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(54) Title: GENES FOR MODIFYING PLANT TRAITS IV

(57) Abstract: The invention relates to plant transcription factor polypeptides, polynucleotides that encode them, homologs from a variety of plant species, and methods of using the polynucleotides and polypeptides to produce transgenic plants having advantageous properties compared to a reference plant. Sequence information related to these polynucleotides and polypeptides can also be used in bioinformatic search methods and is also disclosed.

GENES FOR MODIFYING PLANT TRAITS IV

This application claims priority benefit of: prior U.S application entitled "Plant Trait Modification III," serial no. 60/227,439, filed August 22, 2000; prior U.S. application entitled

5   "Genes for Modifying Plant Traits," attorney docket number MBI-0022, serial no. _____, filed November 16, 2000; and prior U.S. application entitled "Genes for Modifying Plant Traits II," serial no. 09/837,944, filed April 18, 2001. The entire content of each of these applications is hereby incorporated by reference.

10   **Field of the Invention and Introduction**

This invention relates to the field of plant biology. More particularly, the present invention pertains to compositions and methods for phenotypically modifying a plant.

A plant's traits, such as its biochemical, developmental, or phenotypic characteristics, can be

15   controlled through a number of cellular processes. One important way to manipulate that control is through transcription factors - proteins that influence the expression of a particular gene or sets of genes. Transgenic plants that comprise cells having altered levels of at least one selected transcription factor, for example, possess advantageous or desirable traits. Strategies for manipulating traits by altering a plant cell's transcription factor content can therefore result in

20   plants and crops with commercially valuable properties. Applicants have identified polynulceotides encoding transcription factors, developed numerous transgenic plants using these polynucleotides, and have analyzed the plants for a variety of important traits. In so doing, applicants have identified important polynucleotide and polypeptide sequences for producing commercially valuable plants and crops as well as the methods for making them and using them.

25   Other aspects and embodiments of the invention are described below and can be derived from the teachings of this disclosure as a whole.

Background of the Invention

Transcription factors can modulate gene expression, either increasing or decreasing (inducing or

30   repressing) the rate of transcription. This modulation results in differential levels of gene expression at various developmental stages, in different tissues and cell types, and in response to different exogenous (e.g., environmental) and endogenous stimuli throughout the life cycle of the organism.

35   Because transcription factors are key controlling elements of biological pathways, altering the expression levels of one or more transcription factors can change entire biological pathways in an

organism. For example, manipulation of the levels of selected transcription factors may result in increased expression of economically useful proteins or metabolic chemicals in plants or to improve other agriculturally relevant characteristics. Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of unwanted compounds or remove an
5   undesirable trait. Therefore, manipulating transcription factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a plant's traits.

The present invention provides novel transcription factors useful for modifying a plant's phenotype in desirable ways.
10

Summary of the Invention

In a first aspect, the invention relates to a recombinant polynucleotide comprising a nucleotide sequence selected from: (a) a nucleotide sequence of the Sequence Listing, or SEQ ID Nos.: 2N-1 where N=1-232, preferably where N=1-232, or a nucleotide sequence encoding a polypeptide
15   comprising an amino acid sequence selected from those of the Sequence Listing, or SEQ ID Nos: 2N where N=1-232, or a complementary nucleotide sequence of any of these; (b) a nucleotide sequence encoding a polypeptide comprising a variant of a polypeptide of (a) or a variant having one or more, or between 1 and about 5, or between 1 and about 10, or between 1 and about 30, conservative amino acid substitutions; (c) a nucleotide sequence comprising a sequence selected
20   from SEQ ID Nos.: 2N-1 where N=1-232, or a complementary nucleotide sequence thereof; (d) a nucleotide sequence comprising one or more silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence that hybridizes under stringent conditions, high stringent conditions, ultra-high stringent conditions, or ultra-ultra-high stringent conditions over substantially the entire length of a nucleotide sequence of one or more of (a), (b), (c), or (d); (f) a nucleotide
25   sequence comprising at least 10 or 15, or at least about 20, or at least about 30 consecutive nucleotides of a sequence of any of (a)-(e), or at least 10 or 15, or at least about 20, or at least about 30 consecutive nucleotides outside of a region encoding a conserved domain of any of (a)-(e); (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a
30   plant's characteristic, functions as a transcription factor, results in ectopic expression or altered expression in a transgenic plant, or alters the level of transcription of a gene or transgene in a cell; (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60%, or at least 70 %, or at least 80 %, or at least 90 %, or at least 95 % sequence identity to a nucleotide sequence of any of (a)-(g) or a 10
35   or 15 nucleotide, or at least about 20, or at least about 30 nucleotide region of a sequence of (a)-

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(g) that is outside of a region encoding a conserved domain; (j) a nucleotide sequence that encodes a polypeptide having at least 31% sequence identity to a polypeptide listed in the Sequence Listing, or SEQ ID No.: 2N-1 where N=1-232; (k) a nucleotide sequence that encodes a polypeptide having at least 60%, or at least 70 %, or at least 80%, or at least 90 %, or at least 95

5   % sequence identity to a polypeptide listed in the Sequence Listing, or SEQ ID No.: 2N-1 where N=1-232; and (l) a nucleotide sequence that encodes a conserved domain of a polypeptide having at least 85%, or at least 90%, or at least 95%, or at least 98% sequence identity to a conserved domain of a polypeptide listed in the Sequence Listing, or SEQ ID No.: 2N-1 where N=1-232. A recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-specific

10   promoter operably linked to a nucleotide sequence listed above. The invention also relates to compositions comprising at least two of the above-described polynucleotides.

In a second aspect, the invention comprises an isolated or recombinant polypeptide having an amino acid sequence of the Sequence Listing, or SEQ ID Nos.: 2N-1 where N=1-232, or a

15   polypeptide comprising a subsequence of at least about 10, or at least about 15, or at least about 20, or at least about 30 contiguous amino acids encoded by the recombinant or isolated polynucleotide described above, or comprising a subsequence of at least about 8, or at least about 12, or at least about 15, or at least about 20, or at least about 30 contiguous amino acids outside of a conserved domain.

20

In another aspect, the invention is a transgenic plant comprising one or more of the above-described recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above-described polypeptide. Further, the invention is a plant lacking a

25   nucleotide sequence encoding a polypeptide described above or substantially lacking a polypeptide described above. The plant may be any appropriate plant, including, but not limited to, *Arabidopsis,* mustard, soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion,

30   papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, sugarbeet, canola, peanut, rosaceous fruits, vegetable brassicas, and mint or other labiates.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression

35   vector.

In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase, a polymerase and a primer, a cloning vector, or with a cell.

5   Furthermore, the invention relates to a method for producing a plant having a modified trait. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for a modified trait.

10   In another aspect, the invention relates to a method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the

15   polypeptide to a promoter sequence, or by detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity

20   or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in a cell of the plant, the expression level of the polypeptide in a cell of the plant, and the modulation of an activity of the polypeptide in a cell of the plant.

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In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a sequence of the Sequence Listing, SEQ ID Nos.: 1-464, to a polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium

30   may comprise a link between one or more sequence strings to a modified plant trait.

In yet another aspect, the invention is a method for identifying a sequence similar to or homologous to one or more polynucleotides of the invention, or one or more polypeptides encoded by the polynucleotides. The method comprises providing a sequence database, and

35   querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides, such as those of SEQ ID Nos.: 1-464,

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to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences. Such a method may also be a method of identifying a homolog sequence from a database, where the database comprises a plurality of known plant sequences. These sequences can be ESTs, cDNA, or genomic

5   fragments. The database may contain sequences that are not "known" in addition to the known sequences, in that sequences may not be assigned or linked to a function or particular characteristic, yet the sequence itself is known. The method of identifying a homolog comprises inputting sequence information selected from one or more of SEQ ID Nos. 1-464; and querying the database to identify a homolog sequence. In this way, homolog sequences from any number

10   of plant species, cultivars, or strains can be identified from the information of an inputted sequence or a fragment of the sequence. For these methods and for the sequence information, a computer readable medium having stored sequence information of one or more of SEQ ID Nos.: 1-464, or 1-37, or any one particular SEQ ID No., or any group of SEQ ID Nos. in between 1 and 464, can be used. The computer readable medium may include, for example, a floppy disc, a

15   hard drive, random access memory (RAM), read only memory (ROM), and/or CD-ROM.

A method of the invention may comprise linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant phenotype.

20   **Brief Description of the Sequence Listing and the Appendices**

The Sequence Listing provides exemplary polynucleotide (SEQ ID Nos.: 2N-1 where N=1-232) and polypeptide (SEQ ID Nos.: 2N where N=1-232) sequences of the invention. The traits associated with the use of the sequences are included in the Examples or the Appendices.

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The Tables of the Appendices include homologous sequences and homologs of specific polynucleotides and polypeptides, specific information about those sequences, and data concerning exemplary transgenic plants of the invention. The data and sequence information can be prepared according to the methods of the Examples or those known in the art. The Appendices

30   include the Tables of this Appendix and those in the files of the Appendices of the priority documents.

Table 3 in the Appendix is a list of: the first 332 sequences from the Sequence Listing; the corresponding GID number (i.e. G28) used throughout to refer to both the cDNA and protein

35   sequence of a particular transcription factor, and referred to or used in the Appendices of the U.S.

priority documents; and the identification of conserved amino acid domain start and stop sites (conserved domain) within the protein sequence.

Table 4 in the Appendix is a list of: selected sequences from the Sequence Listing; their
5   corresponding GID number; the type of transgenic plant produced to determine ectopic expression, altered expression, or trait (either Knockout of overexpressor as in the Examples); and general descriptions and specific characteristics of the transgenic plant's traits as compared to a wild type, reference, or control plant.

10   Table 5 of the Appendix is a list of: selected sequences from the Sequence Listing; their corresponding GID number; the identification of the one or more homolog sequences and the corresponding GID numbers; the type of sequence of the particular SEQ ID No.; and the identification of conserved amino acid domain start and stop sites (conserved domain) within the protein sequence.
15

Table 6 of the Appendix is a list of selected homologs identified from genomic, EST, or other database, as referred to in the Examples. Table 6 includes: the particular SEQ ID No. in the Sequence Listing used to identify exemplary homologs; the corresponding GID number of the SEQ ID No. sequence; the Genbank NID reference number associated with the exemplary
20   homolog identified (from which one of skill in the art can produce a genomic, cDNA, and/or EST sequence and corresponding polynucleotide); the P-value related to the particular, exemplary homolog comparison to the GID sequence; the percent identity between the GID sequence and the homolog; and the species the exemplary homolog sequence is derived from. All of the sequences referred to in the Table, as well as fragments or parts of these sequences,
25   can be used in accordance with this invention, for example to produce transgenic plants with ectopic expression or altered expression.

Detailed Description of Exemplary Embodiments

In an important aspect, the present invention relates to polynucleotides and polypeptides, e.g. for
30   modifying phenotypes of plants. Throughout this disclosure, various information sources are referred to and/or are specifically incorporated. The information sources include scientific journal articles, patent documents, textbooks, and web pages, for example. While the reference to these information sources clearly indicates that they can be used by one of skill in the art, applicants specifically incorporate each and every one of the information sources cited herein, in
35   their entirety, whether or not a specific mention of "incorporation by reference" is noted. The

contents and teachings of each and every one of the information sources can be relied on and
used to make and use embodiments of the invention.

The polynucleotides of the invention encode plant transcription factors or fragments of them.
5   As one of ordinary skill in the art recognizes, transcription factors can be identified by the
presence of a region or domain of structural similarity or identity to a specific consensus
sequence or the presence of a specific consensus DNA-binding site (see, for example, Riechmann
et al., Science 290: 2105-2110 (2000)). The plant transcription factors may belong to one of the
following transcription factor families: the AP2 (APETALA2) domain transcription factor family
10   (Riechmann and Meyerowitz (1998) Biol. Chem. 379:633-646); the MYB transcription factor
family (Martin and Paz-Ares, (1997) Trends Genet. 13:67-73); the MADS domain transcription
factor family (Riechmann and Meyerowitz (1997) Biol. Chem. 378:1079-1101); the WRKY
protein family (Ishiguro and Nakamura (1994) Mol. Gen. Genet. 244:563-571); the ankyrin-
repeat protein family (Zhang et al. (1992) Plant Cell 4:1575-1588); the zinc finger protein (Z)
15   family (Klug and Schwabe (1995) FASEB J. 9: 597-604); the homeobox (HB) protein family
(Duboule (1994) Guidebook to the Homeobox Genes, Oxford University Press); the CAAT-
element binding proteins (Forsburg and Guarente (1989) Genes Dev. 3:1166-1178); the
squamosa promoter binding proteins (SPB) (Klein et al. (1996) Mol. Gen. Genet. 250:7-16); the
NAM protein family (Souer et al. (1996) Cell 85:159-170); the IAA/AUX proteins (Rouse et al.
20   (1998) Science 279:1371–1373); the HLH/MYC protein family (Littlewood et al. (1994) Prot.
Profile 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) EMBO J.
13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) FASEB J. 8:192-
200); the Box P-binding protein (the BPF-1) family (da Costa e Silva et al. (1993) Plant J.
4:125-135); the high mobility group (HMG) family (Bustin and Reeves (1996) Prog. Nucl.
25   Acids Res. Mol. Biol. 54:35-100); the scarecrow (SCR) family (Di Laurenzio et al. (1996) Cell
86:423-433); the GF14 family (Wu et al. (1997) Plant Physiol. 114:1421-1431); the polycomb
(PCOMB) family (Kennison (1995) Annu. Rev. Genet. 29:289-303); the teosinte branched (TEO)
family (Luo et al. (1996) Nature 383:794-799; the ABI3 family (Giraudat et al. (1992) Plant Cell
4:1251-1261); the triple helix (TH) family (Dehesh et al. (1990) Science 250:1397-1399); the
30   EIL family (Chao et al. (1997) Cell 89:1133-44); the AT-HOOK family (Reeves and Nissen
(1990) Journal of Biological Chemistry 265:8573-8582); the S1FA family (Zhou et al. (1995)
Nucleic Acids Res. 23:1165-1169); the bZIPT2 family (Lu and Ferl (1995) Plant Physiol.
109:723); the YABBY family (Bowman et al. (1999) Development 126:2387-96); the PAZ
family (Bohmert et al. (1998) EMBO J. 17:170-80); a family of miscellaneous (MISC)
35   transcription factors including the DPBF family (Kim et al. (1997) Plant J. 11:1237-1251) and
the SPF1 family (Ishiguro and Nakamura (1994) Mol. Gen. Genet. 244:563-571); the golden

(GLD) family (Hall et al. (1998) *Plant Cell* 10:925-936), the TUBBY family (Boggin et al,
(1999) *Science* 286:2119-2125), the heat shock family (Wu C (1995) *Annu Rev Cell Dev Biol*
11:441-469), the ENBP family (Christiansen et al (1996) *Plant Mol Biol* 32:809-821), the RING-
zinc family (Jensen et al. (1998*) FEBS letters* 436:283-287), the PDBP family (Janik et al

5   *Virology.* (1989) 168:320-329), the PCF family (Cubas P, et al. *Plant J.* (1999) 18:215-22), the
SRS (SHI-related) family (Fridborg et al *Plant Cell* (1999) 11:1019-1032), the CPP (cysteine-
rich polycomb-like) family (Cvitanich et al *Proc. Natl. Acad. Sci.* U S A. (2000) 97:8163-8168),
the ARF (auxin response factor) family (Ulmasov, et al. (1999) *Proc. Natl. Acad. Sci.* USA 96:
5844-5849), the SWI/SNF family (Collingwood et al *J. Mol. End.* 23:255-275), the ACBF

10   family (Seguin et al *Plant Mol Biol.* (1997) 35:281-291), PCGL (CG-1 like) family (*Plant Mol
Biol.* (1994) 25:921-924) the ARID family (Vazquez et al *Development.* (1999) 126: 733-42), the
Jumonji family, Balciunas et al (*Trends Biochem Sci.* (2000) 25: 274-276), the bZIP-NIN family
(Schauser et al *Nature.* (1999) 402: 191-195), the E2F family Kaelin et al (1992) *Cell* 70: 351-
364) and the GRF-like family (Knaap et al (2000) *Plant Physiol.* 122: 695-704. As indicated by

15   any part of the list above and as known in the art, transcription factors have been sometimes
categorized by class, family, and sub-family according to their structural content and consensus
DNA-binding site, for example. All of the classes and many of the families and sub-families are
listed here. However, the inclusion of one sub-family and not another, or the inclusion of one
family and not another, does not mean that the invention does not encompass polynucleotides or

20   polypeptides of a certain family or sub-family. The list provided here is merely an example of
the types of transcription factors and the knowledge available concerning the consensus
sequences and DNA-binding site motifs that help define them (each of the references noted
above are specifically incorporated herein by reference).

25   In addition to methods for modifying a plant phenotype by employing one or more
polynucleotides and polypeptides of the invention described herein, the polynucleotides and
polypeptides of the invention have a variety of additional uses. These uses include their use in
the recombinant production (i.e, expression) of proteins; as regulators of plant gene expression;
as diagnostic probes for the presence of complementary or partially complementary nucleic acids

30   (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g.,
mutation reactions, PCR reactions, or the like; as substrates for cloning e.g., including digestion
or ligation reactions; and/or for identifying exogenous or endogenous modulators of the
transcription factors.

35   A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotide
residues, e.g., at least about 15 consecutive polymerized nucleotide residues, optionally at least

about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a
polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain
or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an
enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions,
5   a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or
double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a
modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such
as an mRNA), a cDNA, a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like.
The polynucleotide can comprise a sequence in either sense or antisense orientations.
10

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the
polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a
context other than that in which it is naturally found, e.g., separated from nucleotide sequences
with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide
15   sequences with which it typically is not in proximity. For example, the sequence at issue can be
cloned into a vector, or otherwise recombined with one or more additional nucleic acid. A
recombinant polynucleotide of the invention can be a cDNA or cDNA-derived polynucleotide
that contains the entire coding region of a protein but does not contain the introns of genomic
DNA. A recombinant polynucleotide of the invention can also be, or be derived from, a
20   fragment of an isolated genomic DNA that is a full length coding region in that it contains the
start of translation of a particular protein through the termination of translation of that same
protein, where the start and termination sites are known.

An "isolated polynucleotide" is a polynucleotide or nucleic acid molecule, whether naturally
25   occurring or recombinant, that is present outside the cell in which it is typically found in nature,
whether purified or not. Optionally, an isolated polynucleotide is subject to one or more
enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or
the like.

30   A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant
polynucleotide. An "isolated polypeptide," whether a naturally occurring or a recombinant
polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a
wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than
about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%,
35   120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment
is not the result of a natural response of a wild type plant. Alternatively, or additionally, the

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isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

5   The term "transgenic plant" refers to a plant that contains genetic material not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation, but any method can be used as one of skill in the art

10   recognizes.

    A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the

15   expression of the polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cell or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

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    The phrase "ectopic expression or altered expression," or the terms "ectopic expression" or "altered expression" in reference to a polynucleotide or polypeptide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. For example, the polynucleotide or

25   polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression

30   patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the phrase "ectopic expression or altered expression," or the terms "ectopic expression" or altered expression" may further relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous

35   modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

The term "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain is a subsequence of the polypeptide that performs at least one biological function of the intact polypeptide in substantially the same

5   manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding site or domain that binds to a DNA promoter region, an activation domain, or a domain for protein-protein interaction. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and

10   more preferably at least about 60 amino acids in length. In reference to a nucleotide sequence, "a fragment" refers to any subsequence of a polynucleotide, typically of at least about 15 consecutive nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50, of any of the sequences provided herein. A fragment or domain can be referred to as outside a consensus sequence or outside a consensus DNA-binding site that is known to exist or that

15   exists for a particular transcription factor class, family, or sub-family. In this case, the fragment or domain will not include the exact amino acids of a consensus sequence or consensus DNA-binding site of a transcription factor class, family or sub-family, or the exact amino acids of a particular transcription factor consensus sequence or consensus DNA-binding site. Furthermore, a particular fragment, region, or domain of a polypeptide, or a polynucleotide encoding a

20   polypeptide, can be "outside a conserved domain" if all the amino acids of the fragment, region, or domain fall outside of a defined conserved domain(s) for a polypeptide or protein. The conserved domains for polypeptides of the Sequence Listing are listed in the Tables of the Appendices. Also, many of the polypeptides of the Appendices have conserved domains specifically indicated by start and stop sites. A comparison of the regions of the polypeptides in

25   the Sequence Listing, or of those in the Appendices, allows one of skill in the art to identify conserved domain(s) for any of the polypeptides listed or referred to in this disclosure, including those in the Appendices and homologs from other species, strains, or cultivars.

The term "trait" refers to a physiological, morphological, biochemical or physical characteristic

30   of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by biochemical techniques, such as detecting the protein, starch or oil content of seed or leaves, or by the observation of the expression level of a gene or genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays or reporter gene expression systems, or by agricultural observations such

35   as stress tolerance, yield or pathogen tolerance. Any technique can be used to measure the

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amount of, comparative level of, or difference in any selected chemical compound or macromolecule in the transgenic plants, however.

"Trait modification" refers to a detectable difference in a characteristic in a plant ectopically
5   expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least
10   about a 70%, or at least about a 100%, or an even greater difference. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.

15   Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like; decreased
20   herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins,
25   cellulose, tannins, prenyllipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds
30   during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture
35   characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

Polnucleotides and Polypeptides of the Invention

The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides and homologue polypeptide-encoding

5   polynucleotides (homologs), and isolated or recombinant polynucleotides encoding the polypeptides, or novel variant polypeptides or polynucleotides encoding novel variants of transcription factors derived from the specific sequences provided here. These polypeptides and polynucleotides may be employed to modify one or more of a plant's characteristics or traits.

10   Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as

15   transcription factors.

Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length

20   coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5' and 3' ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5' and 3' ends. Exemplary sequences are provided in

25   the Sequence Listing.

The polynucleotides of the invention can be or were ectopically expressed in overexpressor or knockout plants and the changes in the characteristic(s) or trait(s) of the plants observed. Therefore, the polynucleotides and polypeptides can be employed to improve the characteristics

30   of plants.

Producing Polypeptides

The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as

35   unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides

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can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription

5   factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription

10   factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in

15   Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed., and 3rd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, ("Sambrook"); Current Protocols in Molecular Biology, F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2001) ("Ausubel"); and

20   Current Protocols in Cell Biology, Bonifacino, J.S. et al. (eds.) 2001 John Wiley & Sons, Inc.

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro

25   amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger, Sambrook, and Ausubel, as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis).

30   Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR

35   expansion and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel, Sambrook and Berger, all supra.

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically

5   ligated to produce a desired sequence, e.g., a polynucletotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-69; and Matthes et al. (1984) EMBO J. 3:801-5. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable

10   vectors. And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

Homologous Sequences

Sequences homologous, i.e., that share significant sequence identity or similarity, to those

15   provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as

20   banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype

25   can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such pine, poplar and eucalyptus, or mint or other labiates.

30

Transcription factors that are homologous to the listed sequences will typically share at least about 30% amino acid sequence identity, or at least about 30% amino acid sequence identity outside of a known consensus sequence or consensus DNA-binding site. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75%

35   or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences, or with the listed sequences but excluding or outside a known consensus sequence or

15

consensus DNA-binding site, or with the listed sequences excluding or outside one or all conserved domain. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences, or to the listed sequences but excluding or outside a known consensus sequence or consensus DNA-

5   binding site or outside one or all conserved domain. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences, or to a listed sequence but excluding or outside a known consensus sequence or consensus DNA-

10   binding site, or outside one or all conserved domain. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity, and more preferably at

15   least 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 90%, or at least about 95%, or at least about 98% sequence identity. Transcription factors that are homologous to the listed sequences should share at least 30%, or at least about 60%, or at least about 75%, or at least about 80%, or at least about 90%, or at least about 95% amino acid sequence identity over the entire length of the polypeptide or the homolog.

20

Identifying Polynucleotides or Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of

25   well characterized physico-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in

30   both the hybridization and wash solutions and incubations (and number), as described in more detail in the references cited above.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern

35   blot is about 5°C to 20°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH)

at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid
molecules that hybridize under stringent conditions will typically hybridize to a probe based on
either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under
wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C. For example, high stringency

5   is about 0.2 x SSC, 0.1% SDS at 65° C. Ultra-high stringency will be the same conditions except
the wash temperature is raised about 3 or about 5° C, and ultra-ultra-high stringency will be the
same conditions except the wash temperature is raised about 6 or about 9°C. For identification
of less closely related homologs, washes can be performed at a lower temperature, e.g., 50° C.
In general, stringency is increased by raising the wash temperature and/or decreasing the

10   concentration of SSC, as known in the art.

As another example, stringent conditions can be selected such that an oligonucleotide that is
perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide
with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the

15   perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known
as of the filing date of the application. Conditions can be selected such that a higher signal to
noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or
more. Accordingly, the subject nucleic acid hybridizes to the unique coding oligonucleotide with
at least a 2x higher signal to noise ratio as compared to hybridization of the coding

20   oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise
ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will
depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a
radioactive label, or the like.

25   Alternatively, transcription factor homolog polypeptides can be obtained by screening an
expression library using antibodies specific for one or more transcription factors. With the
provision herein of the disclosed transcription factor, and transcription factor homolog nucleic
acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous
expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific

30   for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides
derived from transcription factor, or transcription factor homologue, amino acid sequences.
Methods of raising antibodies are well known in the art and are described in Harlow and Lane
(1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such
antibodies can then be used to screen an expression library produced from the plant from which it

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is desired to clone additional transcription factor homologues, using the methods described
above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

Sequence Variations

5   It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide
sequences is capable of encoding the transcription factors and transcription factor homologue
polypeptides of the invention. Due to the degeneracy of the genetic code, many different
polynucleotides can encode identical and/or substantially similar polypeptides in addition to
those sequences illustrated in the Sequence Listing.

10

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT
all encode the same amino acid - serine. Accordingly, at each position in the sequence where
there is a codon for serine, any of the above trinucleotide sequences can be used without altering
the encoded polypeptide.

15   **Table 1**

Amino acid			Possible Codons					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	TGC	TGT				
Aspartic acid	Asp	D	GAC	GAT				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	TTC	TTT				
Glycine	Gly	G	GGA	GGC	GGG	GGT		
Histidine	His	H	CAC	CAT				
Isoleucine	Ile	I	ATA	ATC	ATT			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT
Methionine	Met	M	ATG					
Asparagine	Asn	N	AAC	AAT				
Proline	Pro	P	CCA	CCC	CCG	CCT		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT

Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT
Threonine	Thr	T	ACA	ACC	ACG	ACT		
Valine	Val	V	GTA	GTC	GTG	GTT		
Tryptophan	Trp	W	TGG					
Tyrosine	Tyr	Y	TAC	TAT				

Sequence alterations that do not change the amino acid sequence encoded by the
polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG,
5   encoding methionine and tryptophan, respectively, any of the possible codons for the same amino
acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the
art. Accordingly, any and all such variations of a sequence selected from the above table are a
feature of the invention.

10   In addition to silent variations, other conservative variations that alter one, or a few amino acids
in the encoded polypeptide, can be made without altering the function of the polypeptide. These
conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in
15   the Sequence Listing are also envisioned by the invention. Such sequence modifications can be
engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol.
217, Academic Press) or the other methods noted below. Amino acid substitutions are typically
of single residues; insertions usually will be on the order of about from 1 to 10 amino acid
residues; and deletions will range about from 1 to 30 residues. In preferred embodiments,
20   deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of
two residues. Substitutions, deletions, insertions or any combination thereof can be combined to
arrive at a sequence. The mutations that are made in the polynucleotide encoding the
transcription factor should not place the sequence out of reading frame and should not create
complementary regions that could produce secondary mRNA structure. Preferably, the
25   polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has
been removed and a different residue inserted in its place. Such substitutions generally are made
in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2
30   shows amino acids which can be substituted for an amino acid in a protein and which are
typically regarded as conservative substitutions.

Table 2

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser;Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

5

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The

10   substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side

chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

5   **Further Modifying Sequences of the Invention – Mutation/Forced Evolution**

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to

10   change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution

15   methods are described, e.g., by Stemmer (1994) Nature 370:389-391, and Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751, and U.S. Patents 5,811,238; 5,811,654; 6,251,604; and 6,177,263. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

20   Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These

25   modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the

30   products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant

35   RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be

modified to reflect host preference. For example, preferred stop codons for *S. cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

5   The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to

10 change codon preference, to introduce splice sites, etc.

Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA binding domain derived

15 from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from

20 bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

Expression and Modification of Polypeptides
Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or

25 RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

30

The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been

35 inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably

linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

General texts that describe molecular biological techniques useful herein, including the use and
5   production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic
10   Press, and Gelvin et al., (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642, for dicotyledonous plants.

15   Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature
20   embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for Agrobacterium-mediated DNA transfer (Ishida et al. (1996) Nature Biotech 14: 745-750).

25   Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start
30   site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-
35   level expression in most plant tissues (*see*, e.g., Odel et al. (1985) Nature 313:810); the nopaline

synthase promoter (An et al. (1988) Plant Physiol 88:547); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977).

5   A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known promoters have
10   been characterized and can favorable be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the
15   tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al, (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol Biol
20   26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et al. (1998)
25   38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wunl*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-
30   396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

35

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region

5   of potato or the octopine or nopaline synthase 3' terminator regions.

Specific initiation signals can aid in efficient translation of coding sequences. These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression

10   vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural

15   and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

The present invention also relates to host cells which are transduced with vectors of the

20   invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e, nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acid, *etc.* The

25   engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook and Ausubel.

30

The host cell can be an eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al., (1985)

35   Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York)

pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA

5   plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

       The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the

10   cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants, which include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

15   For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the

20   vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

25   **Modified Amino Acids**

       Polypeptides of the invention may contain one or more modified amino acids. The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid(s) are modified, for example, co-translationally or post-translationally during

30   recombinant production or modified by synthetic or chemical means.

       Non-limiting examples of a modified amino acid include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated

35   amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References adequate to guide one of skill in the modification of amino acids are replete throughout the literature.

26

Identification of Additional Factors

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phentoype or trait of interest. On the one
5   hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene with which is
10   subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homolog of the invention is expressed in a host cell, e.g, a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of
15   protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the
20   promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) Nature
25   Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method
30   suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al.,
35   (1991), Proc. Natl. Acad. Sci. USA 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins:

one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are

5   transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library

10 plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be performed.

15 **Identification of Modulators**

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a

20 plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northerns, quantitative PCR, or any other technique for monitoring changes in

25 mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998, and supplements through 2001). Such changes in the expression levels can be correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

30

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-

35 based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator

composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

5   In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

10

A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the

15   number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines,

20   Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

Preparation and screening of combinatorial or other libraries is well known to those of skill in

25   the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, Int. J. Pept. Prot. Res. 37:487-493 (1991) and Houghton et al. Nature 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used.

30   In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for

35   high-throughput screening of potential modulators. The nature and implementation of

modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

5   Indeed, entire high throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

10

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of
15   relevant nucleic acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is,
20   known transcriptional activators or inhibitors can be incubated with cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators that inhibit transcriptional activation or transcriptional
25   repression. Either expression of the nucleic acids and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test
30   compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In
35   some cases, an alteration in a plant phenotype can be detected following contact of a plant (or

30

plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention.

Subsequences

5   Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra- high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like,

10   according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18

15   nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologs of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended

20   along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a

25   subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

30

Production of Transgenic Plants
Modification of Traits
The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve

35   the seed characteristics of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or

transcription factor homologues) of the invention, as compared with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative example of trait modification, improved characteristics, by altering expression levels of a particular transcription factor is described further in the Examples.

5

Antisense and Cosuppression Approaches

In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention,

10   e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University, Oxford, England. In general, sense or anti-

15   sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription

20   factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or

25   gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably, the

30   introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the

35   endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a
ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity.
The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent
No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer

5   RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that
hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense
inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription factor homologue

10   cDNA is over-expressed can also be used to obtain co-suppression of a corresponding
endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such
co-suppression (also termed sense suppression) does not require that the entire transcription factor
cDNA be introduced into the plant cells, nor does it require that the introduced sequence be
exactly identical to the endogenous transcription factor gene of interest. However, as with

15   antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization
is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity
between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences

20   comprising one or more stop codon, or nonsense mutation) can also be used to suppress
expression of an endogenous transcription factor, thereby reducing or eliminating it's activity and
modifying one or more traits. Methods for producing such constructs are described in U.S.
Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop
codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene

25   silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-
DNA of Agrobacterium tumefaciens. After generating the insertion mutants, the mutants can be
screened to identify those containing the insertion in a transcription factor or transcription factor

30   homologue gene. Plants containing a single transgene insertion event at the desired gene can be
crossed to generate homozygous plants for the mutation (Koncz et al. (1992) Methods in
Arabidopsis Research, World Scientific).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a

35   transcription factor or transcription factor homologue, e.g., by homologous recombination
(Kempin et al. (1997) Nature 389:802).

A plant trait can also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the

5   intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the

10   endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery

15   in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (See, e.g., PCT Publications WO 96/06166 and WO 98/53057, which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

20   The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the

25   polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue

30   of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledenous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover,

35   etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcurbitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.),

Solanaceae (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture –Crop Species. Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

5

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given

10   plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence into a plant in a manner

15   to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471;

20   5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or

25   herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally,

30   to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

35   **Integrated Systems – Sequence Identity**

35

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link

5   certain functional benefits, such improved characteristics, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madision, WI). Public

10   sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of

15   Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence

20   similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

A variety of methods for determining sequence relationships can be used, including manual

25   alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of skill.

30   One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length

35   W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the

neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters

5   M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring

10   residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62

15   scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915). Unless otherwise indicated, "sequence identity" here refers to the % sequence identity generated from a tblastx using the NCBI version of the algorithm at the default settings using gapped alignments with the filter "off" (http://www.ncbi.nlm.nih.gov/).

20   In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see*, e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For

25   example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using

30   progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character

35   strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity.

The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element, which displays an alignment produced by the alignment instruction set.

5   The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may be implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in

10   certain preferred embodiments, the computers may be components of an intranet or an internet.

Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant

15   phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database.

20   This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a

25   remote terminal or computer across an internet or intranet.

Examples
The following examples are intended to illustrate, but not limit, the scope of the present invention.

30

Example I: Full Length Gene Identification and Cloning
Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of –4 or –5 or lower,

35   depending on the length of the query sequence. Putative transcription factor sequence hits were

then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

5   Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60°C) and labeled with ^{32}P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO$_4$ pH 7.0, 7% SDS, 1 % w/v

10   bovine serum albumin) and hybridized overnight at 60°C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSCC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA

15   amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

20   Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5'

25   and 3' ends of the gene by end-to-end PCR.

Example II: Construction of Expression Vectors

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20

30   or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-58) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide

35   staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were

ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

5

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

Example III: Transformation of *Agrobacterium* with the Expression Vector

10   After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached.

15   Cells were harvested by centrifugation at 4,000 x g for 15 min at 4°C. Cells were then resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl

20   aliquots, quickly frozen in liquid nitrogen, and stored at -80°C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of

25   *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28°C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100

30   µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28°C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

Example IV: Transformation of *Arabidopsis* Plants with *Agrobacterium tumefaciens* with

35   **Expression Vector**

40

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0

5   is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 µM benzylamino purine (Sigma), 200 µl/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

10   Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 µE/m²/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After

15   flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat

20   surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

25   **Example V: Identification of *Arabidopsis* Primary Transformants**

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H_2O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second

30   wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H_2O. The

35   seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH),

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1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin).
Seeds were germinated under continuous illumination (50-75 $\mu E/m^2/sec$) at 22-23° C. After 7-10
days of growth under these conditions, kanamycin resistant primary transformants (T_1
generation) were visible and obtained. These seedlings were transferred first to fresh selection
5   plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX
potting medium).

Primary transformants were crossed and progeny seeds (T_2) collected; kanamycin resistant
seedlings were selected and analyzed.   The expression levels of the recombinant
10   polynucleotides in the transformants varies from about a 5% expression level increase to a least a
100% expression level increase.   Similar observations are made with respect to polypeptide level
expression.

Example VI: Identification of *Arabidopsis* Plants with Transcription Factor Gene
15   **Knockouts**
The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known
target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly,
gene-specific primers, nested by 5-250 base pairs to each other, were designed from the 5' and 3'
regions of a known target gene. Similarly, nested sets of primers were also created specific to
20   each of the T-DNA or transposon ends (the "right" and "left" borders). All possible
combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an
insertion event within or close to the target gene. The amplified DNA fragments were then
sequenced which allows the precise determination of the T-DNA/transposon insertion point
relative to the target gene. Insertion events within the coding or intervening sequence of the
25   genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique
mutant plant for functional characterization. The method is described in more detail in Yu and
Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

Example VII: Identification of Modified Phenotypes in Overexpression or Gene Knockout
30   **Plants**
Experiments were performed to identify those transformants or knockouts that exhibited
modified biochemical characteristics. Among the biochemicals that were assayed were
insoluble sugars, such as arabinose, fucose, galactose, mannose, rhamnose or xylose or the like;
prenyl lipids, such as lutein, beta-carotene, xanthophyll-1, xanthophyll-2, chlorophylls A or B, or
35   alpha-, delta- or gamma-tocopherol or the like; fatty acids, such as 16:0 (palmitic acid), 16:1
(palmitoleic acid), 18:0 (stearic acid), 18:1 (oleic acid), 18:2 (linoleic acid), 20:0 , 18:3 (linolenic

acid), 20:1 (eicosenoic acid), 20:2, 22:1 (erucic acid) or the like; waxes, such as by altering the levels of C29, C31, or C33 alkanes; sterols, such as brassicasterol, campesterol, stigmasterol, sitosterol or stigmastanol or the like, glucosinolates, protein or oil levels.

5   Fatty acids were measured using two methods depending on whether the tissue was from leaves or seeds. For leaves, lipids were extracted and esterified with hot methanolic H_2SO_4 and partitioned into hexane from methanolic brine. For seed fatty acids, seeds were pulverized and extracted in methanol:heptane:toluene:2,2-dimethoxypropane:H_2SO_4 (39:34:20:5:2) for 90 minutes at 80°C. After cooling to room temperature the upper phase, containing the seed fatty
10   acid esters, was subjected to GC analysis. Fatty acid esters from both seed and leaf tissues were analyzed with a Supelco SP-2330 column.

Glucosinolates were purified from seeds or leaves by first heating the tissue at 95°C for 10 minutes. Preheated ethanol:water (50:50) is and after heating at 95°C for a further 10 minutes,
15   the extraction solvent is applied to a DEAE Sephadex column which had been previously equilibrated with 0.5 M pyridine acetate. Desulfoglucosinolates were eluted with 300 ul water and analyzed by reverse phase HPLC monitoring at 226 nm.

For wax alkanes, samples were extracted using an identical method as fatty acids and extracts
20   were analyzed on a HP 5890 GC coupled with a 5973 MSD. Samples were chromatographed on a J&W DB35 mass spectrometer (J&W Scientific).

To measure prenyl lipids levels, seeds or leaves were pulverized with 1 to 2% pyrogallol as an antioxidant. For seeds, extracted samples were filtered and a portion removed for tocopherol and
25   carotenoid/chlorophyll analysis by HPLC. The remaining material was saponified for sterol determination. For leaves, an aliquot was removed and diluted with methanol and chlorophyll A, chlorophyll B, and total carotenoids measured by spectrophotometry by determining absorbance at 665.2 nm, 652.5 nm, and 470 nm. An aliquot was removed for tocopherol and carotenoid/chlorophyll composition by HPLC using a Waters uBondapak C18 column (4.6 mm x
30   150 mm). The remaining methanolic solution was saponified with 10% KOH at 80°C for one hour. The samples were cooled and diluted with a mixture of methanol and water. A solution of 2% methylene chloride in hexane was mixed in and the samples were centrifuged. The aqueous methanol phase was again re-extracted 2% methylene chloride in hexane and, after centrifugation, the two upper phases were combined and evaporated. 2% methylene chloride in
35   hexane was added to the tubes and the samples were then extracted with one ml of water. The upper phase was removed, dried, and resuspended in 400 ul of 2% methylene chloride in hexane

and analyzed by gas chromatography using a 50 m DB-5ms (0.25 mm ID, 0.25 um phase, J&W Scientific).

Insoluble sugar levels were measured by the method essentially described by Reiter et al., Plant
5   Journal 12:335-345. This method analyzes the neutral sugar composition of cell wall polymers found in *Arabidopsis* leaves. Soluble sugars were separated from sugar polymers by extracting leaves with hot 70% ethanol. The remaining residue containing the insoluble polysaccharides was then acid hydrolyzed with allose added as an internal standard. Sugar monomers generated by the hydrolysis were then reduced to the corresponding alditols by treatment with NaBH4, then
10   were acetylated to generate the volatile alditol acetates which were then analyzed by GC-FID. Identity of the peaks was determined by comparing the retention times of known sugars converted to the corresponding alditol acetates with the retention times of peaks from wild-type plant extracts. Alditol acetates were analyzed on a Supelco SP-2330 capillary column (30 m x 250 um x 0.2 um) using a temperature program beginning at 180° C for 2 minutes followed by an
15   increase to 220° C in 4 minutes. After holding at 220° C for 10 minutes, the oven temperature is increased to 240° C in 2 minutes and held at this temperature for 10 minutes and brought back to room temperature.

To identify plants with alterations in total seed oil or protein content, 150mg of seeds from T2
20   progeny plants were subjected to analysis by Near Infrared Reflectance (NIR) using a Foss NirSystems Model 6500 with a spinning cup transport system.

Experiments were performed to identify those transformants or knockouts that exhibited an improved pathogen tolerance. For such studies, the transformants were exposed to biotropic
25   fungal pathogens, such as *Erisyphe orontii*, and necrotropic fungal pathogens, such as *Fusarium oxysporum*. *Fusarium oxysporum* isolates cause vascular wilts and damping off of various annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko (1994) Molecular Plant-Microbe Interactions 7: 378-383). For *Fusarium oxysporum* experiments, plants grown on petri dishes were sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension was
30   prepared as follows: A plug of fungal hyphae from a plate culture was placed on a fresh potato dextrose agar plate and allowed to spread for one week. 5 ml sterile water was then added to the plate, swirled, and pipetted into 50 ml Armstrong Fusarium medium. Spores were grown overnight in Fusarium medium and then sprayed onto plants using a Preval paint sprayer. Plant tissue was harvested and frozen in liquid nitrogen 48 hours post infection.
35

Erysiphe orontii is a causal agent of powdery mildew. For *Erysiphe orontii* experiments, plants were grown approximately 4 weeks in a greenhouse under 12 hour light (20 C, ~30% relative humidity (rh)). Individual leaves were infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants were transferred to a Percival growth chamber (20 C, 80%

5   rh.). Plant tissue was harvested and frozen in liquid nitrogen 7 days post infection.

Botrytis cinerea is a necrotrophic pathogen. Botrytis cinerea was grown on potato dextrose agar in the light. A spore culture was made by spreading 10 ml of sterile water on the fungus plate, swirling and transferring spores to 10 ml of sterile water. The spore inoculum (approx. 105

10   spores/ml) was used to spray 10 day-old seedlings grown under sterile conditions on MS (-sucrose) media. Symptoms were evaluated every day up to approximately 1 week.

Infection with bacterial pathogens Pseudomonas syringae pv maculicola strain 4326 and pv maculicola strain 4326 was performed by hand inoculation at two doses. Two inoculation doses

15   allows the differentiation between plants with enhanced susceptibility and plants with enhanced resistance to the pathogen. Plants were grown for 3 weeks in the greenhouse, then transferred to the growth chamber for the remainder of their growth. Psm ES4326 was hand inoculated with 1 ml syringe on 3 fully-expanded leaves per plant (4 1/2 wk old), using at least 9 plants per overexpressing line at two inoculation doses, OD=0.005 and OD=0.0005. Disease scoring

20   occured at day 3 post-inoculation with pictures of the plants and leaves taken in parallel.

In some instances, expression patterns of the pathogen-induced genes (such as defense genes) was monitored by microarray experiments. cDNAs were generated by PCR and resuspended at a final concentration of ~ 100 ng/ul in 3X SSC or 150mM Na-phosphate (Eisen and Brown (1999)

25   *Meth. in Enzymol.* 303:179-205). The cDNAs were spotted on microscope glass slides coated with polylysine. The prepared cDNAs were aliquoted into 384 well plates and spotted on the slides using an x-y-z gantry (OmniGrid) purchased from GeneMachines (Menlo Park, CA) outfitted with quill type pins purchased from Telechem International (Sunnyvale, CA). After spotting, the arrays were cured for a minimum of one week at room temperature, rehydrated and

30   blocked following the protocol recommended by Eisen and Brown (1999).

Sample total RNA (10 ug) samples were labeled using fluorescent Cy3 and Cy5 dyes. Labeled samples were resuspended in 4X SSC/0.03% SDS/4 ug salmon sperm DNA/2 ug tRNA/ 50mM Na-pyrophosphate, heated for 95°C for 2.5 minutes, spun down and placed on the array. The

35   array was then covered with a glass coverslip and placed in a sealed chamber. The chamber was then kept in a water bath at 62°C overnight. The arrays were washed as described in Eisen and

Brown (1999) and scanned on a General Scanning 3000 laser scanner. The resulting files are subsequently quantified using Imagene software purchased from BioDiscovery (Los Angeles, CA).

5   Experiments were performed to identify those transformants or knockouts that exhibited an improved environmental stress tolerance. For such studies, the transformants were exposed to a variety of environmental stresses. Plants were exposed to chilling stress (6 hour exposure to 4-8° C), heat stress (6 hour exposure to 32-37° C), high salt stress (6 hour exposure to 200 mM NaCl), drought stress (168 hours after removing water from trays), osmotic stress (6 hour

10   exposure to 3 M mannitol), or nutrient limitation (nitrogen, phosphate, and potassium) (Nitrogen: all components of MS medium remained constant except N was reduced to 20mg/L of $NH_4 NO_3$, or Phosphate: All components of MS medium except $KH_2 PO_4$, which was replaced by K_2SO_4, Potassium: All components of MS medium except removal of KNO_3 and KH_2PO_4, which were replaced by NaH_4PO_4).

15

Experiments were performed to identify those transformants or knockouts that exhibited a modified structure and development characteristics. For such studies, the transformants were observed by eye to identify novel structural or developmental characteristics associated with the ectopic expression of the polynucleotides or polypeptides of the invention.

20

Experiments were performed to identify those transformants or knockouts that exhibited modified sugar-sensing. For such studies, seeds from transformants were germinated on media containing 5% glucose or 9.4% sucrose which normally partially restrict hypocotyl elongation. Plants with altered sugar sensing may have either longer or shorter hypocotyls than normal plants

25   when grown on this media. Additionally, other plant traits may be varied such as root mass.

Flowering time was measured by the number of rosette leaves present when a visible inflorescence of approximately 3 cm is apparent. Rosette and total leaf number on the progeny stem are tightly correlated with the timing of flowering (Koornneef et al (1991) *Mol. Gen. Genet*

30   229:57-66). The vernalization response was measured. For vernalization treatments, seeds were sown to MS agar plates, sealed with micropore tape, and placed in a 4°C cold room with low light levels for 6-8 weeks. The plates were then transferred to the growth rooms alongside plates containing freshly sown non-vernalized controls. Rosette leaves were counted when a visible inflorescence of approximately 3 cm was apparent.

35

Modified phenotypes observed for particular overexpressor or knockout plants are provided in Table 4 of the Appendix and the Appendices of the priority documents. For a particular overexpressor that shows a less beneficial characteristic, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that

5   shows a less beneficial characteristic, it may be more useful to select a plant with an increased expression of the particular transcription factor.

The sequences of the Sequence Listing SEQ ID Nos. 1-464 or those disclosed here can be used to prepare transgenic plants and plants with altered traits. The specific transgenic plants listed

10   below are produced from the sequences of the Sequence Listing, as noted. The Tables of the Appendix and the Appendices of the priority documents provide exemplary polynucleotide (cDNA) and polypeptide (protein) sequences of the invention. The Tables includeSEQ ID Nos., the corresponding reference number (GID), and/or the identification of the start and stop residues of any conserved domain in the polypeptide sequence.

15

The transgenic plants of the invention display an ectopic expression or altered expression of one or more polypeptides encoded by the full length coding regions in the Sequence Listing, the homologs and/or fragments of the Tables of the Appendices, and/or another polypeptide described in this document, when the transgenic plant is compared to a wild type, control, or

20   reference plant. As a result, the transgenic plants possess advantageous traits, as detailed by the limited and exemplary discussion of comparison data below.

Some of the polypeptides encoded by the full length coding regions in the Sequence Listing and the homologs and fragments of them noted in the Tables of the Appendices modulate a plant's

25   defense response and even confer multipathogen resistance. These traits are extremely useful in many commercial crops and plants. For example, plants overexpressing G28 (SEQ ID NO.: 1 and 2) are more tolerant to infection by fungal pathogens, such as Erysiphe orontii, Sclerotinia sclerotiorum, or Botrytis cinerea. Similarly, plants overexpressing G1792 (SEQ ID NO.: 5 and 6) are more tolerant to infection by necrotrophic fungal pathogens, such as Fusarium oxysporum

30   or Botrytis cinerea, and display increased resistance to fungal pathogens and to Erysiphe orontii. Increased tolerance to infection by Fusarium oxysporum is observed in G1047 (SEQ ID NO.: 23 and 24) and G1363 (SEQ ID NO.: 29 and 30) overexpressing plants. Knockout mutants also demonstrate the particular polypeptide's involvement in a defense response. A G1880 (SEQ ID NO.: 435 and 436) knockout mutant is more tolerant to Botrytis cinerea. G1196 (SEQ ID NO.:

35   27 and 28) knockout mutant plants show increased susceptibility to Botrytis cinerea.
Manipulating the content or expression of any of these polypeptides, or fragments or homologs

of them, can therefore improve a plant's defense response, tolerance, or susceptibility to
pathogens and infection.

5 A number of the polypeptides encoded by the full length coding regions in the Sequence Listing,
and homologs and fragments of them noted in the Tables of the Appendices, regulate the
transition from vegetative to reproductive growth. These traits can be useful in crops and plants
where fruit or seed is commercially valuable, for example. Overexpression of G180 (SEQ ID
NO.: 53 and 54), G227 (SEQ ID NO.: 313 and 314), G1841 (SEQ ID NO.: 455 and 456), and
G2347 (SEQ ID NO.: 477 and 478) results in an early flowering phenotype, whereas
10 overexpression of G748 (SEQ ID NO.: 125 and 126) or G2007 (SEQ ID NO.: 457 and 458)
results in late flowering. Other polypeptides and polynucleotides for modulating flowering time
include G590 (SEQ ID NO.: 107 and 108), G1760 (SEQ ID NO.: 31 and 32), G1820 (SEQ ID
NO.: 33 and 34), and G2010 (SEQ ID NO.: 37 and 38).

15 The response to a variety of abiotic or environmental stresses is modified by an additional set of
polypeptides encoded by the full length coding regions of the Sequence Listing and the homologs
and fragments listed in the Tables of the Appendices. These traits can be useful in manipulating
the growth medium or environment for plants, for example. G226 overexpressing plants are
more tolerant to low nitrogen and high salt stress. G2130 (SEQ ID NO.: 417 and 418)
20 overexpressors show improved heat stress tolerance in a germination assay. G867 (SEQ ID NO.:
15 and 16) and G1930 (SEQ ID NO.: 35 and 36) overexpressing plants show increased seedling
vigor in germination assays on both high salt and high sucrose containing media. G912 (SEQ ID
NO.: 19 and 20) is a member of the AP2 family related to the CBF1, CBF2 and CBF3 genes.
Plants overexpressing G912 (SEQ ID NO.: 19 and 20) exhibit increased freezing and drought
25 tolerance. Additional polypeptides and polynucleotides modifying stress responses include G175
(SEQ ID NO.: 9 and 10), G926 (SEQ ID NO,: 459 and 460), and G1820 (SEQ ID NO.: 33 and
34).

Several transcription factors have been identified that can affect metabolic processes. These
30 plants can be used to optimize or improve production of various plants extracts used for
commercial products including, for example, foodstuffs, paper and paper-related products, edible
plants, fruits and vegetables with improved properties, organic compounds, oils and alcohols,
additives and binders for pharmaceutical or cosmetic products, and industrial products. For
instance, plants overexpressing G1750 (SEQ ID NO.: 395 and 396) produce seed with increased
35 seed oil content. Overexpression of G280 (SEQ ID NO.: 461 and 462) results in an increase in
gamma and delta tocopherol in leaves. G663 (SEQ ID NO.: 13 and 14) overexpressors exhibit

48

constitutive anthocyanin production in seeds, leaves and roots. In contrast, seeds of G156 (SEQ
ID NO.: 7 and 8) knockout mutant plants exhibit a colorless phenotype indicative of the
involvement of the gene in the regulation of the anthocyanin pathway.

5   Also of particular interest are polypeptides involved in plant growth and development. The
following polypeptides encoded by the full length coding regions of the Sequence Listing and the
homologs and fragments listed in the Tables of the Appendices are some examples. Transgenic
plants overexpressing G1073 exhibit a substantial increase in size. An increase in size is also
observed in G189 (SEQ ID NO.: 11 and 12) overexpressing plants. Transgenic plants
10   overexpressing G634 (SEQ ID NO.: 3 and 4) exhibit a substantial increase in trichome number.
Null mutations in G374 (SEQ ID NO.: 463 and 464) and in G877 (SEQ ID NO.: 17 and 18)
result in embryo lethality. A G979 (SEQ ID NO.: 153 and 154) knockout mutation results in
delayed seed ripening.

15   G987 (SEQ ID NO.: 21 and 22) knockout mutant plants can only be grown on sucrose-
containing medium. In addition, G987 appears to control an aspect of thylakoid membrane
development and the tocopherol, carotenoid, and/or chlorophyll content of the plant is altered.
Since the compounds represented by these groups are commercially important in a number of
industries, including use as dietary supplements, a transgenic plant's altered tocopherol,
20   carotenoid, and/or chlorophyll content is an advantageous and valuable trait.

**G634 (SEQ ID. Nos 3 and 4), G1841 (SEQ ID. Nos 455 and 456), G979 (SEQ ID. Nos 153
and 154): modified plant development**

25   **G634:** Overexpression of G634 produced an increase in trichome density on later arising rosette
leaves, cauline leaves, inflorescence stems and sepals. Trichomes of 35S::G634 plants also
appeared slightly larger than those of wild type, and stem trichomes were more highly branched.
These effects were not apparent in young seedlings and became most prominent at the later
vegetative and early reproductive phase. The trichome phenotype was apparent in approximately
30   50% of primary transformants and two out of the three T2 lines.

G1841: Overexpression of G1841 markedly reduced the time to flowering. This early flowering
phenotype was consistently observed over multiple plantings for each of the three T2 lines, and
in a majority of primary transformants. Additionally, 35S::G1841 plants appeared slightly pale
35   and had rather flat leaves compared to wild-type controls.

In continuous light conditions, 35S::G1841 plants produced flower buds up to five days earlier than wild-type controls. In repeat sowings the plants appeared to grow slightly faster than controls; although they switched to making flower buds several days early, they had a similar number of primary rosette leaves to wild type.

5

In addition to showing accelerated flowering under 24 hours light, plants from all three T2 populations produced flowers up to 2 weeks earlier than controls under a 12 hour photoperiod.

G979: Seeds homozygous for a T-DNA insertion within G979 showed delayed ripening, slow
10 germination, and developed into small, poorly fertile plants, indicating that G979 might be involved in seed development processes.

Siliques of heterozygous plants were examined for seed abnormalities. Approximately 25% of the seeds contained in young green siliques were pale in coloration. In older, brown siliques,
15 approximately 25% of the seeds were green and appeared slow ripening, whereas the remaining seeds were brown. Thus, it seemed likely that the seeds with altered development were homozygous for the T-DNA insertion, whereas the normal seeds were wild type and heterozygous segregants.

20 Furthermore, it was observed that approximately 25% of the seed from G979 KO heterozygous plants showed impaired (delayed) germination. Upon germination, these seeds produced extremely tiny seedlings that often did not survive transplantation. A few homozygous plants, small and sickly looking, could be grown, and produced siliques that contained seeds that were small and wrinkled compared to wild type.

25

On the basis of these results obtained with G979 knockout mutant lines, G979 can be used to alter or modify seed germination properties and performance.

G1792 (SEQ ID. Nos 5 and 6), G2130 (SEQ ID. Nos 417 and 418), G926 (SEQ ID. Nos.
30 **459 and 460): modified stress response**

G1792: 35S::G1792 plants were more tolerant to the fungal pathogens *Fusarium oxysporum* and *Botrytis cinerea*: they showed fewer symptoms after inoculation with a low dose of each pathogen. This result was confirmed using individual T2 lines.

35

35S::G1792 plants also showed more tolerance to growth under nitrogen-limiting conditions. In a root growth assay under conditions of limiting N, 35S::G1792 lines were slightly less stunted. In a germination assay that monitors the effect of C on N signaling through anthocyanin production on high sucrose plus and minus, the 35S::G1792 lines make less anthocyanin on high

5   sucrose plus glutamine, suggesting that the gene could be involved in the plants ability to monitor their carbon and nitrogen status.

G1792 overexpressing plants also showed several mild morphological alterations such as abnormal phyllotaxy, alterations in leaf and flower development, and flowering time.

10

G2130: G2130 overexpressing lines show more seedling vigor in a heat stress tolerance germination assay compared to wild-type controls. No difference from wild-type was detected in the heat stress response assay performed on older seedlings suggesting the phenotype could be specific for germination in the G2130 overexpressors. Lines G2130-3 and G2130-4 show the

15   heat tolerant phenotype, line G2130-2 show the weakest phenotype. G2130 overexpressing lines are also somewhat more sensitive to chilling, the plants are more chlorotic and stunted when grown at 8oC compared to the wild-type controls. They also show more disease symptoms following inoculation with a low dose of the fungal pathogen *Botrytis cinerea* in two separate experiments.

20

G926: G926 knockout mutant plants show more tolerance to osmotic stress in a germination assay in three separate experiments. They show more seedling vigor than wild-type controls when germinated on plates containing high salt and high sucrose. They also show insensitivity to ABA in repeated germination assays.

25

These analyses revealed that in the absence of G926 function, plants are more tolerant to osmotic stress. This osmotic stress tolerance could be related to the plant's apparent insensitivity to the growth hormone ABA because ABA plays an important regulatory role in the initiation and maintenance of seed dormancy. G926 may function as part of a checkpoint for germinating

30   seeds and loss of G926 function promotes germination regardless of the osmotic status of the environment. G926 has utility in modifying plant stress responses.

G280 (SEQ ID. Nos. 461 and 462), G1323 (SEQ ID. Nos 203 and 204): modified biochemistry

G280: Overexpression of G280 in Arabidopsis resulted in an increase in leaf gamma and delta tocopherol in all three lines tested. Overexpression of G280 produced a reduction in overall plant size and accelerated the rate of leaf senescence in the rosette.

5   G1323: In two G1323 overexpressing lines, line 5 and 7, seeds had more protein and less oil than controls. Otherwise, overexpression of G1323 in Arabidopsis did not result in any biochemical phenotype. These experiments were repeated and a similar biochemical phenotype was observed.

10   <u>G2557 (SEQ ID Nos. 289 and 290), G2143 (SEQ ID Nos. 285 and 286), G1063 (SEQ ID Nos 167 and 168) (HLH/MYC)</u>

Overexpression of each of these genes affected plant growth, inflorescence architecture, and resulted in the development of carpelloid tissues in ectopic positions.

15   G2557: Twenty independent 35S::G2557 Arabidopsis primary transformants were obtained. Of these plants, 19/20 exhibited carpelloid tissue in the outer whorl organs of flowers. In some instances ovules developed from these ectopic carpels. The central carpel of 35S::G2557 flowers was also sometimes borne on a long pedicel-like structure, indicating that overexpression of this gene could influence determinacy of the floral meristem. Additionally, 35S::G2557 plants were

20   often smaller, darker green and possessed narrow leaves and elongated cotyledons compared to wild type.

G2143: Twenty independent 35S::G2143 Arabidopsis primary transformants were obtained. All 20 plants developed ectopic carpelloid tissue. In some cases entire flowers were replaced by

25   a disorganized mass of this tissue. Additionally, 35S::G2143 plants were often smaller, darker green and possessed narrow leaves and elongated cotyledons compared to wild type. In some cases the shoot tips of G2413 plants aborted in a 'pin-like' structure.

G1063: Seventeen independent 35S::G1063 Arabidopsis primary transformants were obtained.

30   5/17 of these lines exhibited flowers in which outer whorl organs displayed carpelloid features. In some cases flowers were completely replaced by a carpelloid mass of tissue and defined individual organs could not be distinguished. The shoots of these plants also occasionally terminated in a 'pin-like' structure. The majority of 35S::G1063 plants were smaller than wild type and often had altered leaf shape.

35

Based on the above phenotypes, these genes might be applied to manipulate flower structure and development, fertility, seed-pod development, leaf coloration and overall plant architecture. Specifically, the genes might be used to manipulate floral organ identity or instigate the formation of carpel-derived structures including ovules, embryos and seeds.

5

G2509 (SEQ ID Nos 287 and 288) (AP2)

Twenty independent 35S::G2509 *Arabidopsis* primary transformants were obtained. All plants exhibited increased secondary shoot development and loss of apical dominance, leading to a shorter bushier stature than wild type. G2509 could be used to modify plant architecture. This could produce plants more resistant to wind and rain and influence yield. Additionally, changing plant architecture could generate novel interesting forms for the ornamental plant market.

10

G353 (SEQ ID Nos 79 and 80) and G354 (SEQ ID Nos. 81 and 82) (Z(C2H2))

G353 and G354 constitute a pair of closely related Z(C2H2) genes that influence shoot architecture. Both genes produced comparable effects when overexpressed.

15

G353: A consistent phenotype was noted on inflorescences of 35S::G353 plants. Flowers were oriented downwards and pedicels of flowers and siliques were reduced in length or absent. Floral internodes were also very short. Furthermore, secondary shoots were often observed to grow in a downward direction. These phenotypes were observed in both primary transformants and T2 generation plants. Overexpression of G353 produced additional effects; 35S::G353 were sometimes smaller than wild-type, had abnormal branching patterns and flat leaves.

20

G354: 35S::G354 plants displayed abnormal inflorescences in which flowers were oriented downwards and pedicels were absent or reduced in length. Floral internodes were also short. Additionally, many of the 35S::G354 plants were reduced in size compared to wild type.

25

These genes could be used to modify plant architecture. Specifically, altering the length of flower and fruit stalks could permit more efficient harvesting. In species such as strawberry, changing the length of the fruit stalk could allow fruits to develop above the leaf canopy and reduce the likelihood of fungal infection. The genes might also have applications in producing novel forms of ornamental species in which branches, flowers and fruits develop with unusual orientations.

30

35

<u>G1494 (SEQ ID Nos. 223 and 224) (HLH/MYC)</u>

The phenotype of transgenic *Arabidopsis*, over-expressing G1494, indicates that this gene is a core component of the plant light perception/response machinery. 35S::G1494 seedlings displayed very long hypocotyls, bolted early, and exhibited elongation of rosette internodes.

5   This latter characteristic resulted in the absence of a defined rosette. The plants also possessed very spindly stems, and narrow pale leaves with elongated petioles. Such features were consistently observed in both primary transformants and T2 generation plants. These phenotypes are comparable to those of mutants defective in the *PHYTOCHROME* genes, which encode proteins involved in the perception of light conditions. In particular, the 35S::G1494 phenotype

10   is almost identical to that described for the *phyA;phyB;phyD* triple mutant (Devlin et al., Plant Physiology 119, 909-915). Based upon the 35S::G1494 phenotype, this gene might be applied to manipulate many of the traits which are influenced by the perception and response to light, including seed germination, flowering time, shade response, leaf orientation, architecture and growth habit.

15

Additional phenotypes that were observed included G634 (SEQ ID Nos. 3 and 4) (overexpressors had substantially more trichomes on its leaf surfaces), G971 (SEQ ID Nos. 17 and 18) (overexpressors enhanced terpenoid biosynthesis levels) and G1792 (SEQ ID Nos. 5 and 6) (overexpressors showed a broad-based disease resistance).

20

Example VIII: Identification of Homologous Sequences

Homologous sequences from *Arabidopsis* and plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool

25   (BLAST) (Altschul et al. (1990) J. Mol. Biol. 215:403-410; and Altschul et al. (1997) Nucl. Acid Res. 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919).

30   Identified *Arabidopsis* homologous sequences are provided in the Tables of the Appendices. The percent sequence identity among these sequences can be as low as 47%, or even 31% or lower sequence identity. Additionally, the entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and

35   excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences are compared to sequences representing genes of SEQ IDs Nos. 1-16 using the Washington

University TBLASTX algorithm (version 2.0a19MP) at the default settings using gapped

alignments with the filter "off,"as performed on July 16, 2001 or previously. For each gene of the

Sequence Listing, individual comparisons were ordered by probability score (P-value), where the

score reflects the probability that a particular alignment occurred by chance. For example, a score

5   of 3.6e-40 is 3.6 x 10^{-40}. In addition to P-values, comparisons were also scored by percentage

identity. Percentage identity reflects the degree to which two segments of DNA or protein are

identical over a particular length.

In addition to computer-based methods for identifying homologs, or indeed in conjunction with

10   them, a fragment of a sequence from the sequence listing, from the Tables of the Appendices, or

derived from a homolog sequence identified from a database, is radiolabeled with ^{32}P by random

priming (Sambrook et al., *Molecular Cloning. A Laboratory Manual*, 2nd Ed., or 3rd Ed., Cold

Spring Harbor Laboratory Press, New York) and used to screen a plant cDNA or genomic

library. As merely one example, total plant DNA from *Arabidopsis thaliana, Nicotiana tabacum,*

15   *Lycopersicon pimpinellifolium, Prunus avium, Prunus cerasus, Cucumis sativus,* or *Oryza sativa*

is isolated (Stockinger, E.J., et al., (1996), *J. Heredity*, 87:214-218). Alternatively, cDNA clones

of a selected cDNA library are used. Approximately 2 to 10 μg of each DNA sample is

restriction digested, transferred to nylon membrane (Micron Separations, Westboro, MA) and

hybridized. Alternatively, a library is plated out on growth medium and partially transferred *in*

20   *situ* to the nylon membrane for hybridization. Exemplary hybridization conditions are: 42°C in

50% formamide, 5X SSC, 20 mM phosphate buffer, 1X Denhardt's, 10% dextran sulfate, and

100 μg/ml herring sperm DNA. Four low stringency washes at RT in 2X SSC, 0.05% sodium

sarcosyl and 0.02% sodium pyrophosphate are performed prior to high stringency washes at

55°C in 0.2X SSC, 0.05% sodium sarcosyl and 0.01% sodium pyrophosphate. High stringency

25   washes are performed until no counts are detected in the washout (Walling, L.L., et al., Nucl.

Acids Res. 16:10477-10492(1988)). The areas of radioactivity on the membrane correspond to

homologous sequences from the library or genomic DNA sample and the associated DNA can be

identified, isolated, and cloned into an appropriate vector so that any homologous sequence(s)

can be used. Alterations in the stringency of washes, such as employing ultra-high stringency,

30   and ultra-ultra-high stringency, can also be made.

Example IX

As noted previously, the introduction of polynucleotides of the invention and full length coding

sequences of the invention into the target plant or cell can be accomplished by a variety of

35   techniques known in the art, such as calcium phosphate-DNA precipitation, electroporation,

microinjection, Agrobacterium infection, liposomes, or microprojectile bombardment, for example. Those of ordinary skill in the art can refer to the literature for details and select suitable techniques without undue experimentation. For some plants, using Agrobacterium is a preferred and easy method for transforming plants and cells. This type of transformation has been used for

5   genetic manipulation of more than 120 species of at least 35 different families of plants, including major economic crops such as vegetables, ornamentals, medicinals, fruit, trees and pasture plants (see, for example, Birch, R.G., Annual Rev. Plant Physiology and Plant Molec. Biology 48:297-326 (1997); Gould J.H., Transformation of the Cereals using Agrobacterium, In: R.S. Tuan (Ed.), Methods in Molecular Biology, Humana Press Inc., Totowa, NJ, vol. 62:489-

10   499 (1997)). In fact, this method has become so routine and commonplace that the idea that some species cannot accept the integration of foreign DNA into its genome or that a species lacks the capacity to be transformed has become unacceptable in the art (see de la Riva et al., Electr. J. Biotechnol. Agrobacterium tumefaciens: a natural tool for plant transformation, vol. 1, no. 13, issue of Dec. 15, 1998).

15

A number of vectors can be used to produce transgenic plants. Some of these vectors can replicate in bacterial hosts, plant host cells, and Agrobacterium, as known through many techniques of the art. Expression vectors typically comprise a cassette or region for inserting a coding sequence or transgene that is flanked by a promoter/enhancer and a poly A site. Many

20   variations are possible, including the use of sequences incorporating preferred codons, 5' UTR, 3' UTR, splice donor and acceptor or other intron sequences, internal ribosome entry sites, repressor or suppressor binding sequences, tissue-specific promoters and enhancers, developmentally regulated promoters and enhancers, and inducible promoters and enhancers, for example. Examples of inducible promoters useful in plants include those induced by chemical

25   means, such as the yeast metallothionein promoter, which is activated by concentrations of copper or heavy metal ions. Any appropriate inducible promoter, enhancer, or promoter/enhancer can be selected. One skilled in the art can devise many variations and permutations in selecting and using expression vectors. The vectors may also contain selectable markers for more easily identifying transformed plants. Many types of selectable marker genes

30   are known in the art.

If using Agrobacterium, one can select armed or disarmed Ti genes for transforming cells and plants. Either Ti plasmids of Agrobacterium tumefaciens (A. tumefaciens) or root-inducing (Ri) plasmids of Agrobacterium rhizogenes (A. rhizogenes) can be selected. (For reviews of

35   exemplary techniques see, for example, Weissbach & Weissbach, (1988) Methods for Plant Molecular Biology, Academic Press, NY, Section VIII, pp. 421-463; and Grierson & Corey

(1988) Plant Molecular Biology, 2d Ed., Blackie, London, Ch. 7-9, and Horsch et al., Science
227:1229 (1985), incorporated herein by reference). The selection of either A. tumefaciens or A.
rhizogenes will depend on the plant being transformed. In general A. tumefaciens is the
preferred organism for transformation. Most dicotyledons, some gymnosperms, and a few
5   monocotyledons (e.g. certain members of the Liliales and Arales) are easily susceptible to
infection with A. tumefaciens. A. rhizogenes also has a wide host range, including most dicots
and gymnosperms, which includes members of the Leguminosae, Compositae and
Chenopodiaceae. Selecting a type of vector and the components of the vector is well within the
ordinary skill of the art.
10

A general and exemplary method for plant transformation with Agrobacterium follows. The
polynucleotide or the full length coding region (transgene) is inserted into an intermediate or
shuttle vector capable of replicating in E. coli and suitable for the type of plant used and typically
containing a selectable marker. The vector is introduced into an acceptor A. tumefaciens strain
15   through triparental mating (reciprocal recombination between the intermediate vector and the T-
DNA region of the acceptor plasmid occurs during triparental mating and the transgene is now
part of the T-DNA region that will be transferred). The engineered A. tumefaciens strain
containing the transgene is cocultivated with a plant explant, from which regenerated plants can
be obtained. The explants are cultured in the presence of a selection agent and selecting resistant
20   cells grow shoots and rooted-shoots. These are regenerated into plants and the regenerated plants
screened for the expression of the transgene and selectable marker. The progeny of the
transgenic plant is grown and the inheritance of the introduced transgene is determined.

A transgenic plant transformed using Agrobacterium typically contains a single copy of the
25   introduced transgene on one chromosome – it is heterozygous for the transgene. Homozygous
plants can also be prepared and can be preferred or more stable in certain plants. One skilled in
the art is familiar with breeding and crossing techniques to produce homozygous plants
regardless of the type of transformation used. For example, homozygous transgenic plants can
be produced through sexually mating an independent segregant that contains a single transgene,
30   germinating the seed of the plant, and selecting the plants produced for the transgene. In
addition, two transformed or transgenic plants can be mated to produce plants having two
independently segregating transgenes. Sexually mating progeny produces homozygous plants for
both transgenes. Those of skill in the art are also familiar with techniques, such as back-crossing
to parental plants, out-crossing with a wild type or non-transgenic plant, and vegetative
35   propagation, for example, to manipulate plants having one or more transgenes. Any of these

techniques can be employed to produce transgenic plants, seeds, plant cells, or plant tissue or extracts having a polynucleotide or polypeptide of the invention.

5   Another common transformation protocol employs plant protoplasts using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation, and combinations of these. The selection of a protoplast method depends upon the ability to regenerate that particular plant strain from protoplasts. Many methods for regenerating plants from protoplasts exist and any can be selected for use (see, for example Shillito, R.D. and Saul, M.W., Protoplast Isolation and Transformation, In: Plant molecular biology, A Practical

10   Approach, IRL Press, UK (1988), particularly pp. 161-186; Methods in Enzymology, vol. 118, (Plant Molecular Biology), eds. Weissbach, A. and Weissbach, H., Academic Press, Orlando, Florida (1985); Methods in Enzymology, vol. 153 (Recombinant DNA), eds. Wu, R. and Grossman, L., Academic Press, Orlando, Florida, (1987).

15   To transform plant strains that cannot be successfully regenerated from protoplasts, other ways to introduce DNA into intact cells or tissues can be utilized. For example, plants can be regenerated from immature embryos or explants following introduction of vector or expression cassette DNA containing the transgene. The methods used to regenerate transformed cells into whole plants are not critical to this invention and any method suitable for the target plant can be employed. The

20   literature describes numerous techniques for regenerating specific plant types (for example, somatic embryogenesis, Umbeck, P., et al., Genetically transformed cotton (Gossypium hirsutum L.) plants, Bio/Technology 5:263 266 (1987)), and other techniques are continually becoming known. One of ordinary skill in the art can refer to the literature for details and select suitable techniques without undue experimentation. In practice, a large number of transformed plants can

25   be routinely regenerated from a transformed plant cell or tissue to increase and maintain a sterile line. Many methods for culturing plant cells and regenerating transformed plants from cells are known in the art and any appropriate method can be selected (see, for example, Plant Tissue and Cell Culture, C. E. Green, D. A. et al., (Eds.), Alan R. Liss, Inc., New York; Experiments in Plant Tissue Culture, Dodds, J. H. et al. (Eds.), 1985, Cambridge University Press; Cell Structure

30   and Somatic Cell Genetics of Plants, Vasil, I. K. (Ed.), 1984, Academic Press; Handbook of Plant Cell Culture, Volume 4, Techniques and Applications, Evans, D.A. et al. (Eds.), 1986, Macmillan Publishing Company).

In addition, microprojectile bombardment techniques can be used and many have been described

35   in the art. Here, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles (see, for example McCabe et al., Bio/Technology 6:923 (1988)). The metal

particles penetrate through several layers of cells and allow the transformation of cells within tissue explants. These explants or cells of them can then be regenerated into plants.

5   For example, if soybean is selected, the following method can be used. Somatic embryos, cotyledons, 3-5 mm in length, are dissected from surface of sterilized, immature seeds of the soybean cultivar chosen, and the embryos cultured in light or darkness at 26°C on an appropriate agar medium for 6-10 weeks. Somatic embryos that produce secondary embryos are then excised and placed into a suitable liquid medium. After repeated selection for clusters of somatic embryos that multiply, the suspensions are maintained in suspension culture.

10

The soybean embryogenic suspension cultures can maintained in 35 ml liquid media on a rotary shaker, 150 rpm, at 26°C with florescent lighting on a 16:8 hour day/night schedule. Sub-culturing every two weeks by inoculating approximately 35 mg of tissue into 35 ml of liquid medium maintains the cells.

15

A DuPont BioliStic PDS1000/HE instrument, a BIO RAD PDS-1000/He or other microprojectile device can be used for these transformations. DNA-coated microcarriers, typically tungsten or gold microparticles, are used according to the instruction manual. To 50 μl of a 60 mg/ml 1 μm gold particle suspension is added 5 μl DNA (1 μg/μl), 20 μl spermidine (0.1 M), and 50 μl CaCl2

20   (2.5 M). The particle preparation is agitated for three minutes, spun in a microfuge for 10 seconds, and the supernatant is removed. The DNA-coated particles are then washed once in 400 μl 70% ethanol and resuspended in 40 μl of anhydrous ethanol. The DNA/particle suspension can be sonicated three times for one second each. Five μl of the DNA-coated gold particles is loaded on the disk or appropriate carrier for the particle gun.

25

Approximately 300-400 mg of a two-week-old suspension culture is placed in an empty petri dish and the residual liquid removed from the tissue with a pipette. For each transformation, approximately 5-10 plates of tissue are normally used. Membrane rupture pressure is set at approximately 1100 psi. The tissue is placed approximately 3.5 inches away from the retaining

30   screen and bombarded three times. Following treatment, the tissue can be divided in half and placed back into liquid and cultured as above.

Five to seven days post bombardment, the liquid media is exchanged with fresh media, and eleven to twelve days post bombardment with fresh media containing selection media (if the

35   vector or DNA used also encodes a selectable marker, as it preferably will). The selection media is replaced approximately ever week. Seven to eight weeks post bombardment, green,

transformed tissue may be observed growing from un-transformed, necrotic embryogenic clusters. Isolated green tissue is removed and inoculated into individual flasks to generate new, clonally propagated, transformed embryogenic suspension cultures. Each new line may be treated independently. These suspensions can then be sub-cultured and maintained as clusters of

5   immature embryos or regenerated into whole plants by maturation and germination of individual somatic embryos.

If maize is selected, immature embryos are excised from cleaned and sterilized ears and placed embryo axis side down (scutellum side up) in a petri plate. These are cultured in 560L medium

10   for 4 days in the dark. To prepare for bombardment, the embryos are transferred to 560Y medium for 4 hours and arranged within the device target zone.

The DNA is prepared with Tungsten microparticles, for example, using 1 ug DNA in Tris EDTA buffer, 2.5 M CaCl2, and 0.1 M spermidine while vortexing. The mixture is sonicated briefly

15   and incubated under constant vortexing for ten minutes. After a precipitation period, the tubes are centrifuged briefly, and the liquid is removed. The particles are washed with 100% ethanol, centrifuged, and resuspended in 100% ethanol. For particle gun bombardment, the tungsten/DNA particles are briefly sonicated and 10 ul spotted onto the center of each carrier and allowed to dry about 2 minutes before bombardment.

20

All samples receive a single shot at approximately 650 psi. Following bombardment, the embryos are cultured in 560Y medium for 2 days then transferred to 560R selection medium and sub-cultured every 2 weeks. After approximately 10 weeks of selection, selection-resistant callus clones are sampled by PCR for transgene content and/or activity analysis. Positive lines are

25   transferred to 288J medium to initiate plant regeneration. Following somatic embryo maturation period of 2-4 weeks, well-developed somatic embryos are transferred to 272V medium for germination and then transferred to a lighted culture room. Approximately 7-10 days later, developing plantlets are transferred to 272V medium in tubes for 7-10 days until plantlets are well established. Plants are then transferred to potting soil and grown for 1 week in a growth

30   chamber, and subsequently grown 1-2 weeks in the greenhouse, then grown to maturity.

Example X. Transformation of Cereal Plants with Expression Vector
A cereal plant, such as corn, wheat, rice, sorghum or barley, can also be transformed with a plasmid vector containing a sequence or polynucleotide of the invention, together with an

35   operably linked constitutive or inducible promoter, to modify a trait or produce ectopic or altered expression. In these cases, a cloning vector, pMEN020 for example, is modified to replace the

NptII coding region with the BAR gene of Streptomyces hygroscopicus to confer resistance to phosphinothricin. The KpnI and BglII sites of the Bar (bialaphos resistance) gene are removed by site-directed mutagenesis with silent codon changes. Preferably, a maize or other plant ubiquitin promoter is inserted in place of the 35S promoter of pMEN020 (see, for example,

5   Christensen et al., Plant Mol. Biol. 12:619-632 (1992); and Christensen, et al., Plant Mol. Biol. 18:675-689 (1992); Christensen et al., Transgenic Res. 5:213-8(1996)). The polypeptide-encoding sequence or cDNA is then inserted downstream of the promoter. Additional expression vector elements can also be inserted, as discussed elsewhere in this document, to optimize expression.

10

Plasmids according to the present invention may be transformed into corn embryogenic cells derived from immature scutellar tissue by using microprojectile bombardment, with the A188XB73 genotype as the preferred genotype (Fromm et al., Bio/Technology 8: 833-839 (1990); Gordon-Kamm et al., Plant Cell 2: 603-618 (1990)). After microprojectile bombardment

15   the tissues are selected on phosphinothricin to identify the transgenic embryogenic cells (Gordon-Kamm et al., Plant Cell 2: 603-618 (1990)). Transgenic plants are regenerated by standard corn regeneration techniques (Fromm et al., Bio/Technology 8: 833-839 (1990); Gordon-Kamm et al., Plant Cell 2: 603-618 (1990)).

20   Various homologs, derivative polypeptides, or polypeptide-encoding polynucleotides can be identified and produced from the information in this document. Any technique available can be used and the examples below are merely exemplary.

To identify exemplary variant or derivative polypeptides, polynucleotides, and homologs of the

25   sequences listed here, many techniques, such as using the BLAST program to screen a public (NCBI for example) or commercial (Incyte for example) sequence databases, screening a cDNA or genomic library by hybridization at low or high stringency, and using PCR techniques using degenerate or non-degenerate primers designed to hybridise against the gene you wish to clone, are known in the art. Any GID polynucleotide or cDNA clone can be selected as well as any

30   sequence of the sequence listing. For example, G1073 can be selected. Transgenic plants overexpressing G1073 have the advantageous properties of being large, late flowering, and/or have serrated leaves. The large size and/or late flowering traits would be extremely useful in crops where the vegetative portion of the plant can be commercially harvested (often, vegetative growth stops when plants make the transition to flowering). In this case, it would be

35   advantageous to prevent or delay flowering in order to increase yield or biomass. The plants would also be extremely useful in preparing recombinant therapeutic proteins, such as antibodies

or single chain antibodies. Prevention of flowering would also be useful in plants and crops in order to prevent the spread of transgenic pollen and/or to prevent seed set. G1073 can also be used to manipulate leaf shape.

5   In this example, a homolog of G1073 from Glycine max is identified and a construct expressing this Glycine max cDNA is provided. As noted in the Appendices, the NCBI database is screened using the BLAST algorithm and sequences similar to G1073 are identified, including Glycine max cDNA clones or genomic sequences (BF067277, AW349284 and AI736668).

10   Using standard techniques, a Glycine max cDNA library is screened using probes derived from the sequence BF067277, AW349284 or AI736668 and a full-length clone is isolated. This full length Glycine max clone can be subcloned into an appropriate expression vector using restriction sites or full-length sequences can be amplified from cDNA or genomic DNA by PCR and subcloned into an appropriate expression vector. Also using standard techniques, a fragment

15   incorporating all or part of the Glycine max sequence, or a fragment of another homolog, is produced with substitution or site-specific mutations. This fragment can be used in PCR amplification to replace all or any of the nucleotides to result in amino acid changes or codon changes. Alternatively, oligos incorporating the substitution change(s) can be used in homologous recombination techniques to replace nucleotides in a sequence. Other available

20   techniques, known in the art, can also be used. Once the sequence differences between any sequence listed or described here to that of a known sequence is displayed, one of skill in the art can use any available method to make one or more substitution changes in the nucleotides or the polypeptides. These changes will preferably result in changes in the amino acid sequence of the encoded polypeptide, creating a derivative or variant polypeptide.

25

The changes or substitutions can also incorporate preferred codons for a particular species or group of plants. Preferred codons for a number of different plants are known in the art. The changes can also delete or add amino acid residues. One skilled in the art is familiar with a variety of techniques for manipulating a polypeptide-encoding sequence to make one or more

30   changes, substitutions, deletions, or additions, as desired.

As shown here, the sequences listed have homologs in other plant species. Any of the manipulations, procedures for producing transgenic plants, or analysis of the transgenic plants, can be performed using the homolog sequence in place of the specifically listed sequence. Thus,

35   for example, transgenic plants employing the homolog of G1073 from, for example, Lycopersicon esculentum, Medicago truncatula, Oryza sativa, Hordeum vulgare, Glycine max,

Lotus japonicus, Solanum tuberosum, Sorghum propinquum, Pinus taeda, Triticum aestivum, Pisum sativu, Antirrhinum majus, Daucus carota, Nicotiana tabacum, Brassica napus, Zea mays, Volvox carteri f. nagariensis, or Chlamydomonas reinhardtii can be used to create plants having ectopic expression or altered expression of the G1073 homolog. Chimeric sequences, employing

5   parts of more than one homolog or parts of a specific sequence, such as G1073, and its homolog(s), can also be created and used. More than one homolog or recombinant polynucleotide can be introduced into a plant to produce a transgenic plant, as known in the art.

10   All references, publications, patent documents, web pages, links, sequences of Genbank identifiers, sequences of genomic or EST database identifiers, and other documents cited or mentioned herein are hereby incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to specific embodiments and examples, it should be understood that one of ordinary skill can make various modifications without

15   departing from the spirit of the invention. The scope of the invention is not limited to the specific embodiments and examples provided.

What is claimed is:

1.   A transgenic plant comprising a recombinant polynucleotide having a nucleotide
sequence selected from the group:

5   (a) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence selected
from those of SEQ ID NOs.: 2N where N= 1-232, or a complementary nucleotide sequence
thereof;

(b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant
of a polypeptide of (a);

10   (c) one of SEQ ID NOs.: 2N-1 where N=1-232, or a complementary nucleotide sequence thereof;

(d) a nucleotide sequence comprising one or more silent substitutions in a nucleotide sequence of
(c);

(e) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of
one or more of: (a), (b), (c), or (d);

15   (f) a nucleotide sequence comprising at least 15 consecutive nucleotides outside of a conserved
domain of any of (a)-(e);

(g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which
subsequence or fragment encodes a polypeptide that modifies one or more of a plant's traits;

(h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any

20   of (a)-(g);

(i) a nucleotide sequence having at least 60% sequence identity to a nucleotide sequence of any
of (a)-(g);

(j) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of any
of (a)-(g);

25   (k) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity outside
of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.:
2N where N=1-232;

(l) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity outside
of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.:

30   2N where N=1-232; or

(m) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity outside
of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.:
2N where N=1-232;

(n) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity outside

35   of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.:
2N where N=1-232;

(o) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least 86% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;

(p) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least

5   about 90% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;

(q) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 95% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;

10   (r) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 98% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;

(s) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity over the entire length of a polypeptide of one of SEQ ID Nos.: 2N where N=1-232;

15   (t) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity over the entire length of a polypeptide of one of SEQ ID Nos.: 2N where N=1-232;

(u) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity over the entire length of a polypeptide of one of SEQ ID Nos. 2N where N=1-232;

(v) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity over the

20   entire length of a polypeptide of one of SEQ ID Nos. 2N where N=1-232,

wherein the plant possesses an altered trait as compared to a wild type or reference plant, or the plant exhibits an altered phenotype as compared to a wild type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a

25   plant trait as compared to a wild type plant.

2.   The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to said recombinant nucleotide.

30   3.   The transgenic plant of claim 1, wherein the plant is selected from the following group: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, *Arabidopsis*, spinach, squash, sweet corn, tobacco, tomato, watermelon, mint and

35   other labiates, rosaceous fruits, and vegetable brassicas.

4.   An isolated or recombinant polynucleotide having a nucleotide sequence selected
from the following group:
(a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from those of
SEQ ID Nos: 2N where N=1-232, or a complementary nucleotide sequence thereof;

5   (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant
of a polypeptide of (a);
(c) one of SEQ ID NOs. 2N-1 where N=1-232, or a complementary nucleotide sequence thereof;
(d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
(e) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of

10   one or more of: (a), (b), (c), or (d);
(f) a nucleotide sequence comprising at least 15 consecutive nucleotides outside of a conserved
domain of any of (a)-(e);
(g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which
subsequence or fragment encodes a polypeptide that modifies one or more of a plant's traits;

15   (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any
of (a)-(g);
(i) a nucleotide sequence having at least 60% sequence identity to a nucleotide sequence of any
of (a)-(g);
(j) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of any

20   of (a)-(g);
(k) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity outside
of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.:
2N where N=1-232;
(l) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity outside

25   of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.:
2N where N=1-232; or
(m) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity outside
of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.:
2N where N=1-232;

30   (n) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity outside
of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.:
2N where N=1-232;
(o) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least 86%
sequence identity to a conserved domain of a polypeptide having an amino acid sequence of one

35   of SEQ ID Nos.: 2N where N=1-232;

(p) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least
about 90% sequence identity to a conserved domain of a polypeptide having an amino acid
sequence of one of SEQ ID Nos.: 2N where N=1-232;

(q) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least

5   about 95% sequence identity to a conserved domain of a polypeptide having an amino acid
sequence of one of SEQ ID Nos.: 2N where N=1-232; and

(r) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least
about 98% sequence identity to a conserved domain of a polypeptide having an amino acid
sequence of one of SEQ ID Nos.: 2N where N=1-232;

10   (s) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity over the
entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where
N=1-232;

(t) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity over the
entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where

15   N=1-232;

(u) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity over the
entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where
N=1-232;

(v) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity over the

20   entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where
N=1-232.

5.   The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive,
inducible, or tissue-specific promoter operably linked to the polynucleotide nucleotide.

25

6.   An isolated or recombinant polypeptide comprising a subsequence of at least about 15
contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.

7.   A method of using the isolated or recombinant polynucleotide of claim 4 for producing a

30   plant having a modified trait, the method comprising selecting a polynucleotide that encodes a
polypeptide, inserting the polynucleotide into an expression vector, introducing the vector into a
plant or a cell of a plant to overexpress the polypeptide, thereby producing a modified plant, and
selecting for a modified trait.

35   8.   The transgenic plant of claim 1, wherein the trait is selected from the group: enhanced
tolerance to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced

tolerance to drought; enhanced tolerance to water saturation; enhanced tolerance to radiation; enhanced tolerance to ozone; enhanced tolerance to microbial disease; enhanced tolerance to fungal disease; enhanced tolerance to viral disease; enhanced tolerance to pest infestation; decreased herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up

5   heavy metals; and enhanced growth under poor photoconditions.

9.   The transgenic plant of claim 1, wherein the trait is an alteration in the level of one or more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins,

10   prenyllipids, glucosinolates, and terpenoids.

10.   The transgenic plant of claim 1, wherein the trait is an alteration in one or more physical characteristics selected from the group: number of trichomes; fruit and seed size and number; yield of stems; yield of leaves; yield of roots; stability of seeds during storage; susceptibility of

15   the seed to shattering; root hair length; root hair quantity; internode distances; and the quality of seed coat.

11.   The transgenic plant of claim 1, wherein the trait is an alteration in a plant growth characteristic selected from the group: growth rate; germination rate of seeds; vigor of plants;

20   vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time; flower abscission; rate of nitrogen uptake; biomass; transpiration characteristics; apical dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.

12.   The transgenic plant of claim 1, wherein the trait is an alteration in one or more

25   characteristics selected from the group: protein production; oil production; seed protein production; seed oil production; insoluble sugar level; soluble sugar level; and starch composition.

13.   The method of claim 7, wherein the trait is selected from the group: enhanced tolerance

30   to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced tolerance to drought; enhanced tolerance to water saturation; enhanced tolerance to radiation; enhanced tolerance to ozone; enhanced tolerance to microbial disease; enhanced tolerance to fungal disease; enhanced tolerance to viral disease; enhanced tolerance to pest infestation; decreased herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up heavy

35   metals; and enhanced growth under poor photoconditions.

14.   The method of claim 7, wherein the trait is an alteration in the level of one or more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyllipids, glucosinolates, and terpenoids.

5

15.   The method of claim 7, wherein the trait is an alteration in one or more physical characteristics selected from the group: number of trichomes; fruit and seed size and number; yield of stems; yield of leaves; yield of roots; stability of seeds during storage; susceptibility of the seed to shattering; root hair length; root hair quantity; internode distances; and the quality of

10   seed coat.

16.   The method of claim 7, wherein the trait is an alteration in a plant growth characteristic selected from the group: growth rate; germination rate of seeds; vigor of plants; vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time; flower

15   abscission; rate of nitrogen uptake; biomass; transpiration characteristics; apical dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.

17.   The method of claim 7, wherein the trait is an alteration in one or more characteristics selected from the group: protein production; oil production; seed protein production; seed oil

20   production; insoluble sugar level; soluble sugar level; and starch composition.

18.   A plant produced by the method of claim 13.

19.   A plant produced by the method of claim 14.

25

20.   A plant produced by the method of claim 15.

21.   A plant produced by the method of claim 16.

30   22.   A plant produced by the method of claim 17.

23.   A method of using the isolated or recombinant polynucleotide of claim 4 for producing a plant having a modified trait, the method comprising selecting a polynucleotide that when expressed produces an antisense nucleic acid, inserting the polynucleotide into an expression

35   vector, introducing the vector into a plant or a cell of a plant to express the antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait.

24.   The method of claim 23, wherein the trait is selected from the group: enhanced tolerance to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced tolerance to drought; enhanced tolerance to water saturation; enhanced tolerance to radiation; enhanced

5   tolerance to ozone; enhanced tolerance to microbial disease; enhanced tolerance to fungal disease; enhanced tolerance to viral disease; enhanced tolerance to pest infestation; decreased herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up heavy metals; and enhanced growth under poor photoconditions.

10   25.   The method of claim 23, wherein the trait is an alteration in the level of one or more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyllipids, glucosinolates, and terpenoids.

15   26.   The method of claim 23, wherein the trait is an alteration in one or more physical characteristics selected from the group consisting of: the number of trichomes, fruit and seed size and number, yield of stems, leaves, or roots, stability of seeds during storage, susceptibility of the seed to shattering, root hair length and quantity, internode distances, or the quality of seed coat.

20   27.   The method of claim 23, wherein the trait is an alteration in a plant growth characteristic selected from the group: growth rate; germination rate of seeds; vigor of plants; vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time; flower abscission; rate of nitrogen uptake; biomass; transpiration characteristics; apical dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.

25

28.   The method of claim 23, wherein the trait is an alteration in one or more characteristics selected from the group: protein production; oil production; seed protein production; seed oil production; insoluble sugar level; soluble sugar level; and starch composition.

30   29.   A plant produced by the method of claim 24.

30.   A plant produced by the method of claim 25.

31.   A plant produced by the method of claim 26.

35

32.   A plant produced by the method of claim 27.

33.   A plant produced by the method of claim 28.

34.   An isolated or recombinant polypeptide comprising a subsequence of at least about 10

5   contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim

            4, wherein the contiguous amino acids are outside of a conserved domain.

35.   An isolated or recombinant polypeptide comprising a subsequence of at least about 20

            contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim

10   4, wherein the contiguous amino acids are outside of a conserved domain.

36.   An isolated or recombinant polypeptide comprising a subsequence of at least about 30

            contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim

            4, wherein the contiguous amino acids are outside of a conserved domain.

15

37.   An isolated or recombinant polypeptide comprising a subsequence of at least about 10

            contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim

            4, wherein the contiguous amino acids are within a conserved domain.

20   38.   An isolated or recombinant polypeptide comprising a subsequence of at least about 20

            contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim

            4, wherein the contiguous amino acids are within a conserved domain.

39.   An isolated or recombinant polypeptide comprising a subsequence of at least about 30

25   contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim

            4, wherein the contiguous amino acids are within a conserved domain.

40.   An isolated or recombinant polypeptide having at least 31% sequence identity over the

            entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N

30   where N=1-232, or the length of the polypeptide itself.

41.   An isolated or recombinant polypeptide having at least 60% sequence identity over the

            entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N

            where N=1-232, or the length of the polypeptide itself.

35

42.   An isolated or recombinant polypeptide having at least 75% sequence identity over the
        entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N
        where N=1-232, or the length of the polypeptide itself.

5   43.   An isolated or recombinant polypeptide having at least 95% sequence identity over the
        entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N
        where N=1-232, or the length of the polypeptide itself.

44.   An isolated or recombinant polynucleotide having the sequence one of SEQ ID NOs.:
10   2N-1 where N=1-232, or a complementary nucleotide sequence thereof..

45.   The polynucleotide of claim 44, which has the sequence of one of SEQ ID Nos.: 1, 3, 5,
        7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 37.

15 46.   The polynucleotide of claim 44, which has the sequence of one of SEQ ID Nos.: 53, 79,
        81, 107, 125, 153, 167, 203, 223, 289, 285, or 287.

47.   The polynucleotide of claim 44, which has the sequence of one of SEQ ID Nos.: 313,
        345, 365, 395, 417, 425, 435, 455, 457, 459, 461, or 463.

20

48.   A computer readable medium having stored sequence information comprising the
        polynucleotide sequence of claim 44.

49.   The computer readable medium of claim 48, having stored sequence information
25   comprising the sequence of one of SEQ ID Nos.: 1-37.

50.   The computer readable medium of claim 48, having stored sequence information
        comprising the sequence of one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125,
        126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.

30

51.   The computer readable medium of claim 48, having stored sequence information
        comprising the polynucleotide sequence of one of SEQ ID Nos.: 313, 314, 345, 346, 365,
        366, 395, 396, 461, 462, 417, 418, 425, 426, 435, 436, 455, 456, 457, 458, 459, 460, 461,
        462, 463, or 464.

35

52.   A method of identifying a homolog sequence from a database comprising a plurality of known plant sequences, the method comprising: inputting sequence information selected from one or more of SEQ ID Nos. 1-464; and querying the database to identify a homolog sequence.

53.   The method of claim 52, wherein the database being queried comprises a database of known genomic, cDNA, EST, or protein sequences.

54.   The method of claim 52, wherein inputting sequence information comprises copying the sequence information from a CD.

55.   The method of claim 52, wherein the sequence data comprises one of SEQ ID Nos.: 1-37.

56.   The method of claim 52, wherein the sequence data comprises one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.

57.   The method of claim 52, wherein the sequence data comprises of SEQ ID Nos.: 313, 314, 345, 346, 365, 366, 395, 396, 461, 462, 417, 418, 425, 426, 435, 436, 455, 456, 457, 458, 459, 460, 461, 462, 463, or 464.

58.   The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acid region of one of SEQ ID Nos.: 1-37.

59.   The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acids region one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.

60.   The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acid region of one of SEQ ID Nos.: 313, 314, 345, 346, 365, 366, 395, 396, 461, 462, 417, 418, 425, 426, 435, 436, 455, 456, 457, 458, 459, 460, 461, 462, 463, or 464.

61.   A homolog identified by the method of claim 52.

62.   The homolog of claim 61, identified by the method of claim 53.

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63.   The homolog of claim 61, identified by the method of claim 54.

64.   The homolog of claim 61, identified by the method of claim 55.

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65.   The homolog of claim 61, identified by the method of claim 55.

66.   The homolog of claim 61, identified by the method of claim 56.

10   67.   The homolog of claim 61, identified by the method of claim 57.

68.   The homolog of claim 61, identified by the method of claim 58.

69.   The homolog of claim 61, identified by the method of claim 59.

15

70.   The homolog of claim 61, identified by the method of claim 60.

SEQUENCE LISTING

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<110>  Pilgrim, Marsha
Creelman, Robert
Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
Keddie, James
Adam, Luc
Ratcliffe, Oliver
Reuber, T. Lynne
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Yu, Guo-Liang
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Ser Ile Arg Arg His Leu Leu Gly Glu Ser Glu Pro Ile Leu Ser Glu
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tcg aca gcg agt tcg gtt act caa tct tgt gta acc ggt cag agc att
203
Ser Thr Ala Ser Ser Val Thr Gln Ser Cys Val Thr Gly Gln Ser Ile
            35                  40                  45

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251
Lys Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys
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Phe Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu
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443
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        130   135   140

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539
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635
Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Arg Ala
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964

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Met Ser Met Thr Ala Asp Ser Gln Ser Asp Tyr Ala Phe Leu Glu Ser
1   5   10   15

Ile Arg Arg His Leu Leu Gly Glu Ser Glu Pro Ile Leu Ser Glu Ser
            20   25   30

Thr Ala Ser Ser Val Thr Gln Ser Cys Val Thr Gly Gln Ser Ile Lys
            35   40   45

Pro Val Tyr Gly Arg Asn Pro Ser Phe Ser Lys Leu Tyr Pro Cys Phe
        50   55   60

Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu Asp
65   70   75   80

Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp Glu
                85   90   95

Pro Ser Ser Ser Ser Ser Asp Glu Asp Arg Ser Ser Phe Pro Ser Val
            100   105   110

Lys Ile Glu Thr Pro Glu Ser Phe Ala Ala Val Asp Ser Val Pro Val
            115   120   125

Lys Lys Glu Lys Thr Ser Pro Val Ser Ala Ala Val Thr Ala Ala Lys
        130   135   140

Gly Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
145   150   155   160

Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
                165   170   175

Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Arg Ala Ala
            180   185   190

Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val
            195   200   205

3

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Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Lys Ser Lys Arg Ser Ser
    210             215             220

Phe Ser Ser Ser Asn Glu Asn Gly Ala Pro Lys Lys Arg Arg Thr Val
225             230             235                 240

Ala Ala Gly Gly Gly Met Asp Lys Gly Leu Thr Val Lys Cys Glu Val
                245             250             255

Val Glu Val Ala Arg Gly Asp Arg Leu Leu Val Leu
            260             265
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<221> CDS <222> (1)..(798) <223> G634

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atg gag caa gga gga ggt ggt ggt ggt aat gaa gtt gtg gag gaa gct
48
Met Glu Gln Gly Gly Gly Gly Gly Gly Asn Glu Val Val Glu Glu Ala
1               5               10              15

tca cct att agt tca aga cct cct gct aac aac tta gaa gag ctt atg
96
Ser Pro Ile Ser Ser Arg Pro Pro Ala Asn Asn Leu Glu Glu Leu Met
            20              25              30

aga ttc tca gcc gcc gcg gat gac ggt gga tta gga ggt gga ggt gga
144
Arg Phe Ser Ala Ala Ala Asp Asp Gly Gly Leu Gly Gly Gly Gly Gly
        35              40              45

gga gga gga gga gga agt gct tct tct tca tcg gga aat cga tgg ccg
192
Gly Gly Gly Gly Gly Ser Ala Ser Ser Ser Ser Gly Asn Arg Trp Pro
    50              55              60

aga gaa gaa act tta gct ctt ctt cgg atc cga tcc gat atg gat tct
240
Arg Glu Glu Thr Leu Ala Leu Leu Arg Ile Arg Ser Asp Met Asp Ser
65              70              75              80

act ttt cgt gat gct act ctc aaa gct cct ctt tgg gaa cat gtt tcc
288
Thr Phe Arg Asp Ala Thr Leu Lys Ala Pro Leu Trp Glu His Val Ser
            85              90              95

agg aag cta ttg gag tta ggt tac aaa cga agt tca aag aaa tgc aaa
336
Arg Lys Leu Leu Glu Leu Gly Tyr Lys Arg Ser Ser Lys Lys Cys Lys
            100             105             110

gag aaa ttc gaa aac gtt cag aaa tat tac aaa cgt act aaa gaa act
384
Glu Lys Phe Glu Asn Val Gln Lys Tyr Tyr Lys Arg Thr Lys Glu Thr
        115             120             125
```

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cgc ggt ggt cgt cat gat ggt aaa gct tac aag ttc ttc tct cag ctt
432
Arg Gly Gly Arg His Asp Gly Lys Ala Tyr Lys Phe Phe Ser Gln Leu
    130             135             140

gaa gct ctc aac act act cct cct cct cct cct tct cat cct cac gct
480
Glu Ala Leu Asn Thr Thr Pro Pro Pro Pro Pro Ser His Pro His Ala
145             150             155             160

cat caa cca gaa cag aaa caa caa caa caa cca caa caa gag atg gtc
528
His Gln Pro Glu Gln Lys Gln Gln Gln Gln Pro Gln Gln Glu Met Val
                165             170             175

atg agc tcg gaa caa tca tca tta cca tca tca tca aga tgg cca aag
576
Met Ser Ser Glu Gln Ser Ser Leu Pro Ser Ser Ser Arg Trp Pro Lys
                180             185             190

gca gag att cta gcg ctt ata aac ctg aga agt gga atg gaa cca agg
624
Ala Glu Ile Leu Ala Leu Ile Asn Leu Arg Ser Gly Met Glu Pro Arg
            195             200             205

tac caa gat aat gta cct aaa gga ctt cta tgg gaa gag atc tca act
672
Tyr Gln Asp Asn Val Pro Lys Gly Leu Leu Trp Glu Glu Ile Ser Thr
    210             215             220

tca atg aag aga atg gga tac aac aga aac gct aag aga tgt aaa gag
720
Ser Met Lys Arg Met Gly Tyr Asn Arg Asn Ala Lys Arg Cys Lys Glu
225             230             235             240

aaa tgg gaa aac ata aac aaa tac tac aag aaa gtt aaa gaa agc aac
768
Lys Trp Glu Asn Ile Asn Lys Tyr Tyr Lys Lys Val Lys Glu Ser Asn
                245             250             255

aac agc aac tac aac aac aag aat caa tga
798
Asn Ser Asn Tyr Asn Asn Lys Asn Gln
                260             265


<210> 4 <211> 265 <212> PRT <213> Arabidopsis thaliana <400> 4

Met Glu Gln Gly Gly Gly Gly Gly Gly Asn Glu Val Val Glu Glu Ala
1               5               10              15

Ser Pro Ile Ser Ser Arg Pro Pro Ala Asn Asn Leu Glu Glu Leu Met
            20              25              30

Arg Phe Ser Ala Ala Ala Asp Asp Gly Gly Leu Gly Gly Gly Gly Gly
        35              40              45

Gly Gly Gly Gly Gly Ser Ala Ser Ser Ser Ser Gly Asn Arg Trp Pro
```

                50   55   60

Arg Glu Glu Thr Leu Ala Leu Leu Arg Ile Arg Ser Asp Met Asp Ser
65   70   75   80

Thr Phe Arg Asp Ala Thr Leu Lys Ala Pro Leu Trp Glu His Val Ser
                85   90   95

Arg Lys Leu Leu Glu Leu Gly Tyr Lys Arg Ser Ser Lys Lys Cys Lys
            100   105   110

Glu Lys Phe Glu Asn Val Gln Lys Tyr Tyr Lys Arg Thr Lys Glu Thr
            115   120   125

Arg Gly Gly Arg His Asp Gly Lys Ala Tyr Lys Phe Phe Ser Gln Leu
        130   135   140

Glu Ala Leu Asn Thr Thr Pro Pro Pro Pro Pro Ser His Pro His Ala
145   150   155   160

His Gln Pro Glu Gln Lys Gln Gln Gln Pro Gln Gln Glu Met Val
                165   170   175

Met Ser Ser Glu Gln Ser Ser Leu Pro Ser Ser Ser Arg Trp Pro Lys
            180   185   190

Ala Glu Ile Leu Ala Leu Ile Asn Leu Arg Ser Gly Met Glu Pro Arg
            195   200   205

Tyr Gln Asp Asn Val Pro Lys Gly Leu Leu Trp Glu Glu Ile Ser Thr
    210   215   220

Ser Met Lys Arg Met Gly Tyr Asn Arg Asn Ala Lys Arg Cys Lys Glu
225   230   235   240

Lys Trp Glu Asn Ile Asn Lys Tyr Tyr Lys Lys Val Lys Glu Ser Asn
            245   250   255

Asn Ser Asn Tyr Asn Asn Lys Asn Gln
            260   265

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<221> CDS <222> (77)..(496) <223> G1792

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60

6

tagaacacca aagtta atg gag agc tca aac agg agc agc aac aac caa tca
112
                         Met Glu Ser Ser Asn Arg Ser Ser Asn Asn Gln Ser
                         1   5   10

caa gat gac aag caa gct cgt ttc cgg gga gtt cga aga agg cct tgg
160
Gln Asp Asp Lys Gln Ala Arg Phe Arg Gly Val Arg Arg Arg Pro Trp
        15   20   25

gga aag ttt gca gca gag att cga gac ccg tcg aga aac ggt gcc cgt
208
Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Ser Arg Asn Gly Ala Arg
        30   35   40

ctt tgg ctc ggg aca ttt gag acc gct gag gag gca gca agg gct tat
256
Leu Trp Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr
45   50   55   60

gac cga gca gcc ttt aac ctt agg ggt cat ctc gct ata ctc aac ttc
304
Asp Arg Ala Ala Phe Asn Leu Arg Gly His Leu Ala Ile Leu Asn Phe
                65   70   75

cct aat gag tat tat cca cgt atg gac gac tac tcg ctt cgc cct cct
352
Pro Asn Glu Tyr Tyr Pro Arg Met Asp Asp Tyr Ser Leu Arg Pro Pro
            80   85   90

tat gct tct tct tct tcg tcg tcg tca tcg ggt tca act tct act aat
400
Tyr Ala Ser Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Thr Asn
        95   100   105

gtg agt cga caa aac caa aga gaa gtt ttc gag ttt gag tat ttg gac
448
Val Ser Arg Gln Asn Gln Arg Glu Val Phe Glu Phe Glu Tyr Leu Asp
    110   115   120

gat aag gtt ctt gaa gaa ctt ctt gat tca gaa gaa agg aag aga taa
496
Asp Lys Val Leu Glu Glu Leu Leu Asp Ser Glu Glu Arg Lys Arg
125   130   135

tcacgattag ttttgttttg atattttatg tggcactgtt gtggctacct acgtgcatta
556

tgtgcatgta taggtcgctt gattagtact ttataacatg catgccacga ccataaattg
616

taagagaaga cgtactttgc gttttcatga aatatgaatg ttagatggtt tgagtacaaa
676

aaaaaaaaaa aaaaaaaaaa
696

<210> 6 <211> 139 <212> PRT <213> Arabidopsis thaliana <400> 6

Met Glu Ser Ser Asn Arg Ser Ser Asn Asn Gln Ser Gln Asp Asp Lys
1   5   10   15

Gln Ala Arg Phe Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala
            20   25   30

Ala Glu Ile Arg Asp Pro Ser Arg Asn Gly Ala Arg Leu Trp Leu Gly
            35   40   45

Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ala Ala
    50   55   60

Phe Asn Leu Arg Gly His Leu Ala Ile Leu Asn Phe Pro Asn Glu Tyr
65   70   75   80

Tyr Pro Arg Met Asp Asp Tyr Ser Leu Arg Pro Pro Tyr Ala Ser Ser
            85   90   95

Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Thr Asn Val Ser Arg Gln
            100   105   110

Asn Gln Arg Glu Val Phe Glu Phe Glu Tyr Leu Asp Asp Lys Val Leu
        115   120   125

Glu Glu Leu Leu Asp Ser Glu Glu Arg Lys Arg
    130   135

<210> 7 <211> 944 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (39)..(755) <223> G156

 <400> 7
aggaagaggg agccactcat aagaggaaga agagagag atg ggt aga ggg aag ata
56
                                    Met Gly Arg Gly Lys Ile
                                    1   5

gag ata aag aag ata gag aat cag acg gcg agg caa gtg acc ttc tcc
104
Glu Ile Lys Lys Ile Glu Asn Gln Thr Ala Arg Gln Val Thr Phe Ser
            10   15   20

aag aga aga act ggt ctt ata aag aag act cgt gag ctc tct att ctc
152
Lys Arg Arg Thr Gly Leu Ile Lys Lys Thr Arg Glu Leu Ser Ile Leu
            25   30   35

tgt gac gct cac atc ggt ctc atc gtc ttc tca gcc acc gga aag ctt
200
Cys Asp Ala His Ile Gly Leu Ile Val Phe Ser Ala Thr Gly Lys Leu
        40   45   50

```
tcc gag ttc tgc tcc gaa cag aac agg atg cct caa ctc att gac cga
248
Ser Glu Phe Cys Ser Glu Gln Asn Arg Met Pro Gln Leu Ile Asp Arg
55                  60              65                  70

tac ttg cat acc aac gga ttg cga ctt cct gat cat cat gac gac cag
296
Tyr Leu His Thr Asn Gly Leu Arg Leu Pro Asp His His Asp Asp Gln
                75              80                  85

gag caa ttg cac cat gag atg gaa cta cta aga aga gag aca tgt aac
344
Glu Gln Leu His His Glu Met Glu Leu Leu Arg Arg Glu Thr Cys Asn
            90              95                  100

ctt gag ctt cgt ctg cgt cca ttc cat gga cat gac tta gcc tcc att
392
Leu Glu Leu Arg Leu Arg Pro Phe His Gly His Asp Leu Ala Ser Ile
        105             110                 115

cct cct aat gag ctt gac gga ctc gag aga cag cta gaa cat tct gtc
440
Pro Pro Asn Glu Leu Asp Gly Leu Glu Arg Gln Leu Glu His Ser Val
        120             125                 130

ctc aaa gtc cgt gag cgt aag agg agg atg cta gaa gaa gat aac aac
488
Leu Lys Val Arg Glu Arg Lys Arg Arg Met Leu Glu Glu Asp Asn Asn
135                 140             145                 150

aac atg tac cgt tgg ctt cat gag cat cgt gca gcg atg gag ttt caa
536
Asn Met Tyr Arg Trp Leu His Glu His Arg Ala Ala Met Glu Phe Gln
                155             160                 165

caa gct ggg ata gat acc aaa cca ggg gag tat caa cag ttt ata gag
584
Gln Ala Gly Ile Asp Thr Lys Pro Gly Glu Tyr Gln Gln Phe Ile Glu
                170             175                 180

cag ctt cag tgc tat aaa cca ggg gag tat cag cag ttt cta gag cag
632
Gln Leu Gln Cys Tyr Lys Pro Gly Glu Tyr Gln Gln Phe Leu Glu Gln
            185             190                 195

cag caa caa caa cca aac agc gtt ctt cag ctt gct aca ctt cct tct
680
Gln Gln Gln Gln Pro Asn Ser Val Leu Gln Leu Ala Thr Leu Pro Ser
        200             205             210

gag att gat cct act tac aat ctc cag ctt gct cag cct aat ctt caa
728
Glu Ile Asp Pro Thr Tyr Asn Leu Gln Leu Ala Gln Pro Asn Leu Gln
215                 220             225                 230

aac gat cca acg gcc cag aat gat taa tacaattctc aatagatatc
775
Asn Asp Pro Thr Ala Gln Asn Asp
                235
```

tactctttct ttatggagac agattcatga acttttatta cctatatttt gataagccag
835

tgtcttcttt tgtgtggcta tggaaacctt gtttaaagca caatgcactt gagttcttgg
895

ttatataatt aatcatcatt attacataaa aaaaaaaaaa aaaaaaaa
944

<210> 8 <211> 238 <212> PRT <213> Arabidopsis thaliana <400> 8

Met Gly Arg Gly Lys Ile Glu Ile Lys Lys Ile Glu Asn Gln Thr Ala
1   5   10   15

Arg Gln Val Thr Phe Ser Lys Arg Arg Thr Gly Leu Ile Lys Lys Thr
            20   25   30

Arg Glu Leu Ser Ile Leu Cys Asp Ala His Ile Gly Leu Ile Val Phe
            35   40   45

Ser Ala Thr Gly Lys Leu Ser Glu Phe Cys Ser Glu Gln Asn Arg Met
    50   55   60

Pro Gln Leu Ile Asp Arg Tyr Leu His Thr Asn Gly Leu Arg Leu Pro
65   70   75   80

Asp His His Asp Asp Gln Glu Gln Leu His His Glu Met Glu Leu Leu
                85   90   95

Arg Arg Glu Thr Cys Asn Leu Glu Leu Arg Leu Arg Pro Phe His Gly
            100   105   110

His Asp Leu Ala Ser Ile Pro Pro Asn Glu Leu Asp Gly Leu Glu Arg
        115   120   125

Gln Leu Glu His Ser Val Leu Lys Val Arg Glu Arg Lys Arg Arg Met
    130   135   140

Leu Glu Glu Asp Asn Asn Asn Met Tyr Arg Trp Leu His Glu His Arg
145   150   155   160

Ala Ala Met Glu Phe Gln Gln Ala Gly Ile Asp Thr Lys Pro Gly Glu
                165   170   175

Tyr Gln Gln Phe Ile Glu Gln Leu Gln Cys Tyr Lys Pro Gly Glu Tyr
            180   185   190

Gln Gln Phe Leu Glu Gln Gln Gln Gln Gln Pro Asn Ser Val Leu Gln

10

```
          195                    200                    205


       Leu Ala Thr Leu Pro Ser Glu Ile Asp Pro Thr Tyr Asn Leu Gln Leu
          210                    215                    220


       Ala Gln Pro Asn Leu Gln Asn Asp Pro Thr Ala Gln Asn Asp
       225                    230                    235


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<221>  CDS <222>  (429)..(2135) <223>  G175

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atttctaaaa atagttaaac tgttggtgat ttttgtggaa ctgattaatt aacacaattg
60

gagaaaacaa attgaaactt ttttgtttgt tagagagtta aggagaaatt ttatctaacc
120

aagctgtgta aatctcttgt agtttttctg ccgatataca ttttcattgt gttgagggta
180

aacgataatc aagaacgaga gagagagaga gcaagagcaa agatttcta ctacagaaga
240

tttattatat tgatcatttt gtgtgatcaa cccataaaaa cagagagaca tagacaagtc
300

catgtttcga tgtttcgatc tctcttactg tctaaacggc gaaataaaaa gtctgatggg
360

tgtcacttat tgcatgtata ttagtaaatc agcttgagcc caagttaaag ctgaaacttg
420

ggtttgca atg gct ggt att gat aat aaa gct gct gta atg gga gaa tgg
470
         Met Ala Gly Ile Asp Asn Lys Ala Ala Val Met Gly Glu Trp
           1               5                    10

ttc gac tgt agt act act aac cac agg aag aga tcg aaa gcg gaa ctt
518
Phe Asp Cys Ser Thr Thr Asn His Arg Lys Arg Ser Lys Ala Glu Leu
15                  20                  25                  30

ggt aga gag ttt tct tta aat tac atc aag aat gag gat tct ttg caa
566
Gly Arg Glu Phe Ser Leu Asn Tyr Ile Lys Asn Glu Asp Ser Leu Gln
                35                  40                  45

acc acc ttt caa gaa agt tca cga gga gct ctt cgt gaa agg att gct
614
Thr Thr Phe Gln Glu Ser Ser Arg Gly Ala Leu Arg Glu Arg Ile Ala
            50                  55                  60

gcg aga tcc ggg ttt aat gca ccg tgg tta aac act gag gat att ctt
662
Ala Arg Ser Gly Phe Asn Ala Pro Trp Leu Asn Thr Glu Asp Ile Leu
        65                  70                  75
```

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cag tcg aaa tct tta acc atc tct tct cct ggt ctt agt cct gca act
710
Gln Ser Lys Ser Leu Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr
    80                  85                  90

ctg tta gag tct cct gtt ttc ctc tca aac cct ttg cta tct cca aca
758
Leu Leu Glu Ser Pro Val Phe Leu Ser Asn Pro Leu Leu Ser Pro Thr
95                  100                 105                 110

acc ggg aag ctc tca tca gta cct tct gat aag gct aaa gct gag tta
806
Thr Gly Lys Leu Ser Ser Val Pro Ser Asp Lys Ala Lys Ala Glu Leu
            115                 120                 125

ttt gac gac att acc aca tcc tta gcc ttc caa acc att tca gga agt
854
Phe Asp Asp Ile Thr Thr Ser Leu Ala Phe Gln Thr Ile Ser Gly Ser
            130                 135                 140

ggc ctt gat cct act aac atc gct tta gaa ccc gat gat tcc caa gac
902
Gly Leu Asp Pro Thr Asn Ile Ala Leu Glu Pro Asp Asp Ser Gln Asp
        145                 150     -           155

tat gaa gaa aga cag ctc ggc ggt tta gga gac tcg atg gct tgt tgt
950
Tyr Glu Glu Arg Gln Leu Gly Gly Leu Gly Asp Ser Met Ala Cys Cys
    160                 165                 170

gca cct gca gat gat gga tac aac tgg aga aaa tat gga caa aag cta
998
Ala Pro Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu
175                 180                 185                 190

gtt aaa gga agt gag tat ccg cgg agc tat tac aag tgc acg cac ccg
1046
Val Lys Gly Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro
            195                 200                 205

aat tgt gag gcc aag aag aag gtt gaa cgg tct cgg gaa ggt cat att
1094
Asn Cys Glu Ala Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile
            210                 215                 220

ata gag atc ata tac aca gga gat cat ata cac agc aaa cct cca cct
1142
Ile Glu Ile Ile Tyr Thr Gly Asp His Ile His Ser Lys Pro Pro Pro
            225                 230                 235

aac cgc cgg tca ggg att gga tca tcc ggt act ggc caa gac atg caa
1190
Asn Arg Arg Ser Gly Ile Gly Ser Ser Gly Thr Gly Gln Asp Met Gln
    240                 245                 250

ata gat gca acc gaa tac gaa ggt ttt gct gga acc aat gag aac ata
1238
Ile Asp Ala Thr Glu Tyr Glu Gly Phe Ala Gly Thr Asn Glu Asn Ile
255                 260                 265                 270
```

12

gaa tgg aca tca cct gta tct gca gag ctc gaa tac gga agc cat tca
1286
Glu Trp Thr Ser Pro Val Ser Ala Glu Leu Glu Tyr Gly Ser His Ser
                275   280   285

gga tca atg cag gtt caa aac ggg act cat cag ttc ggg tat ggt gat
1334
Gly Ser Met Gln Val Gln Asn Gly Thr His Gln Phe Gly Tyr Gly Asp
            290   295   300

gca gca gct gat gcc tta tat aga gat gaa aac gaa gat gat cgc acg
1382
Ala Ala Ala Asp Ala Leu Tyr Arg Asp Glu Asn Glu Asp Asp Arg Thr
            305   310   315

tcc cac atg agt gtt tcc ctg act tac gat gga gag gta gaa gag tcc
1430
Ser His Met Ser Val Ser Leu Thr Tyr Asp Gly Glu Val Glu Glu Ser
        320   325   330

gaa tca aag aga agg aaa cta gaa gct tat gca aca gaa acg agt gga
1478
Glu Ser Lys Arg Arg Lys Leu Glu Ala Tyr Ala Thr Glu Thr Ser Gly
335   340   345   350

tca acc aga gcc agc cgt gag cca aga gtt gtg gtg cag acc aca agt
1526
Ser Thr Arg Ala Ser Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser
            355   360   365

gac att gac atc ctc gat gat ggt tat cgc tgg cgc aag tat ggg caa
1574
Asp Ile Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln
            370   375   380

aaa gtc gtt aaa gga aac ccg aat cca agg agc tac tat aaa tgc aca
1622
Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr
            385   390   395

gct aat gga tgt acc gta acg aag cat gta gag aga gcc tct gat gac
1670
Ala Asn Gly Cys Thr Val Thr Lys His Val Glu Arg Ala Ser Asp Asp
        400   405   410

ttc aag agc gta cta aca act tat ata ggc aag cac acc cac gtt gta
1718
Phe Lys Ser Val Leu Thr Thr Tyr Ile Gly Lys His Thr His Val Val
415   420   425   430

cca gca gca cgc aac agc agc cac gtc ggt gca ggc agt tca ggg act
1766
Pro Ala Ala Arg Asn Ser Ser His Val Gly Ala Gly Ser Ser Gly Thr
                435   440   445

ctc caa ggc agt tta gcg act cag acc cac aac cac aat gtg cac tat
1814
Leu Gln Gly Ser Leu Ala Thr Gln Thr His Asn His Asn Val His Tyr
                450   455   460

```
cca atg cca cac agt aga tct gag gga ctg gcc aca gcc aac tca tct
1862
Pro Met Pro His Ser Arg Ser Glu Gly Leu Ala Thr Ala Asn Ser Ser
        465             470             475

cta ttt gac ttc cag tca cac ctg agg cat cct aca ggt ttc tcc gtt
1910
Leu Phe Asp Phe Gln Ser His Leu Arg His Pro Thr Gly Phe Ser Val
    480             485             490

tac ata ggc caa tct gag ctt tct gat ctt tca atg cct ggt cta act
1958
Tyr Ile Gly Gln Ser Glu Leu Ser Asp Leu Ser Met Pro Gly Leu Thr
495             500             505             510

att ggg caa gag aag ctt acc agc ctg cag gcg cct gac att ggg gat
2006
Ile Gly Gln Glu Lys Leu Thr Ser Leu Gln Ala Pro Asp Ile Gly Asp
            515             520             525

cca act ggc cta atg ttg cag tta gca gca cag ccg aag gtg gaa cca
2054
Pro Thr Gly Leu Met Leu Gln Leu Ala Ala Gln Pro Lys Val Glu Pro
            530             535             540

gtg tca cca caa cag gga ctt gat ttg tca gcg agc tca ttg ata tgc
2102
Val Ser Pro Gln Gln Gly Leu Asp Leu Ser Ala Ser Ser Leu Ile Cys
            545             550             555

aga gag atg ttg agt aga tta cga cag ata tga aacaaatctc tttgttcact
2155
Arg Glu Met Leu Ser Arg Leu Arg Gln Ile
        560             565

gattgctcaa atttttgaat aaatgaaaaa ttgagaaaaa aaaaaaaaaa aaaaaaaaaa
2215


<210> 10 <211> 568 <212> PRT <213> Arabidopsis thaliana <400>
10

Met Ala Gly Ile Asp Asn Lys Ala Ala Val Met Gly Glu Trp Phe Asp
1               5               10              15


Cys Ser Thr Thr Asn His Arg Lys Arg Ser Lys Ala Glu Leu Gly Arg
            20              25              30


Glu Phe Ser Leu Asn Tyr Ile Lys Asn Glu Asp Ser Leu Gln Thr Thr
        35              40              45


Phe Gln Glu Ser Ser Arg Gly Ala Leu Arg Glu Arg Ile Ala Ala Arg
    50              55              60


Ser Gly Phe Asn Ala Pro Trp Leu Asn Thr Glu Asp Ile Leu Gln Ser
65              70              75              80
```

Lys Ser Leu Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr Leu Leu
                    85   90   95

Glu Ser Pro Val Phe Leu Ser Asn Pro Leu Leu Ser Pro Thr Thr Gly
            100   105   110

Lys Leu Ser Ser Val Pro Ser Asp Lys Ala Lys Ala Glu Leu Phe Asp
        115   ·120   125

Asp Ile Thr Thr Ser Leu Ala Phe Gln Thr Ile Ser Gly Ser Gly Leu
    130   135   140

Asp Pro Thr Asn Ile Ala Leu Glu Pro Asp Asp Ser Gln Asp Tyr Glu
145   150   155   160

Glu Arg Gln Leu Gly Gly Leu Gly Asp Ser Met Ala Cys Cys Ala Pro
            165   170   175

Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu Val Lys
            180   185   190

Gly Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro Asn Cys
        195   200   205

Glu Ala Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile Ile Glu
    210   215   220

Ile Ile Tyr Thr Gly Asp His Ile His Ser Lys Pro Pro Pro Asn Arg
225   230   235   240

Arg Ser Gly Ile Gly Ser Ser Gly Thr Gly Gln Asp Met Gln Ile Asp
            245   250   255

Ala Thr Glu Tyr Glu Gly Phe Ala Gly Thr Asn Glu Asn Ile Glu Trp
            260   265   270

Thr Ser Pro Val Ser Ala Glu Leu Glu Tyr Gly Ser His Ser Gly Ser
        275   280   285

Met Gln Val Gln Asn Gly Thr His Gln Phe Gly Tyr Gly Asp Ala Ala
        290   295   300

Ala Asp Ala Leu Tyr Arg Asp Glu Asn Glu Asp Asp Arg Thr Ser His
305   310   315   · 320

15

Met Ser Val Ser Leu Thr Tyr Asp Gly Glu Val Glu Glu Ser Glu Ser
                325   330   335

Lys Arg Arg Lys Leu Glu Ala Tyr Ala Thr Glu Thr Ser Gly Ser Thr
                340   345   350

Arg Ala Ser Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser Asp Ile
                355   360   365

Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val
    370   375   380

Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Ala Asn
385   390   395   400

Gly Cys Thr Val Thr Lys His Val Glu Arg Ala Ser Asp Asp Phe Lys
                405   410   415

Ser Val Leu Thr Thr Tyr Ile Gly Lys His Thr His Val Val Pro Ala
                420   425   430

Ala Arg Asn Ser Ser His Val Gly Ala Gly Ser Ser Gly Thr Leu Gln
                435   440   445

Gly Ser Leu Ala Thr Gln Thr His Asn His Asn Val His Tyr Pro Met
    450   455   460

Pro His Ser Arg Ser Glu Gly Leu Ala Thr Ala Asn Ser Ser Leu Phe
465   470   475   480

Asp Phe Gln Ser His Leu Arg His Pro Thr Gly Phe Ser Val Tyr Ile
                485   490   495

Gly Gln Ser Glu Leu Ser Asp Leu Ser Met Pro Gly Leu Thr Ile Gly
                500   505   510

Gln Glu Lys Leu Thr Ser Leu Gln Ala Pro Asp Ile Gly Asp Pro Thr
    515   520   525

Gly Leu Met Leu Gln Leu Ala Ala Gln Pro Lys Val Glu Pro Val Ser
    530   535   540

Pro Gln Gln Gly Leu Asp Leu Ser Ala Ser Ser Leu Ile Cys Arg Glu
545   550   555   560

Met Leu Ser Arg Leu Arg Gln Ile

16

565

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                                    1               5
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cgg aat tac atc tcc ggc gtc gga gct gat agc ttc gcc gtt caa gaa
102
Arg Asn Tyr Ile Ser Gly Val Gly Ala Asp Ser Phe Ala Val Gln Glu
        10   15   20

gca gct gct tca gga ctc aaa agt atc gaa aat ttc atc ggt tta atg
150
Ala Ala Ala Ser Gly Leu Lys Ser Ile Glu Asn Phe Ile Gly Leu Met
    25   30   35

tct cgt gat agc ttt aac tct gat cag cca tct tct tct tcc gcc tcc
198
Ser Arg Asp Ser Phe Asn Ser Asp Gln Pro Ser Ser Ser Ser Ala Ser
40   45   50   55

gcc tcc gcc tcc gcc gcc gca gat ctt gaa tca gct cgt aac aca acg
246
Ala Ser Ala Ser Ala Ala Ala Asp Leu Glu Ser Ala Arg Asn Thr Thr
                60   65   70

gcg gac gcg gct gtt tca aag ttt aaa aga gtc ata tct ctc tta gat
294
Ala Asp Ala Ala Val Ser Lys Phe Lys Arg Val Ile Ser Leu Leu Asp
            75   80   85

cga act cga acc gga cac gcc cgg ttt aga cgt gct ccg gtt cat gtt
342
Arg Thr Arg Thr Gly His Ala Arg Phe Arg Arg Ala Pro Val His Val
            90   95   100

att tct ccg gtt ctt tta caa gaa gaa cca aaa acg acg ccg ttt cag
390
Ile Ser Pro Val Leu Leu Gln Glu Glu Pro Lys Thr Thr Pro Phe Gln
        105   110   115

tct cct ctt cct cct ccg ccg caa atg atc cga aaa ggt tcg ttt tct
438
Ser Pro Leu Pro Pro Pro Pro Gln Met Ile Arg Lys Gly Ser Phe Ser
120   125   130   135

tca tcg atg aaa acg att gat ttc tca tct ctc tcc tct gta aca acg
486
Ser Ser Met Lys Thr Ile Asp Phe Ser Ser Leu Ser Ser Val Thr Thr
            140   145   150

gaa tca gac aac cag aag aag att cat cat cat caa cgt ccc tct gaa
534
Glu Ser Asp Asn Gln Lys Lys Ile His His His Gln Arg Pro Ser Glu
            155   160   165

17

```
acg gcg ccg ttt gcg tct caa act caa agc ctc tcc acg acg gtc tcg
582
Thr Ala Pro Phe Ala Ser Gln Thr Gln Ser Leu Ser Thr Thr Val Ser
        170                 175                 180

tct ttc tca aaa tca aca aag aga aaa tgt aac tct gag aat ctt ctc
630
Ser Phe Ser Lys Ser Thr Lys Arg Lys Cys Asn Ser Glu Asn Leu Leu
        185                 190                 195

acc gga aaa tgc gct tcc gct tct tcc tcc ggt cgt tgt cat tgc tcg
678
Thr Gly Lys Cys Ala Ser Ala Ser Ser Ser Gly Arg Cys His Cys Ser
200                 205                 210                 215

aag aaa aga aag ata aaa cag agg aga ata att agg gtt ccg gcg ata
726
Lys Lys Arg Lys Ile Lys Gln Arg Arg Ile Ile Arg Val Pro Ala Ile
                220                 225                 230

agt gca aaa atg tcc gat gta cca ccg gac gat tat tca tgg agg aaa
774
Ser Ala Lys Met Ser Asp Val Pro Pro Asp Asp Tyr Ser Trp Arg Lys
            235                 240                 245

tac gga caa aaa cca att aaa gga tct cca cat cca aga gga tat tat
822
Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr
        250                 255                 260

aag tgt agt agc gta aga ggt tgt cca gca cgt aaa cat gtt gag aga
870
Lys Cys Ser Ser Val Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg
        265                 270                 275

gca gct gat gat tcg tcc atg ttg att gtt act tat gaa gga gat cat
918
Ala Ala Asp Asp Ser Ser Met Leu Ile Val Thr Tyr Glu Gly Asp His
280                 285                 290                 295

aat cat tct ctc tcc gcc gct gat ctc gcc gga gcc gcc gtt gct gat
966
Asn His Ser Leu Ser Ala Ala Asp Leu Ala Gly Ala Ala Val Ala Asp
                300                 305                 310

ctt att ttg gaa tcg tct tga aaagaacaaa tctttattta aggcttttat
1017
Leu Ile Leu Glu Ser Ser
                315

aatataaatt tagatcctta cttagtgaag tactcaaact atgaatgaaa tcaatgtaat
1077

caaaatcaaa aagcttttgc taaaaaaaaa aaaaaaa
1115


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12
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Met Ala Val Glu Leu Met Thr Arg Asn Tyr Ile Ser Gly Val Gly Ala
1               5                   10              15

Asp Ser Phe Ala Val Gln Glu Ala Ala Ala Ser Gly Leu Lys Ser Ile
            20              25              30

Glu Asn Phe Ile Gly Leu Met Ser Arg Asp Ser Phe Asn Ser Asp Gln
        35              40              45

Pro Ser Ser Ser Ser Ala Ser Ala Ser Ala Ser Ala Ala Ala Asp Leu
    50              55              60

Glu Ser Ala Arg Asn Thr Thr Ala Asp Ala Ala Val Ser Lys Phe Lys
65              70              75              80

Arg Val Ile Ser Leu Leu Asp Arg Thr Arg Thr Gly His Ala Arg Phe
            85              90              95

Arg Arg Ala Pro Val His Val Ile Ser Pro Val Leu Leu Gln Glu Glu
            100             105             110

Pro Lys Thr Thr Pro Phe Gln Ser Pro Leu Pro Pro Pro Gln Met
        115             120             125

Ile Arg Lys Gly Ser Phe Ser Ser Ser Met Lys Thr Ile Asp Phe Ser
    130             135             140

Ser Leu Ser Ser Val Thr Thr Glu Ser Asp Asn Gln Lys Lys Ile His
145             150             155             160

His His Gln Arg Pro Ser Glu Thr Ala Pro Phe Ala Ser Gln Thr Gln
            165             170             175

Ser Leu Ser Thr Thr Val Ser Ser Phe Ser Lys Ser Thr Lys Arg Lys
            180             185             190

Cys Asn Ser Glu Asn Leu Leu Thr Gly Lys Cys Ala Ser Ala Ser Ser
        195             200             205

Ser Gly Arg Cys His Cys Ser Lys Lys Arg Lys Ile Lys Gln Arg Arg
    210             215             220

Ile Ile Arg Val Pro Ala Ile Ser Ala Lys Met Ser Asp Val Pro Pro
225             230             235             240

Asp Asp Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser
```

                        245   250   255

Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Ser Val Arg Gly Cys Pro
            260   265   270

Ala Arg Lys His Val Glu Arg Ala Ala Asp Asp Ser Ser Met Leu Ile
        275   280   285

Val Thr Tyr Glu Gly Asp His Asn His Ser Leu Ser Ala Ala Asp Leu
    290   295   300

Ala Gly Ala Ala Val Ala Asp Leu Ile Leu Glu Ser Ser
305   310   315

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60

aagttttaga ataatccgat aaaatacttt tatattaatt ttctttggt cc atg gag
118
                                                              Met Glu
                                                               1

ggt tcg tcc aaa ggg ttg agg aaa ggt gca tgg act gct gaa gaa gat
166
Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu Glu Asp
            5   10   15

agt ctc ttg agg cta tgt att gat aag tat gga gaa ggc aaa tgg cat
214
Ser Leu Leu Arg Leu Cys Ile Asp Lys Tyr Gly Glu Gly Lys Trp His
    20   25   30

caa gtt cct ttg aga gct ggg cta aat cga tgc aga aag agt tgt aga
262
Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser Cys Arg
35   40   45   50

cta aga tgg ttg aac tat ttg aag cca agt atc aag aga gga aga ctt
310
Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly Arg Leu
                55   60   65

agc aat gat gaa gtt gat ctt ctt ctt cgc ctt cat aag ctt cta gga
358
Ser Asn Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu Leu Gly
                70   75   80

aat agg tgg tcc ttg att gct ggt cga ttg cct ggt cgg acc gct aat
406
Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr Ala Asn
            85   90   95

```
gat gtc aaa aat tac tgg aac acc cat ctg agt aaa aaa cat gag tct
454
Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His Glu Ser
    100                 105                 110

tcg tgt tgt aag tct aaa atg aaa aag aaa aac att att tcc cct cct
502
Ser Cys Cys Lys Ser Lys Met Lys Lys Lys Asn Ile Ile Ser Pro Pro
·115                120                 125·                 130

aca aca ccg gtc caa aaa atc ggt gtt ttt aag cct cga cct cga tcc
550
Thr Thr Pro Val Gln Lys Ile Gly Val Phe Lys Pro Arg Pro Arg Ser
                135                 140                 145

ttc tct gtt aac aat ggt tgc agc cat ctc aat ggt ctg cca gaa gtt
598
Phe Ser Val Asn Asn Gly Cys Ser His Leu Asn Gly Leu Pro Glu Val
                150                 155                 160

gat tta att cct tca tgc ctt gga ctc aag aaa aat aat gtt tgt gaa
646
Asp Leu Ile Pro Ser Cys Leu Gly Leu Lys Lys Asn Asn Val Cys Glu
            165                 170                 175

aat agt atc aca tgt aac aaa gat gat gag aaa gat gat ttt gtg aat
694
Asn Ser Ile Thr Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe Val Asn
    180                 185                 190

aat cta atg aat gga gat aat atg tgg ttg gag aat tta ctg ggg gaa
742
Asn Leu Met Asn Gly Asp Asn Met Trp Leu Glu Asn Leu Leu Gly Glu
195                 200                 205                 210

aac caa gaa gct gat gcg att gtt cct gaa gcg acg aca gct gaa cat
790
Asn Gln Glu Ala Asp Ala Ile Val Pro Glu Ala Thr Thr Ala Glu His
                215                 220                 225

ggg gcc act ttg gcg ttt gac gtt gag caa ctt tgg agt ctg ttt gat
838
Gly Ala Thr Leu Ala Phe Asp Val Glu Gln Leu Trp Ser Leu Phe Asp
                230                 235                 240

gga gag act gtt gaa ctt gat tag tgtttctcac cgtttgttta agattgtggg
892
Gly Glu Thr Val Glu Leu Asp
            245

tggcttttct ttcgtatttt agtaatgtat ttttctgtat gaagtaaaga atttcagcat
952

tttaagaaaa atggttatgt ttctacgtaa taaaaaaaaa cgttatttat aaaaaaaaaa
1012

aaaaaaaaaa aaaaaaaaaa a
1033
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21

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14

Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu
1   5   10   15

Glu Asp Ser Leu Leu Arg Leu Cys Ile Asp Lys Tyr Gly Glu Gly Lys
            20   25   30

Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
        35   40   45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
    50   55   60

Arg Leu Ser Asn Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
65   70   75   80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
                85   90   95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
            100   105   110

Glu Ser Ser Cys Cys Lys Ser Lys Met Lys Lys Lys Asn Ile Ile Ser
        115   120   125

Pro Pro Thr Thr Pro Val Gln Lys Ile Gly Val Phe Lys Pro Arg Pro
    130   135   140

Arg Ser Phe Ser Val Asn Asn Gly Cys Ser His Leu Asn Gly Leu Pro
145   150   155   160

Glu Val Asp Leu Ile Pro Ser Cys Leu Gly Leu Lys Lys Asn Asn Val
                165   170   175

Cys Glu Asn Ser Ile Thr Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe
            180   185   190

Val Asn Asn Leu Met Asn Gly Asp Asn Met Trp Leu Glu Asn Leu Leu
        195   200   205

Gly Glu Asn Gln Glu Ala Asp Ala Ile Val Pro Glu Ala Thr Thr Ala
    210   215   220

Glu His Gly Ala Thr Leu Ala Phe Asp Val Glu Gln Leu Trp Ser Leu
225   230   235   240

```
Phe Asp Gly Glu Thr Val Glu Leu Asp
                245
```

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cacaacacaa acacatttct gttttctcca ttgtttcaaa ccataaaaaa aaacacagat
60
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taa atg gaa tcg agt agc gtt gat gag agt act aca agt aca ggt tcc
108
    Met Glu Ser Ser Ser Val Asp Glu Ser Thr Thr Ser Thr Gly Ser
    1               5                   10                  15
```

```
atc tgt gaa acc ccg gcg ata act ccg gcg aaa aag tcg tcg gta ggt
156
Ile Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly
            20                  25                  30
```

```
aac tta tac agg atg gga agc gga tca agc gtt gtg tta gat tca gag
204
Asn Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu
        35                  40                  45
```

```
aac ggc gta gaa gct gaa tct agg aag ctt ccg tcg tca aaa tac aaa
252
Asn Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys
        50                  55                  60
```

```
ggt gtg gtg cca caa cca aac gga aga tgg gga gct cag att tac gag
300
Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu
    65                  70                  75
```

```
aaa cac cag cgc gtg tgg ctc ggg aca ttc aac gaa gaa gac gaa gcc
348
Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala
80                  85                  90                  95
```

```
gct cgt gcc tac gac gtc gcg gtt cac agg ttc cgt cgc cgt gac gcc
396
Ala Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala
            100                 105                 110
```

```
gtc aca aat ttc aaa gac gtg aag atg gac gaa gac gag gtc gat ttc
444
Val Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe
            115                 120                 125
```

```
ttg aat tct cat tcg aaa tct gag atc gtt gat atg ttg agg aaa cat
492
Leu Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His
        130                 135                 140
```

```
act tat aac gaa gag tta gag cag agt aaa cgg cgt cgt aat ggt aac
540
Thr Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn
```

```
        145                    150                    155

gga aac atg act agg acg ttg tta acg tcg ggg ttg agt aat gat ggt
588
Gly Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly
160                165                170                175

gtt tct acg acg ggg ttt aga tcg gcg gag gca ctg ttt gag aaa gcg
636
Val Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala
              180                185                190

gta acg cca agc gac gtt ggg aag cta aac cgt ttg gtt ata ccg aaa
684
Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys
          195                200                205

cat cac gca gag aaa cat ttt ccg tta ccg tca agt aac gtt tcc gtg
732
His His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val
          210                215                220

aaa gga gtg ttg ttg aac ttt gag gac gtt aac ggg aaa gtg tgg agg
780
Lys Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg
      225                230                235

ttc cgt tac tcg tat tgg aac agt agt cag agt tat gtt ttg act aaa
828
Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
240                245                250                255

ggt tgg agc agg ttc gtt aag gag aag aat cta cgt gct ggt gac gtg
876
Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val
              260                265                270

gtt agt ttc agt aga tct aac ggt cag gat caa cag ttg tac att ggg
924
Val Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly
              275                280                285

tgg aag tcg aga tcc ggg tca gat tta gat gcg ggt cgg gtt ttg aga
972
Trp Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg
          290                295                300

ttg ttc gga gtt aac att tca ccg gag agt tca aga aac gac gtc gta
1020
Leu Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val
          305                310                315

gga aac aaa aga gtg aac gat act gag atg tta tcg ttg gtg tgt agc
1068
Gly Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser
320                325                330                335

aag aag caa cgc atc ttt cac gcc tcg taa caactcttct tctttttttt
1118
Lys Lys Gln Arg Ile Phe His Ala Ser
              340
```

tcttttgttg ttttaataat ttttaaaaac tccattttcg ttttctttat ttgcatcggt
1178

ttctttcttc ttgtttacca aaggttcatg agttgttttt gttgtattga tgaactgtaa
1238

attttattta taggataaat tttaaaaaaa aaaaaaaaaa aaa
1281

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Met Glu Ser Ser Ser Val Asp Glu Ser Thr Thr Ser Thr Gly Ser Ile
1   5   10   15

Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly Asn
            20   25   30

Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu Asn
        35   40   45

Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly
    50   55   60

Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
65   70   75   80

His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
                85   90   95

Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala Val
            100   105   110

Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe Leu
            115   120   125

Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr
    130   135   140

Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn Gly
145   150   155   160

Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly Val
                165   170   175

Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala Val
            180   185   190

```
Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His
      ·195                 200                 205

His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val Lys
    210                 215                 220

Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe
225                 230                 235                 240

Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
            245                 250                 255

Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val
            260                 265                 270

Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly Trp
      275                 280                 285

Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg Leu
    290                 295                 300

Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val Gly
305                 310                 315                 320

Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser Lys
            325                 330                 335

Lys Gln Arg Ile Phe His Ala Ser
            340
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60

agttgtaaag ttttgatttt tttttctggg tttttttctgt gagacccaga agaagaacag
120

agagaggaag aaggagaaga aaaaaatatc tctttctctc cggctttcaa caaaatctct
180

cttttttcct tcatcagtgt taaattcgga tccgggtcgg gtgggttttc ggtttttggt
240

gttcggatca gagcacagtt ggatgttagc gacggaactg aggatttcag tttgcggctg
300
```

```
cggcggctgt gacggtgttt gtgtgtcgtc ttcttttatc aatcaggagt ttcatcacag
360

tttgatcaga gattcagcca aattcttgga tactaa atg gct ggt ttt gat gaa
414
                                        Met Ala Gly Phe Asp Glu
                                        1             5

aat gtt gct gtg atg gga gaa tgg gtg cct cgt agt cct agt ccc ggg
462
Asn Val Ala Val Met Gly Glu Trp Val Pro Arg Ser Pro Ser Pro Gly
        10              15                  20

aca ctt ttc tcc tct gct att gga gaa gag aag agc tcg aaa cgt gtt
510
Thr Leu Phe Ser Ser Ala Ile Gly Glu Glu Lys Ser Ser Lys Arg Val
        25              30                  35

ctt gaa aga gag tta tct ttg aat cat ggt caa gtt att ggt tta gaa
558
Leu Glu Arg Glu Leu Ser Leu Asn His Gly Gln Val Ile Gly Leu Glu
    40              45                  50

gaa gac act agt agt aat cat aac aag gat tct tca caa agc aat gtt
606
Glu Asp Thr Ser Ser Asn His Asn Lys Asp Ser Ser Gln Ser Asn Val
55              60                  65                  70

ttt cga ggt ggt ctc agt gaa aga att gct gca aga gct gga ttt aat
654
Phe Arg Gly Gly Leu Ser Glu Arg Ile Ala Ala Arg Ala Gly Phe Asn
            75                  80                  85

gct cca agg ttg aac act gag aat atc cgc acc aac acc gac ttt tcc
702
Ala Pro Arg Leu Asn Thr Glu Asn Ile Arg Thr Asn Thr Asp Phe Ser
            90                  95                  100

att gac tct aac ctt cga tct cct tgc tta acc atc tct tct cct ggc
750
Ile Asp Ser Asn Leu Arg Ser Pro Cys Leu Thr Ile Ser Ser Pro Gly
        105                 110                 115

ctt agc cct gca aca ctc ttg gaa tct cct gtt ttc ctt tct aac cca
798
Leu Ser Pro Ala Thr Leu Leu Glu Ser Pro Val Phe Leu Ser Asn Pro
    120                 125                 130

ttg gct caa cct tct cca act acc ggg aaa ttt cca ttt ctt cct ggt
846
Leu Ala Gln Pro Ser Pro Thr Thr Gly Lys Phe Pro Phe Leu Pro Gly
135                 140                 145                 150

gtt aat ggt aat gca ttg tct tct gag aaa gcg aaa gac gag ttc ttt
894
Val Asn Gly Asn Ala Leu Ser Ser Glu Lys Ala Lys Asp Glu Phe Phe
            155                 160                 165

gat gat att gga gca tca ttc agc ttc cat cct gtt tca aga tca tct
942
Asp Asp Ile Gly Ala Ser Phe Ser Phe His Pro Val Ser Arg Ser Ser
```

```
          170                    175                    180
tcc tct ttc ttc caa ggc aca aca gag atg atg tca gtt gat tat ggt
990
Ser Ser Phe Phe Gln Gly Thr Thr Glu Met Met Ser Val Asp Tyr Gly
        185                    190                    195

aac tac aac aat aga tct tct tct cat caa tcc gca gaa gaa gta aaa
1038
Asn Tyr Asn Asn Arg Ser Ser Ser His Gln Ser Ala Glu Glu Val Lys
    200                    205                    210

cct ggc tct gaa aac ata gaa agc tcc aat ctt tat ggg att gaa act
1086
Pro Gly Ser Glu Asn Ile Glu Ser Ser Asn Leu Tyr Gly Ile Glu Thr
215                    220                    225                    230

gac aat caa aac ggg cag aac aag aca tct gat gtc act aca aac acc
1134
Asp Asn Gln Asn Gly Gln Asn Lys Thr Ser Asp Val Thr Thr Asn Thr
            235                    240                    245

agt ctt gaa acc gtg gat cat caa gag gaa gaa gaa gag caa aga cgc
1182
Ser Leu Glu Thr Val Asp His Gln Glu Glu Glu Glu Glu Gln Arg Arg
            250                    255                    260

ggt gat tcg atg gct ggt ggt gcg cct gca gag gat gga tat aac tgg
1230
Gly Asp Ser Met Ala Gly Gly Ala Pro Ala Glu Asp Gly Tyr Asn Trp
            265                    270                    275

agg aaa tac gga caa aag ttg gtc aaa gga agt gag tat ccg cga agc
1278
Arg Lys Tyr Gly Gln Lys Leu Val Lys Gly Ser Glu Tyr Pro Arg Ser
    280                    285                    290

tat tac aag tgc aca aac ccg aat tgt cag gtg aag aag aaa gtt gag
1326
Tyr Tyr Lys Cys Thr Asn Pro Asn Cys Gln Val Lys Lys Lys Val Glu
295                    300                    305                    310

aga tca agg gaa ggt cac atc aca gag att ata tac aaa gga gct cat
1374
Arg Ser Arg Glu Gly His Ile Thr Glu Ile Ile Tyr Lys Gly Ala His
            315                    320                    325

aat cat ctt aaa cct cca cct aat cgc cgc tca ggg atg caa gta gat
1422
Asn His Leu Lys Pro Pro Pro Asn Arg Arg Ser Gly Met Gln Val Asp
            330                    335                    340

gga act gaa caa gtt gaa caa caa caa caa cag aga gat tct gct gca
1470
Gly Thr Glu Gln Val Glu Gln Gln Gln Gln Gln Arg Asp Ser Ala Ala
            345                    350                    355

acg tgg gtt agt tgt aat aac act caa caa caa ggt gga agc aat gag
1518
Thr Trp Val Ser Cys Asn Asn Thr Gln Gln Gln Gly Gly Ser Asn Glu
    360                    365                    370
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aac aat gtc gaa gag gga tct acg aga ttc gag tat gga aac caa tct
1566
Asn Asn Val Glu Glu Gly Ser Thr Arg Phe Glu Tyr Gly Asn Gln Ser
375                 380              385                 390


gga tca att caa gct caa acc gga ggt caa tac gag tca ggt gat cct
1614
Gly Ser Ile Gln Ala Gln Thr Gly Gly Gln Tyr Glu Ser Gly Asp Pro
                395              400                 405


gtg gtt gtg gtt gat gct tct tca aca ttc tct aat gat gaa gat gaa
1662
Val Val Val Val Asp Ala Ser Ser Thr Phe Ser Asn Asp Glu Asp Glu
                410              415                 420


gat gat cga ggg aca cat gga agt gtt tct ttg ggt tac gat gga gga
1710
Asp Asp Arg Gly Thr His Gly Ser Val Ser Leu Gly Tyr Asp Gly Gly
            425              430                 435


gga gga ggt ggg gga gga gaa gga gat gaa tca gag tcg aaa aga agg
1758
Gly Gly Gly Gly Gly Gly Glu Gly Asp Glu Ser Glu Ser Lys Arg Arg
    440                  445                  450


aaa cta gaa gct ttt gca gca gag atg agt gga tca aca aga gcc ata
1806
Lys Leu Glu Ala Phe Ala Ala Glu Met Ser Gly Ser Thr Arg Ala Ile
455                  460                  465                  470


cgt gag cca aga gtt gtt gtg cag aca acg agt gat gtt gac att ctt
1854
Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser Asp Val Asp Ile Leu
                475                  480                  485


gat gat ggt tat cgc tgg cga aaa tat ggt cag aaa gtt gtc aaa ggc
1902
Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys Gly
            490              495                  500


aat cca aat cca agg agt tat tac aaa tgc aca gct cca gga tgt aca
1950
Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Ala Pro Gly Cys Thr
        505              510                  515


gtg agg aaa cat gtt gaa aga gct tct cat gat ctc aaa tcc gtt ata
1998
Val Arg Lys His Val Glu Arg Ala Ser His Asp Leu Lys Ser Val Ile
    520              525                  530


aca act tac gaa ggc aaa cat aac cat gac gtc ccc gct gca cgc aac
2046
Thr Thr Tyr Glu Gly Lys His Asn His Asp Val Pro Ala Ala Arg Asn
535              540                  545                  550


agc agc cac gga ggc ggt ggt gat agt ggt aac ggt aac agc ggc ggt
2094
Ser Ser His Gly Gly Gly Gly Asp Ser Gly Asn Gly Asn Ser Gly Gly
            555                  560                  565
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tca gcc gca gtt tct cac cat tac cac aac ggt cat cac tca gag ccg
2142
Ser Ala Ala Val Ser His His Tyr His Asn Gly His His Ser Glu Pro
              570   575   580

cca cgt ggg aga ttc gac aga caa gtc aca act aac aat cag tct cct
2190
Pro Arg Gly Arg Phe Asp Arg Gln Val Thr Thr Asn Asn Gln Ser Pro
          585   590   595

ttt agc cgt ccc ttt agc ttt cag cca cat ttg ggt cct cct tct ggt
2238
Phe Ser Arg Pro Phe Ser Phe Gln Pro His Leu Gly Pro Pro Ser Gly
      600   605   610

ttc tcc ttc ggt tta gga caa acc ggt ttg gtt aat ctt tca atg cct
2286
Phe Ser Phe Gly Leu Gly Gln Thr Gly Leu Val Asn Leu Ser Met Pro
615   620   625   630

ggt tta gcg tat ggt caa ggg aaa atg ccg ggt ttg cct cac ccg tat
2334
Gly Leu Ala Tyr Gly Gln Gly Lys Met Pro Gly Leu Pro His Pro Tyr
                635   640   645

atg aca caa ccg gtt ggg atg agt gaa gca atg atg cag aga ggg atg
2382
Met Thr Gln Pro Val Gly Met Ser Glu Ala Met Met Gln Arg Gly Met
              650   655   660

gaa cca aag gtt gaa ccg gtt tca gat tca gga caa tcg gta tat aac
2430
Glu Pro Lys Val Glu Pro Val Ser Asp Ser Gly Gln Ser Val Tyr Asn
          665   670   675

cag atc atg agt aga tta cct cag att tga aatttactct tcttcttctt
2480
Gln Ile Met Ser Arg Leu Pro Gln Ile
      680   685

cttctgcatt tggtcactcc ttataataac ttttaatttc tgcttcttct tcttctttca
2540

tttattggtt tcaaactttg gggaaggtaa aggctgtttt attgttaaaa aaaaaaaaaa
2600

aaa
2603

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Arg Ser Pro Ser Pro Gly Thr Leu Phe Ser Ser Ala Ile Gly Glu Glu
              20   25   30

Lys Ser Ser Lys Arg Val Leu Glu Arg Glu Leu Ser Leu Asn His Gly
       35   40   45

Gln Val Ile Gly Leu Glu Glu Asp Thr Ser Ser Asn His Asn Lys Asp
       50   55   60

Ser Ser Gln Ser Asn Val Phe Arg Gly Gly Leu Ser Glu Arg Ile Ala
65   70   75   80

Ala Arg Ala Gly Phe Asn Ala Pro Arg Leu Asn Thr Glu Asn Ile Arg
              85   90   95

Thr Asn Thr Asp Phe Ser Ile Asp Ser Asn Leu Arg Ser Pro Cys Leu
             100   105   110

Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr Leu Leu Glu Ser Pro
         115   120   125

Val Phe Leu Ser Asn Pro Leu Ala Gln Pro Ser Pro Thr Thr Gly Lys
    130   135   140

Phe Pro Phe Leu Pro Gly Val Asn Gly Asn Ala Leu Ser Ser Glu Lys
145   150   155   160

Ala Lys Asp Glu Phe Phe Asp Asp Ile Gly Ala Ser Phe Ser Phe His
              165   170   175

Pro Val Ser Arg Ser Ser Ser Ser Phe Phe Gln Gly Thr Thr Glu Met
              180   185   190

Met Ser Val Asp Tyr Gly Asn Tyr Asn Asn Arg Ser Ser Ser His Gln
       195   200   205

Ser Ala Glu Glu Val Lys Pro Gly Ser Glu Asn Ile Glu Ser Ser Asn
    210   215   220

Leu Tyr Gly Ile Glu Thr Asp Asn Gln Asn Gly Gln Asn Lys Thr Ser
225   230   235   240

Asp Val Thr Thr Asn Thr Ser Leu Glu Thr Val Asp His Gln Glu Glu
             245   250   255

Glu Glu Glu Gln Arg Arg Gly Asp Ser Met Ala Gly Gly Ala Pro Ala
             260   265   270

Glu Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu Val Lys Gly

                275   280   285

    Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr Asn Pro Asn Cys Gln
        290   295   300

    Val Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile Thr Glu Ile
    305   310   315   320

    Ile Tyr Lys Gly Ala His Asn His Leu Lys Pro Pro Pro Asn Arg Arg
                 325   330   335

    Ser Gly Met Gln Val Asp Gly Thr Glu Gln Val Glu Gln Gln Gln Gln
                 340   345   350

    Gln Arg Asp Ser Ala Ala Thr Trp Val Ser Cys Asn Asn Thr Gln Gln
                 355   360   365

    Gln Gly Gly Ser Asn Glu Asn Asn Val Glu Glu Gly Ser Thr Arg Phe
        370   375   380

    Glu Tyr Gly Asn Gln Ser Gly Ser Ile Gln Ala Gln Thr Gly Gly Gln
    385   390   395   400

    Tyr Glu Ser Gly Asp Pro Val Val Val Val Asp Ala Ser Ser Thr Phe
                 405   410   415

    Ser Asn Asp Glu Asp Glu Asp Asp Arg Gly Thr His Gly Ser Val Ser
                 420   425   430

    Leu Gly Tyr Asp Gly Gly Gly Gly Gly Gly Gly Glu Gly Asp Glu
                 435   440   445

    Ser Glu Ser Lys Arg Arg Lys Leu Glu Ala Phe Ala Ala Glu Met Ser
        450   455   460

    Gly Ser Thr Arg Ala Ile Arg Glu Pro Arg Val Val Val Gln Thr Thr
    465   470   475   480

    Ser Asp Val Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly
                 485   490   495

    Gln Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys
                 500   505   510

    Thr Ala Pro Gly Cys Thr Val Arg Lys His Val Glu Arg Ala Ser His
                 515   520   525

32

Asp Leu Lys Ser Val Ile Thr Thr Tyr Glu Gly Lys His Asn His Asp
530   535   540

Val Pro Ala Ala Arg Asn Ser Ser His Gly Gly Gly Gly Asp Ser Gly
545   550   555   560

Asn Gly Asn Ser Gly Gly Ser Ala Ala Val Ser His His Tyr His Asn
565   570   575

Gly His His Ser Glu Pro Pro Arg Gly Arg Phe Asp Arg Gln Val Thr
580   585   590

Thr Asn Asn Gln Ser Pro Phe Ser Arg Pro Phe Ser Phe Gln Pro His
595   600   605

Leu Gly Pro Pro Ser Gly Phe Ser Phe Gly Leu Gly Gln Thr Gly Leu
610   615   620

Val Asn Leu Ser Met Pro Gly Leu Ala Tyr Gly Gln Gly Lys Met Pro
625   630   635   640

Gly Leu Pro His Pro Tyr Met Thr Gln Pro Val Gly Met Ser Glu Ala
645   650   655

Met Met Gln Arg Gly Met Glu Pro Lys Val Glu Pro Val Ser Asp Ser
660   665   670

Gly Gln Ser Val Tyr Asn Gln Ile Met Ser Arg Leu Pro Gln Ile
675   680   685

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52
                      Met Asn Pro Phe Tyr Ser Thr Phe Pro Asp Ser
                       1   5   10

ttt ctc tca atc tcc gat cat aga tct ccg gtt tca gac agt agt gag
100
Phe Leu Ser Ile Ser Asp His Arg Ser Pro Val Ser Asp Ser Ser Glu
            15   20   25

tgt tca cca aag tta gct tca agt tgt cca aag aaa cga gct ggg agg
148
Cys Ser Pro Lys Leu Ala Ser Ser Cys Pro Lys Lys Arg Ala Gly Arg
            30   35   40

33

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aag aag ttt cgt gag aca cgt cat ccg att tac aga gga gtt cgt cag
196
Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln
    45                      50                  55

agg aat tct ggt aaa tgg gtt tgt gaa gtt aga gag cct aat aag aaa
244
Arg Asn Ser Gly Lys Trp Val Cys Glu Val Arg Glu Pro Asn Lys Lys
60               65                  70                      75

tct agg att tgg tta ggt act ttt ccg acg gtt gaa atg gct gct cgt
292
Ser Arg Ile Trp Leu Gly Thr Phe Pro Thr Val Glu Met Ala Ala Arg
                80                  85                  90

gct cat gat gtt gct gct tta gct ctt cgt ggt cgc tct gct tgt ctc
340
Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys Leu
            95                  100                 105

aat ttc gct gat tct gct tgg cgg ctt cgt att cct gag act act tgt
388
Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Thr Thr Cys
        110                 115                 120

cct aag gag att cag aaa gct gcg tct gaa gct gca atg gcg ttt cag
436
Pro Lys Glu Ile Gln Lys Ala Ala Ser Glu Ala Ala Met Ala Phe Gln
    125                 130                 135

aat gag act acg acg gag gga tct aaa act gcg gcg gag gca gag gag
484
Asn Glu Thr Thr Thr Glu Gly Ser Lys Thr Ala Ala Glu Ala Glu Glu
140                 145                 150                 155

gcg gca ggg gag ggg gtg agg gag ggg gag agg agg gcg gag gag cag
532
Ala Ala Gly Glu Gly Val Arg Glu Gly Glu Arg Arg Ala Glu Glu Gln
                160                 165                 170

aat ggt ggt gtg ttt tat atg gat gat gag gcg ctt ttg ggg atg ccc
580
Asn Gly Gly Val Phe Tyr Met Asp Asp Glu Ala Leu Leu Gly Met Pro
                175                 180                 185

aac ttt ttt gag aat atg gcg gag ggg atg ctt ttg ccg ccg ccg gaa
628
Asn Phe Phe Glu Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro Glu
        190                 195                 200

gtt ggc tgg aat cat aac gac ttt gac gga gtg ggt gac gtg tca ctc
676
Val Gly Trp Asn His Asn Asp Phe Asp Gly Val Gly Asp Val Ser Leu
    205                 210                 215

tgg agt ttt gac gag taa ttttttggct cttttctgg ataataagtt
724
Trp Ser Phe Asp Glu
220
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34

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Met Asn Pro Phe Tyr Ser Thr Phe Pro Asp Ser Phe Leu Ser Ile Ser
1   5   10   15

Asp His Arg Ser Pro Val Ser Asp Ser Ser Glu Cys Ser Pro Lys Leu
            20   25   30

Ala Ser Ser Cys Pro Lys Lys Arg Ala Gly Arg Lys Lys Phe Arg Glu
            35   40   45

Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly Lys
        50   55   60

Trp Val Cys Glu Val Arg Glu Pro Asn Lys Lys Ser Arg Ile Trp Leu
65   70   75   80

Gly Thr Phe Pro Thr Val Glu Met Ala Ala Arg Ala His Asp Val Ala
                85   90   95

Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser
                100   105   110

Ala Trp Arg Leu Arg Ile Pro Glu Thr Thr Cys Pro Lys Glu Ile Gln
            115   120   125

Lys Ala Ala Ser Glu Ala Ala Met Ala Phe Gln Asn Glu Thr Thr Thr
            130   135   140

Glu Gly Ser Lys Thr Ala Ala Glu Ala Glu Glu Ala Ala Gly Glu Gly
145   150   155   160

Val Arg Glu Gly Glu Arg Arg Ala Glu Glu Gln Asn Gly Gly Val Phe
                165   170   175

Tyr Met Asp Asp Glu Ala Leu Leu Gly Met Pro Asn Phe Phe Glu Asn
            180   185   190

Met Ala Glu Gly Met Leu Leu Pro Pro Pro Glu Val Gly Trp Asn His
            195   200   205

Asn Asp Phe Asp Gly Val Gly Asp Val Ser Leu Trp Ser Phe Asp Glu
            210   215   220

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48
Met Gly Ser Tyr Ser Ala Gly Phe Pro Gly Ser Leu Asp Trp Phe Asp
1   5   10   15

ttt ccc ggt tta gga aac gga tcc tat cta aat gat caa cct ttg tta
96
Phe Pro Gly Leu Gly Asn Gly Ser Tyr Leu Asn Asp Gln Pro Leu Leu
                20   25   30

gat att gga tct gtt cct cct cct cta gac cca tat cct caa cag aat
144
Asp Ile Gly Ser Val Pro Pro Pro Leu Asp Pro Tyr Pro Gln Gln Asn
            35   40   45

ctt gct tct gcg gat gct gat ttc tct gat tct gtt ttg aag tac ata
192
Leu Ala Ser Ala Asp Ala Asp Phe Ser Asp Ser Val Leu Lys Tyr Ile
        50   55   60

agc caa gtt ctt atg gaa gag gac atg gaa gat aag cct tgt atg ttt
240
Ser Gln Val Leu Met Glu Glu Asp Met Glu Asp Lys Pro Cys Met Phe
65   70   75   80

cat gat gct tta tct ctt caa gca gct gag aag tct ctc tat gaa gct
288
His Asp Ala Leu Ser Leu Gln Ala Ala Glu Lys Ser Leu Tyr Glu Ala
                85   90   95

ctc ggc gag aag tac ccg gtt gat gat tct gat cag cct ctg act act
336
Leu Gly Glu Lys Tyr Pro Val Asp Asp Ser Asp Gln Pro Leu Thr Thr
                100   105   110

act act agc ctt gct caa ttg gtt agt agt cct ggt ggt tct tct tat
384
Thr Thr Ser Leu Ala Gln Leu Val Ser Ser Pro Gly Gly Ser Ser Tyr
            115   120   125

gct tca agc acc aca acc act tcc tct gat tca caa tgg agt ttt gat
432
Ala Ser Ser Thr Thr Thr Thr Ser Ser Asp Ser Gln Trp Ser Phe Asp
        130   135   140

tgt ttg gag aat aat agg cct tct tct tgg ttg cag aca ccg atc ccg
480
Cys Leu Glu Asn Asn Arg Pro Ser Ser Trp Leu Gln Thr Pro Ile Pro
145   150   155   160

agt aac ttc att ttt cag tct aca tct act aga gcc agt agc ggt aac
528
Ser Asn Phe Ile Phe Gln Ser Thr Ser Thr Arg Ala Ser Ser Gly Asn
                165   170   175

gcg gtt ttc ggg tca agt ttt agc ggt gat ttg gtt tct aat atg ttt
576
Ala Val Phe Gly Ser Ser Phe Ser Gly Asp Leu Val Ser Asn Met Phe
            180   185   190

36

aat gat act gac ttg gcg tta caa ttc aag aaa ggg atg gag gaa gct
624
Asn Asp Thr Asp Leu Ala Leu Gln Phe Lys Lys Gly Met Glu Glu Ala
        195   200   205

agt aaa ttc ctt cct aag agc tct cag ttg gtt ata gat aac tct gtt
672
Ser Lys Phe Leu Pro Lys Ser Ser Gln Leu Val Ile Asp Asn Ser Val
        210   215   220

cct aac aga tta acc gga aag aag agc cat tgg cgc gaa gaa gaa cat
720
Pro Asn Arg Leu Thr Gly Lys Lys Ser His Trp Arg Glu Glu Glu His
225   230   235   240

ttg act gaa gaa aga agt aag aaa caa tct gct att tat gtt gat gaa
768
Leu Thr Glu Glu Arg Ser Lys Lys Gln Ser Ala Ile Tyr Val Asp Glu
                245   250   255

act gat gag ctt act gat atg ttt gac aat att ctg ata ttt ggc gag
816
Thr Asp Glu Leu Thr Asp Met Phe Asp Asn Ile Leu Ile Phe Gly Glu
                260   265   270

gct aag gaa caa cct gta tgc att ctt aac gag agt ttc cct aag gaa
864
Ala Lys Glu Gln Pro Val Cys Ile Leu Asn Glu Ser Phe Pro Lys Glu
                275   280   285

cct gcg aaa gct tca acg ttt agt aag agt cct aaa ggc gaa aaa ccg
912
Pro Ala Lys Ala Ser Thr Phe Ser Lys Ser Pro Lys Gly Glu Lys Pro
        290   295   300

gaa gct agt ggt aac agt tat aca aaa gag aca cct gat ttg agg aca
960
Glu Ala Ser Gly Asn Ser Tyr Thr Lys Glu Thr Pro Asp Leu Arg Thr
305   310   315   320

atg ctg gtt tct tgt gct caa gct gtt tcg att aac gat cgt aga act
1008
Met Leu Val Ser Cys Ala Gln Ala Val Ser Ile Asn Asp Arg Arg Thr
                325   330   335

gct gac gag ctg tta agt cgg ata agg caa cat tct tca tct tac ggc
1056
Ala Asp Glu Leu Leu Ser Arg Ile Arg Gln His Ser Ser Ser Tyr Gly
                340   345   350

gat gga aca gag aga ttg gct cat tat ttt gct aac agt ctt gaa gca
1104
Asp Gly Thr Glu Arg Leu Ala His Tyr Phe Ala Asn Ser Leu Glu Ala
        355   360   365

cgt ttg gct ggg ata ggt aca cag gtt tat act gcc ttg tct tcc aag
1152
Arg Leu Ala Gly Ile Gly Thr Gln Val Tyr Thr Ala Leu Ser Ser Lys
        370   375   380

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aaa aca tct act tct gac atg ttg aaa gct tat cag aca tat ata tca
1200
Lys Thr Ser Thr Ser Asp Met Leu Lys Ala Tyr Gln Thr Tyr Ile Ser
385                 390                 395                 400

gtc tgt ccg ttc aag aaa atc gca atc ata ttc gcc aac cat agt att
1248
Val Cys Pro Phe Lys Lys Ile Ala Ile Ile Phe Ala Asn His Ser Ile
                405                 410                 415

atg cgg ttg gct tca agt gct aat gcc aaa acc atc cac atc ata gat
1296
Met Arg Leu Ala Ser Ser Ala Asn Ala Lys Thr Ile His Ile Ile Asp
            420                 425                 430

ttt gga ata tct gat ggt ttc cag tgg cct tct ctg att cat cga ctt
1344
Phe Gly Ile Ser Asp Gly Phe Gln Trp Pro Ser Leu Ile His Arg Leu
            435                 440                 445

gct tgg aga cgt ggt tca tct tgt aag ctt cgg ata acc ggt ata gag
1392
Ala Trp Arg Arg Gly Ser Ser Cys Lys Leu Arg Ile Thr Gly Ile Glu
    450                 455                 460

ttg cct caa cgt ggt ttt aga cca gcc gag gga gtt att gag act ggt
1440
Leu Pro Gln Arg Gly Phe Arg Pro Ala Glu Gly Val Ile Glu Thr Gly
465                 470                 475                 480

cgt cgc ttg gct aag tat tgt cag aag ttc aat att ccg ttt gag tac
1488
Arg Arg Leu Ala Lys Tyr Cys Gln Lys Phe Asn Ile Pro Phe Glu Tyr
                485                 490                 495

aat gcg att gcg cag aaa tgg gaa tca atc aag ttg gag gac ttg aag
1536
Asn Ala Ile Ala Gln Lys Trp Glu Ser Ile Lys Leu Glu Asp Leu Lys
            500                 505                 510

cta aaa gaa ggc gag ttt gtt gcg gta aac tct tta ttt cgg ttt agg
1584
Leu Lys Glu Gly Glu Phe Val Ala Val Asn Ser Leu Phe Arg Phe Arg
            515                 520                 525

aat ctt cta gat gag acg gtg gca gtg cat agc ccg aga gat acg gtt
1632
Asn Leu Leu Asp Glu Thr Val Ala Val His Ser Pro Arg Asp Thr Val
            530                 535                 540

ttg aag ctg ata agg aag ata aag cca gac gtg ttc atc ccc ggg atc
1680
Leu Lys Leu Ile Arg Lys Ile Lys Pro Asp Val Phe Ile Pro Gly Ile
545                 550                 555                 560

ctc agc gga tcc tac aac gcg cct ttc ttt gtc acg agg ttt aga gaa
1728
Leu Ser Gly Ser Tyr Asn Ala Pro Phe Phe Val Thr Arg Phe Arg Glu
                565                 570                 575
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gtt ctg ttt cat tac tca tct ctg ttt gac atg tgt gac acg aat cta
1776
Val Leu Phe His Tyr Ser Ser Leu Phe Asp Met Cys Asp Thr Asn Leu
        580   585   590

aca cgg gaa gat cca atg agg gtt atg ttt gag aaa gag ttc tat ggg
1824
Thr Arg Glu Asp Pro Met Arg Val Met Phe Glu Lys Glu Phe Tyr Gly
        595   600   605

cgg gag atc atg aac gtg gtg gcg tgt gag ggg acg gag aga gtg gag
1872
Arg Glu Ile Met Asn Val Val Ala Cys Glu Gly Thr Glu Arg Val Glu
    610   615   620

agg cca gag agt tat aag cag tgg cag gcg agg gcg atg aga gcc ggg
1920
Arg Pro Glu Ser Tyr Lys Gln Trp Gln Ala Arg Ala Met Arg Ala Gly
625   630   635   640

ttt aga cag att ccg ctg gag aag gaa cta gtt cag aaa ctg aag ttg
1968
Phe Arg Gln Ile Pro Leu Glu Lys Glu Leu Val Gln Lys Leu Lys Leu
                645   650   655

atg gtg gaa agt gga tac aaa ccc aaa gag ttt gat gtt gat caa gat
2016
Met Val Glu Ser Gly Tyr Lys Pro Lys Glu Phe Asp Val Asp Gln Asp
                660   665   670

tgt cac tgg ttg ctt cag ggc tgg aaa ggt aga att gta tac ggt tca
2064
Cys His Trp Leu Leu Gln Gly Trp Lys Gly Arg Ile Val Tyr Gly Ser
            675   680   685

tct att tgg gtt cct ttc ttt ttc tat gtg ggc aga gca act agg gtt
2112
Ser Ile Trp Val Pro Phe Phe Phe Tyr Val Gly Arg Ala Thr Arg Val
        690   695   700

ttg atc atg gat cca aac ttc tct gaa tct cta aac ggc ttt gag tat
2160
Leu Ile Met Asp Pro Asn Phe Ser Glu Ser Leu Asn Gly Phe Glu Tyr
705   710   715   720

ttt gat ggt aac cct aat ttg ctt act gat cca atg gaa gat cag tat
2208
Phe Asp Gly Asn Pro Asn Leu Leu Thr Asp Pro Met Glu Asp Gln Tyr
                725   730   735

cca cca cca tct gat act ctg ttg aaa tac gtg agt gag att ctt atg
2256
Pro Pro Pro Ser Asp Thr Leu Leu Lys Tyr Val Ser Glu Ile Leu Met
                740   745   750

gaa gag agt aat gga gat tat aag caa tct atg ttc tat gat tca ttg
2304
Glu Glu Ser Asn Gly Asp Tyr Lys Gln Ser Met Phe Tyr Asp Ser Leu
                755   760   765

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gct tta cga aaa act gaa gaa atg ttg cag caa gtc att act gat tct
2352
Ala Leu Arg Lys Thr Glu Glu Met Leu Gln Gln Val Ile Thr Asp Ser
    770                 775                 780

caa aat cag tcc ttt agt cct gct gat tca ttg att act aat tct tgg
2400
Gln Asn Gln Ser Phe Ser Pro Ala Asp Ser Leu Ile Thr Asn Ser Trp
785                 790                 795                 800

gat gca agc gga agc atc gat gaa tcg gct tat tcg gct gat ccg caa
2448
Asp Ala Ser Gly Ser Ile Asp Glu Ser Ala Tyr Ser Ala Asp Pro Gln
                805                 810                 815

cct gtg aat gaa att atg gtt aag agt atg ttt agt gat gca gaa tca
2496
Pro Val Asn Glu Ile Met Val Lys Ser Met Phe Ser Asp Ala Glu Ser
            820                 825                 830

gct tta cag ttt aag aaa ggg gtt gaa gaa gct agt aaa ttc ctt ccc
2544
Ala Leu Gln Phe Lys Lys Gly Val Glu Glu Ala Ser Lys Phe Leu Pro
        835                 840                 845

aat agt gat caa tgg gtt atc aat ctg gat atc gag aga tcc gaa agg
2592
Asn Ser Asp Gln Trp Val Ile Asn Leu Asp Ile Glu Arg Ser Glu Arg
        850                 855                 860

cgc gat tcg gtt aaa gaa gag atg gga ttg gat cag ttg aga gtt aag
2640
Arg Asp Ser Val Lys Glu Glu Met Gly Leu Asp Gln Leu Arg Val Lys
865                 870                 875                 880

aag aat cat gaa agg gat ttt gag gaa gtt agg agt agt aag caa ttt
2688
Lys Asn His Glu Arg Asp Phe Glu Glu Val Arg Ser Ser Lys Gln Phe
                885                 890                 895

gct agt aat gta gaa gat agt aag gtt aca gat atg ttt gat aag gtt
2736
Ala Ser Asn Val Glu Asp Ser Lys Val Thr Asp Met Phe Asp Lys Val
            900                 905                 910

ttg ctt ctt gac ggt gaa tgc gat ccg caa aca ttg tta gac agc gag
2784
Leu Leu Leu Asp Gly Glu Cys Asp Pro Gln Thr Leu Leu Asp Ser Glu
        915                 920                 925

att caa gcg att cgg agt agt aag aac ata gga gag aaa ggg aag aag
2832
Ile Gln Ala Ile Arg Ser Ser Lys Asn Ile Gly Glu Lys Gly Lys Lys
    930                 935                 940

aag aag aag aag aag agt caa gtg gtt gat ttt cgt aca ctt ctc act
2880
Lys Lys Lys Lys Lys Ser Gln Val Val Asp Phe Arg Thr Leu Leu Thr
945                 950                 955                 960
```

40

cat tgt gca caa gcc att tcc aca gga gat aaa acc acg gct ctt gag
2928
His Cys Ala Gln Ala Ile Ser Thr Gly Asp Lys Thr Thr Ala Leu Glu
            965   970   975

ttt ctg tta cag ata agg caa cag tct tcg cct ctc ggt gac gcg ggg
2976
Phe Leu Leu Gln Ile Arg Gln Gln Ser Ser Pro Leu Gly Asp Ala Gly
            980   985   990

caa aga cta gct cat tgt ttc gct aac gcg ctt gaa gct cgt cta cag
3024
Gln Arg Leu Ala His Cys Phe Ala Asn Ala Leu Glu Ala Arg Leu Gln
            995   1000   .   1005   .

gga agt acc ggt cct atg atc cag act tat tac aat gct tta acc
3069
Gly Ser Thr Gly Pro Met Ile Gln Thr Tyr Tyr Asn Ala Leu Thr
        1010   1015   1020

tcg tcg ttg aag gat act gct gcg gat aca att aga gcg tat cga
3114
Ser Ser Leu Lys Asp Thr Ala Ala Asp Thr Ile Arg Ala Tyr Arg
        1025   1030   1035   .

gtt tat ctt tct tcg tct ccg ttt gtt acc ttg atg tat ttc ttc
3159
Val Tyr Leu Ser Ser Ser Pro Phe Val Thr Leu Met Tyr Phe Phe
        1040   1045   1050

tcc atc tgg atg att ctt gat gtg gct aaa gat gct cct gtt ctt
3204
Ser Ile Trp Met Ile Leu Asp Val Ala Lys Asp Ala Pro Val Leu
        1055   1060   1065

cat ata gtt gat ttt ggg att cta tac ggg ttt caa tgg ccg atg
3249
His Ile Val Asp Phe Gly Ile Leu Tyr Gly Phe Gln Trp Pro Met
        1070   1075   1080

ttt att cag tct ata tca gat cga aaa gat gta ccg cgg aag ctg
3294
Phe Ile Gln Ser Ile Ser Asp Arg Lys Asp Val Pro Arg Lys Leu
        1085   1090   1095

cgg att act ggt atc gag ctt cct cag tgc ggg ttt cgg ccc gcg
3339
Arg Ile Thr Gly Ile Glu Leu Pro Gln Cys Gly Phe Arg Pro Ala
        1100   1105   1110

gag cga ata gag gag aca gga cgg aga ttg gct gag tat tgt aaa
3384
Glu Arg Ile Glu Glu Thr Gly Arg Arg Leu Ala Glu Tyr Cys Lys
        1115   1120   1125

cgg ttt aat gtt ccg ttt gag tac aaa gcc att gcg tct cag aac
3429
Arg Phe Asn Val Pro Phe Glu Tyr Lys Ala Ile Ala Ser Gln Asn
        1130   1135   1140

```
tgg gaa  aca atc cgg ata gaa  gat ctc gat ata cga  cca aac gaa
3474
Trp Glu  Thr Ile Arg Ile Glu  Asp Leu Asp Ile Arg  Pro Asn Glu
    1145                1150                 1155


gtc tta  gcg gtt aat gct gga  ctt aga ctc aag aac  ctt caa gat
3519
Val Leu  Ala Val Asn Ala Gly  Leu Arg Leu Lys Asn  Leu Gln Asp
    1160                1165                 1170


gaa aca  gga agc gaa gag aat  tgc ccg aga gat gct  gtc ttg aag
3564
Glu Thr  Gly Ser Glu Glu Asn  Cys Pro Arg Asp Ala  Val Leu Lys
    1175                1180                 1185


cta ata  aga aac atg aac ccg  gac gtt ttc atc cac  gcg att gtc
3609
Leu Ile  Arg Asn Met Asn Pro  Asp Val Phe Ile His  Ala Ile Val
    1190                1195                 1200


aac ggt  tca ttc aac gca ccc  ttc ttt atc tcg cgg  ttt aaa gaa
3654
Asn Gly  Ser Phe Asn Ala Pro  Phe Phe Ile Ser Arg  Phe Lys Glu
    1205                1210  --        1215


gcg gtt  tac cat tac tcc gct  ctc ttc gac atg ttt  gat tcg acg
3699
Ala Val  Tyr His Tyr Ser Ala  Leu Phe Asp Met Phe  Asp Ser Thr
    1220                1225                 1230


ttg cct  cgg gat aac aaa gag  agg att agg ttc gag  agg gag ttt
3744
Leu Pro  Arg Asp Asn Lys Glu  Arg Ile Arg Phe Glu  Arg Glu Phe
    1235                1240                 1245


tac ggg  aga gag gct atg aac  gtg ata gcg tgc gag  gaa gct gat
3789
Tyr Gly  Arg Glu Ala Met Asn  Val Ile Ala Cys Glu  Glu Ala Asp
    1250                1255                 1260


cga gtg  gag agg cct gag act  tac agg caa tgg cag  gtt aga atg
3834
Arg Val  Glu Arg Pro Glu Thr  Tyr Arg Gln Trp Gln  Val Arg Met
    1265                1270                 1275


gtt aga  gcc ggg ttt aag cag  aaa acg att aag cct  gag ctg gta
3879
Val Arg  Ala Gly Phe Lys Gln  Lys Thr Ile Lys Pro  Glu Leu Val
    1280                1285                 1290


gag ttg  ttt aga gga aag ctg  aag aaa tgg cgt tac  cat aaa gac
3924
Glu Leu  Phe Arg Gly Lys Leu  Lys Lys Trp Arg Tyr  His Lys Asp
    1295                1300                 1305


ttt gtg  gtt gat gaa aat agt  aaa tgg ttg tta caa  ggc tgg aaa
3969
Phe Val  Val Asp Glu Asn Ser  Lys Trp Leu Leu Gln  Gly Trp Lys
    1310                1315                 1320
```

42

ggt cga act ctc tat gct tct tct tgt tgg gtt cct gcc tag
4011
Gly Arg Thr Leu Tyr Ala Ser Ser Cys Trp Val Pro Ala
    1325   1330   1335

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22

Met Gly Ser Tyr Ser Ala Gly Phe Pro Gly Ser Leu Asp Trp Phe Asp
1   5   10   15

Phe Pro Gly Leu Gly Asn Gly Ser Tyr Leu Asn Asp Gln Pro Leu Leu
            20   25   30

Asp Ile Gly Ser Val Pro Pro Pro Leu Asp Pro Tyr Pro Gln Gln Asn
        35   40   45

Leu Ala Ser Ala Asp Ala Asp Phe Ser Asp Ser Val Leu Lys Tyr Ile
    50   55   60

Ser Gln Val Leu Met Glu Glu Asp Met Glu Asp Lys Pro Cys Met Phe
65   70   75   80

His Asp Ala Leu Ser Leu Gln Ala Ala Glu Lys Ser Leu Tyr Glu Ala
            85   90   95

Leu Gly Glu Lys Tyr Pro Val Asp Asp Ser Asp Gln Pro Leu Thr Thr
            100   105   110

Thr Thr Ser Leu Ala Gln Leu Val Ser Ser Pro Gly Gly Ser Ser Tyr
        115   120   125

Ala Ser Ser Thr Thr Thr Thr Ser Ser Asp Ser Gln Trp Ser Phe Asp
    130   135   140

Cys Leu Glu Asn Asn Arg Pro Ser Ser Trp Leu Gln Thr Pro Ile Pro
145   150   155   160

Ser Asn Phe Ile Phe Gln Ser Thr Ser Thr Arg Ala Ser Ser Gly Asn
            165   170   175

Ala Val Phe Gly Ser Ser Phe Ser Gly Asp Leu Val Ser Asn Met Phe
            180   185   190

Asn Asp Thr Asp Leu Ala Leu Gln Phe Lys Lys Gly Met Glu Glu Ala
        195   200   205

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Ser Lys Phe Leu Pro Lys Ser Ser Gln Leu Val Ile Asp Asn Ser Val
    210                 215                 220

Pro Asn Arg Leu Thr Gly Lys Lys Ser His Trp Arg Glu Glu Glu His
225                 230                 235                 240

Leu Thr Glu Glu Arg Ser Lys Lys Gln Ser Ala Ile Tyr Val Asp Glu
                245                 250                 255

Thr Asp Glu Leu Thr Asp Met Phe Asp Asn Ile Leu Ile Phe Gly Glu
                260                 265                 270

Ala Lys Glu Gln Pro Val Cys Ile Leu Asn Glu Ser Phe Pro Lys Glu
                275                 280                 285

Pro Ala Lys Ala Ser Thr Phe Ser Lys Ser Pro Lys Gly Glu Lys Pro
    290                 295                 300

Glu Ala Ser Gly Asn Ser Tyr Thr Lys Glu Thr Pro Asp Leu Arg Thr
305                 310                 315                 320

Met Leu Val Ser Cys Ala Gln Ala Val Ser Ile Asn Asp Arg Arg Thr
                325                 330                 335

Ala Asp Glu Leu Leu Ser Arg Ile Arg Gln His Ser Ser Ser Tyr Gly
                340                 345                 350

Asp Gly Thr Glu Arg Leu Ala His Tyr Phe Ala Asn Ser Leu Glu Ala
                355                 360                 365

Arg Leu Ala Gly Ile Gly Thr Gln Val Tyr Thr Ala Leu Ser Ser Lys
    370                 375                 380

Lys Thr Ser Thr Ser Asp Met Leu Lys Ala Tyr Gln Thr Tyr Ile Ser
385                 390                 395                 400

Val Cys Pro Phe Lys Lys Ile Ala Ile Ile Phe Ala Asn His Ser Ile
                405                 410                 415

Met Arg Leu Ala Ser Ser Ala Asn Ala Lys Thr Ile His Ile Ile Asp
                420                 425                 430

Phe Gly Ile Ser Asp Gly Phe Gln Trp Pro Ser Leu Ile His Arg Leu
                435                 440                 445

Ala Trp Arg Arg Gly Ser Ser Cys Lys Leu Arg Ile Thr Gly Ile Glu
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44

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        450                    455                      460


Leu Pro Gln Arg Gly Phe Arg Pro Ala Glu Gly Val Ile Glu Thr Gly
465              470              475                  480


Arg Arg Leu Ala Lys Tyr Cys Gln Lys Phe Asn Ile Pro Phe Glu Tyr
             485              490                  495


Asn Ala Ile Ala Gln Lys Trp Glu Ser Ile Lys Leu Glu Asp Leu Lys
             500              505                  510


Leu Lys Glu Gly Glu Phe Val Ala Val Asn Ser Leu Phe Arg Phe Arg
         515              520                  525


Asn Leu Leu Asp Glu Thr Val Ala Val His Ser Pro Arg Asp Thr Val
         530              535                  540


Leu Lys Leu Ile Arg Lys Ile Lys Pro Asp Val Phe Ile Pro Gly Ile
545              550              555                  560


Leu Ser Gly Ser Tyr Asn Ala Pro Phe Phe Val Thr Arg Phe Arg Glu
             565              570                  575


Val Leu Phe His Tyr Ser Ser Leu Phe Asp Met Cys Asp Thr Asn Leu
             580              585                  590


Thr Arg Glu Asp Pro Met Arg Val Met Phe Glu Lys Glu Phe Tyr Gly
         595              600                  605


Arg Glu Ile Met Asn Val Val Ala Cys Glu Gly Thr Glu Arg Val Glu
         610              615                  620


Arg Pro Glu Ser Tyr Lys Gln Trp Gln Ala Arg Ala Met Arg Ala Gly
625              630              635                  640


Phe Arg Gln Ile Pro Leu Glu Lys Glu Leu Val Gln Lys Leu Lys Leu
             645              650                  655


Met Val Glu Ser Gly Tyr Lys Pro Lys Glu Phe Asp Val Asp Gln Asp
             660              665                  670


Cys His Trp Leu Leu Gln Gly Trp Lys Gly Arg Ile Val Tyr Gly Ser
         675              680                  685


Ser Ile Trp Val Pro Phe Phe Tyr Val Gly Arg Ala Thr Arg Val
         690              695                  700
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45

```
Leu Ile Met Asp Pro Asn Phe Ser Glu Ser Leu Asn Gly Phe Glu Tyr
705             710             715             720


Phe Asp Gly Asn Pro Asn Leu Leu Thr Asp Pro Met Glu Asp Gln Tyr
                725             730             735


Pro Pro Pro Ser Asp Thr Leu Leu Lys Tyr Val Ser Glu Ile Leu Met
                740             745             750


Glu Glu Ser Asn Gly Asp Tyr Lys Gln Ser Met Phe Tyr Asp Ser Leu
            755             760             765


Ala Leu Arg Lys Thr Glu Glu Met Leu Gln Gln Val Ile Thr Asp Ser
    770             775             780


Gln Asn Gln Ser Phe Ser Pro Ala Asp Ser Leu Ile Thr Asn Ser Trp
785             790             795             800


Asp Ala Ser Gly Ser Ile Asp Glu Ser Ala Tyr Ser Ala Asp Pro Gln
            805             810             815


Pro Val Asn Glu Ile Met Val Lys Ser Met Phe Ser Asp Ala Glu Ser
            820             825             830


Ala Leu Gln Phe Lys Lys Gly Val Glu Glu Ala Ser Lys Phe Leu Pro
        835             840             845


Asn Ser Asp Gln Trp Val Ile Asn Leu Asp Ile Glu Arg Ser Glu Arg
    850             855             860


Arg Asp Ser Val Lys Glu Glu Met Gly Leu Asp Gln Leu Arg Val Lys
865             870             875             880


Lys Asn His Glu Arg Asp Phe Glu Glu Val Arg Ser Ser Lys Gln Phe
                885             890             895


Ala Ser Asn Val Glu Asp Ser Lys Val Thr Asp Met Phe Asp Lys Val
            900             905             910


Leu Leu Leu Asp Gly Glu Cys Asp Pro Gln Thr Leu Leu Asp Ser Glu
        915             920             925


Ile Gln Ala Ile Arg Ser Ser Lys Asn Ile Gly Glu Lys Gly Lys Lys
    930             935             940
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Lys Lys Lys Lys Lys Ser Gln Val Val Asp Phe Arg Thr Leu Leu Thr
945                 950             955                 960


His Cys Ala Gln Ala Ile Ser Thr Gly Asp Lys Thr Thr Ala Leu Glu
            965             970                 975


Phe Leu Leu Gln Ile Arg Gln Gln Ser Ser Pro Leu Gly Asp Ala Gly
            980             985                 990


Gln Arg Leu Ala His Cys Phe Ala  Asn Ala Leu Glu Ala  Arg Leu Gln
        995             1000                1005


Gly Ser  Thr Gly Pro Met Ile  Gln Thr Tyr Tyr Asn  Ala Leu Thr
    1010            1015            1020


Ser Ser  Leu Lys Asp Thr Ala  Ala Asp Thr Ile Arg  Ala Tyr Arg
    1025            1030            1035


Val Tyr  Leu Ser Ser Ser Pro  Phe Val Thr Leu Met  Tyr Phe Phe
    1040            1045            1050


Ser Ile  Trp Met Ile Leu Asp  Val Ala Lys Asp Ala  Pro Val Leu
    1055            1060            1065


His Ile  Val Asp Phe Gly Ile  Leu Tyr Gly Phe Gln  Trp Pro Met
    1070            1075            1080


Phe Ile  Gln Ser Ile Ser Asp  Arg Lys Asp Val Pro  Arg Lys Leu
    1085            1090            1095


Arg Ile  Thr Gly Ile Glu Leu  Pro Gln Cys Gly Phe  Arg Pro Ala
    1100            1105            1110


Glu Arg  Ile Glu Glu Thr Gly  Arg Arg Leu Ala Glu  Tyr Cys Lys
    1115            1120            1125


Arg Phe  Asn Val Pro Phe Glu  Tyr Lys Ala Ile Ala  Ser Gln Asn
    1130            1135            1140


Trp Glu  Thr Ile Arg Ile Glu  Asp Leu Asp Ile Arg  Pro Asn Glu
    1145            1150            1155


Val Leu  Ala Val Asn Ala Gly  Leu Arg Leu Lys Asn  Leu Gln Asp
    1160            1165            1170
```

47

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Glu Thr Gly Ser Glu Glu Asn Cys Pro Arg Asp Ala Val Leu Lys
    1175            1180            1185

Leu Ile Arg Asn Met Asn Pro Asp Val Phe Ile His Ala Ile Val
    1190            1195            1200

Asn Gly Ser Phe Asn Ala Pro Phe Phe Ile Ser Arg Phe Lys Glu
    1205            1210            1215

Ala Val Tyr His Tyr Ser Ala Leu Phe Asp Met Phe Asp Ser Thr
    1220            1225            1230

Leu Pro Arg Asp Asn Lys Glu Arg Ile Arg Phe Glu Arg Glu Phe
    1235            1240            1245

Tyr Gly Arg Glu Ala Met Asn Val Ile Ala Cys Glu Glu Ala Asp
    1250            1255            1260

Arg Val Glu Arg Pro Glu Thr Tyr Arg Gln Trp Gln Val Arg Met
    1265            1270            1275

Val Arg Ala Gly Phe Lys Gln Lys Thr Ile Lys Pro Glu Leu Val
    1280            1285            1290

Glu Leu Phe Arg Gly Lys Leu Lys Lys Trp Arg Tyr His Lys Asp
    1295            1300            1305

Phe Val Val Asp Glu Asn Ser Lys Trp Leu Leu Gln Gly Trp Lys
    1310            1315            1320

Gly Arg Thr Leu Tyr Ala Ser Ser Cys Trp Val Pro Ala
    1325            1330            1335


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<221> CDS <222> (20)..(703) <223> G1047

<400> 23
caattttaaa ccggtcatt atg atg tct act gta ccg gcc ttt acc ttt act
52
                     Met Met Ser Thr Val Pro Ala Phe Thr Phe Thr
                     1               5                       10

gaa ccg ggt ttg gtt aac caa tta tcg gat ttc cag acc gga ttc act
100
Glu Pro Gly Leu Val Asn Gln Leu Ser Asp Phe Gln Thr Gly Phe Thr
            15                  20                      25

cct tgg gaa ttg aac tgc tcc gat ctc ttc tct aca atc cat ctc gaa
148
Pro Trp Glu Leu Asn Cys Ser Asp Leu Phe Ser Thr Ile His Leu Glu
```

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               30                      35                      40
ccg gtc gta ccg agt cct tgt tct ggt gaa tcc gat gcc ggt tct gtc
196
Pro Val Val Pro Ser Pro Cys Ser Gly Glu Ser Asp Ala Gly Ser Val
    45              50              55

aaa att aac acc gat ttt aac ggt ttt gac gaa tcg tgt atc ggt tcc
244
Lys Ile Asn Thr Asp Phe Asn Gly Phe Asp Glu Ser Cys Ile Gly Ser
60              65              70              75

atc aaa act aac tcc ggt tct gat gat tcc aac ctt ttc cac ggc gta
292
Ile Lys Thr Asn Ser Gly Ser Asp Asp Ser Asn Leu Phe His Gly Val
                80              85              90

ccg agt cct caa tcc gac gaa ttg gac tca aaa aac acg aaa atc cga
340
Pro Ser Pro Gln Ser Asp Glu Leu Asp Ser Lys Asn Thr Lys Ile Arg
            95              100             105

agt aac gcc acg aat cat aac cgg aac aaa ttg aac cgg tcg gtt ttg
388
Ser Asn Ala Thr Asn His Asn Arg Asn Lys Leu Asn Arg Ser Val Leu
        110             115             120

cag gtg act gac gac cgt aaa cgc aaa cgg atg gaa tca aac cga gaa
436
Gln Val Thr Asp Asp Arg Lys Arg Lys Arg Met Glu Ser Asn Arg Glu
    125             130             135

tca gcg aag cgg tcg agg atg cgt aaa caa aga cac att gat aat tta
484
Ser Ala Lys Arg Ser Arg Met Arg Lys Gln Arg His Ile Asp Asn Leu
140             145             150             155

aaa gac gaa gca aat cgt ctc ggt tta gaa aac cgg gaa ctc gca aac
532
Lys Asp Glu Ala Asn Arg Leu Gly Leu Glu Asn Arg Glu Leu Ala Asn
            160             165             170

cgg ctt cga att gtt ttg tac aac atc gca tta atg tgt acg gac aac
580
Arg Leu Arg Ile Val Leu Tyr Asn Ile Ala Leu Met Cys Thr Asp Asn
            175             180             185

aat cag ctt ttg tcg gaa caa gag att ctc aga cgg aga ttc ttg gag
628
Asn Gln Leu Leu Ser Glu Gln Glu Ile Leu Arg Arg Arg Phe Leu Glu
        190             195             200

atg agg cag att ttg att ttc aga cag ctt cag ctg aat cca tca ttg
676
Met Arg Gln Ile Leu Ile Phe Arg Gln Leu Gln Leu Asn Pro Ser Leu
    205             210             215

atc atc aat cat cat cat atg att tga aagaaaaaaa aa
715
Ile Ile Asn His His His Met Ile
220             225
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24

Met Met Ser Thr Val Pro Ala Phe Thr Phe Thr Glu Pro Gly Leu Val
1   5   10   15

Asn Gln Leu Ser Asp Phe Gln Thr Gly Phe Thr Pro Trp Glu Leu Asn
            20   25   30

Cys Ser Asp Leu Phe Ser Thr Ile His Leu Glu Pro Val Val Pro Ser
            35   40   45

Pro Cys Ser Gly Glu Ser Asp Ala Gly Ser Val Lys Ile Asn Thr Asp
        50   55   60

Phe Asn Gly Phe Asp Glu Ser Cys Ile Gly Ser Ile Lys Thr Asn Ser
65   70   75   80

Gly Ser Asp Asp Ser Asn Leu Phe His Gly Val Pro Ser Pro Gln Ser
            85   90   95

Asp Glu Leu Asp Ser Lys Asn Thr Lys Ile Arg Ser Asn Ala Thr Asn
            100   105   110

His Asn Arg Asn Lys Leu Asn Arg Ser Val Leu Gln Val Thr Asp Asp
        115   120   125

Arg Lys Arg Lys Arg Met Glu Ser Asn Arg Glu Ser Ala Lys Arg Ser
    130   135   140

Arg Met Arg Lys Gln Arg His Ile Asp Asn Leu Lys Asp Glu Ala Asn
145   150   155   160

Arg Leu Gly Leu Glu Asn Arg Glu Leu Ala Asn Arg Leu Arg Ile Val
            165   170   175

Leu Tyr Asn Ile Ala Leu Met Cys Thr Asp Asn Asn Gln Leu Leu Ser
            180   185   190

Glu Gln Glu Ile Leu Arg Arg Arg Phe Leu Glu Met Arg Gln Ile Leu
        195   200   205

Ile Phe Arg Gln Leu Gln Leu Asn Pro Ser Leu Ile Ile Asn His His
    210   215   220

50

His Met Ile
225

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<221> CDS <222> (297)..(1781) <223> G1062

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60

tatctctatc ttccttttca gatttcgctt cttcaattca tgaaatcctc gtgattctac
120

tttaatgctt ctcttttttt acttttccaa gtctctgaat attcaaagta tatatctttt
180

gttttcaaac ttttgcagaa ttgtcttcaa gcttccaaat ttcagttaaa ggtctcaact
240

ttgcagaatt ttcctctaaa ggttcagact ttggggtaaa ggtgtcaact ttggcg atg
299
                                                                    Met
                                                                     1

ggt ctt gac gga aac aat ggt gga ggg gtt tgg tta aac ggt ggt ggt
347
Gly Leu Asp Gly Asn Asn Gly Gly Gly Val Trp Leu Asn Gly Gly Gly
              5   10   15

gga gaa agg gaa gag aac gag gaa ggt tca tgg gga agg aat caa gaa
395
Gly Glu Arg Glu Glu Asn Glu Glu Gly Ser Trp Gly Arg Asn Gln Glu
           20   25   30

gat ggt tct tct cag ttt aag cct atg ctt gaa ggt gat tgg ttt agt
443
Asp Gly Ser Ser Gln Phe Lys Pro Met Leu Glu Gly Asp Trp Phe Ser
        35   40   45

agt aac caa cca cat cca caa gat ctt cag atg tta cag aat cag cca
491
Ser Asn Gln Pro His Pro Gln Asp Leu Gln Met Leu Gln Asn Gln Pro
50   55   60   65

gat ttc aga tac ttt ggt ggt ttt cct ttt aac cct aat gat aat ctt
539
Asp Phe Arg Tyr Phe Gly Gly Phe Pro Phe Asn Pro Asn Asp Asn Leu
                70   75   80

ctt ctt caa cac tct att gat tct tct tct tct tgt tct cct tct caa
587
Leu Leu Gln His Ser Ile Asp Ser Ser Ser Ser Cys Ser Pro Ser Gln
                85   90   95

gct ttt agt ctt gac cct tct cag caa aat cag ttc ttg tca act aac
635
Ala Phe Ser Leu Asp Pro Ser Gln Gln Asn Gln Phe Leu Ser Thr Asn
           100   105   110

51

```
aac aac aag ggt tgt ctt ctc aat gtt cct tct tct gca aac cct ttt
683
Asn Asn Lys Gly Cys Leu Leu Asn Val Pro Ser Ser Ala Asn Pro Phe
    115             120             125

gat aat gct ttt gag ttt ggc tct gaa tct ggt ttt ctt aac caa atc
731
Asp Asn Ala Phe Glu Phe Gly Ser Glu Ser Gly Phe Leu Asn Gln Ile
130             135             140             145

cat gct cct att tcg atg ggg ttt ggt tct ttg aca caa ttg ggg aac
779
His Ala Pro Ile Ser Met Gly Phe Gly Ser Leu Thr Gln Leu Gly Asn
            150             155             160

agg gat ttg agt tct gtt cct gat ttc ttg tct gct cgg tca ctt ctt
827
Arg Asp Leu Ser Ser Val Pro Asp Phe Leu Ser Ala Arg Ser Leu Leu
            165             170             175

gcg ccg gaa agc aac aac aac aac aca atg ttg tgt ggt ggt ttc aca
875
Ala Pro Glu Ser Asn Asn Asn Asn Thr Met Leu Cys Gly Gly Phe Thr
        180             185             190

gct ccg ttg gag ttg gaa ggt ttt ggt agt cct gct aat ggt ggt ttt
923
Ala Pro Leu Glu Leu Glu Gly Phe Gly Ser Pro Ala Asn Gly Gly Phe
        195             200             205

gtt ggg aac aga gcg aaa gtt ctg aag cct tta gag gtg tta gca tcg
971
Val Gly Asn Arg Ala Lys Val Leu Lys Pro Leu Glu Val Leu Ala Ser
210             215             220             225

tct ggt gca cag cct act ctg ttc cag aaa cgt gca gct atg cgt cag
1019
Ser Gly Ala Gln Pro Thr Leu Phe Gln Lys Arg Ala Ala Met Arg Gln
            230             235             240

agc tct gga agc aaa atg gga aat tcg gag agt tcg gga atg agg agg
1067
Ser Ser Gly Ser Lys Met Gly Asn Ser Glu Ser Ser Gly Met Arg Arg
            245             250             255

ttt agt gat gat gga gat atg gat gag act ggg att gag gtt tct ggg
1115
Phe Ser Asp Asp Gly Asp Met Asp Glu Thr Gly Ile Glu Val Ser Gly
            260             265             270

ttg aac tat gag tct gat gag ata aat gag agc ggt aaa gcg gct gag
1163
Leu Asn Tyr Glu Ser Asp Glu Ile Asn Glu Ser Gly Lys Ala Ala Glu
            275             280             285

agt gtt cag att gga gga gga gga aag ggt aag aag aaa ggt atg cct
1211
Ser Val Gln Ile Gly Gly Gly Gly Lys Gly Lys Lys Lys Gly Met Pro
290             295             300             305
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gct aag aat ctg atg gct gag agg aga agg agg aag aag ctt aat gat
1259
Ala Lys Asn Leu Met Ala Glu Arg Arg Arg Arg Lys Lys Leu Asn Asp
              310   315   320

agg ctt tat atg ctt aga tca gtt gtc ccc aag atc agc aaa atg gat
1307
Arg Leu Tyr Met Leu Arg Ser Val Val Pro Lys Ile Ser Lys Met Asp
              325   330   335

aga gca tca ata ctt gga gat gca att gat tat ctg aag gaa ctt cta
1355
Arg Ala Ser Ile Leu Gly Asp Ala Ile Asp Tyr Leu Lys Glu Leu Leu
          340   345   350

caa agg atc aat gat ctt cac aat gaa ctt gag tca act cct cct gga
1403
Gln Arg Ile Asn Asp Leu His Asn Glu Leu Glu Ser Thr Pro Pro Gly
        355   360   365

tct ttg cct cca act tca tca agc ttc cat ccg ttg aca cct aca ccg
1451
Ser Leu Pro Pro Thr Ser Ser Ser Phe His Pro Leu Thr Pro Thr Pro
370   375   380   385

caa act ctt tct tgt cgt gtc aag gaa gag ttg tgt ccc tct tct tta
1499
Gln Thr Leu Ser Cys Arg Val Lys Glu Glu Leu Cys Pro Ser Ser Leu
              390   395   400

cca agt cct aaa ggc cag caa gct aga gtt gag gtt aga tta agg gaa
1547
Pro Ser Pro Lys Gly Gln Gln Ala Arg Val Glu Val Arg Leu Arg Glu
              405   410   415

gga aga gca gtg aac att cat atg ttc tgt ggt cgt aga ccg ggt ctg
1595
Gly Arg Ala Val Asn Ile His Met Phe Cys Gly Arg Arg Pro Gly Leu
          420   425   430

ttg ctc gct acc atg aaa gct ttg gat aat ctt gga ttg gat gtt cag
1643
Leu Leu Ala Thr Met Lys Ala Leu Asp Asn Leu Gly Leu Asp Val Gln
          435   440   445

caa gct gtg atc agc tgt ttt aat ggg ttt gcc ttg gat gtt ttc cgc
1691
Gln Ala Val Ile Ser Cys Phe Asn Gly Phe Ala Leu Asp Val Phe Arg
450   455   460   465

gct gag caa tgc caa gaa gga caa gag ata ctg cct gat caa atc aaa
1739
Ala Glu Gln Cys Gln Glu Gly Gln Glu Ile Leu Pro Asp Gln Ile Lys
              470   475   480

gca gtg ctt ttc gat aca gca ggg tat gct ggt atg atc tga
1781
Ala Val Leu Phe Asp Thr Ala Gly Tyr Ala Gly Met Ile
              485   490

53

tctgatcctg acttcgagtc cattaagcat ctgttgaagc agagctagaa gaactaagtc
1841

cctttaaatc tgcaatttc ttctcaactt tttttcttat gtcataactt caatctaagc
1901

atgtaatgca attgcaaatg agagttgttt ttaaattaag cttttgagaa cttgaggttg
1961

ttgttgttgg atacataact tcaacctttt attagcaatg ttaacttcca tttatgtttc
2021

atctt
2026

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26

Met Gly Leu Asp Gly Asn Asn Gly Gly Gly Val Trp Leu Asn Gly Gly
1   5   10   15

Gly Gly Glu Arg Glu Glu Asn Glu Glu Gly Ser Trp Gly Arg Asn Gln
            20   25   30

Glu Asp Gly Ser Ser Gln Phe Lys Pro Met Leu Glu Gly Asp Trp Phe
            35   40   45

Ser Ser Asn Gln Pro His Pro Gln Asp Leu Gln Met Leu Gln Asn Gln
    50   55   60

Pro Asp Phe Arg Tyr Phe Gly Gly Phe Pro Phe Asn Pro Asn Asp Asn
65   70   75   80

Leu Leu Leu Gln His Ser Ile Asp Ser Ser Ser Ser Cys Ser Pro Ser
                85   90   95

Gln Ala Phe Ser Leu Asp Pro Ser Gln Gln Asn Gln Phe Leu Ser Thr
            100   105   110

Asn Asn Asn Lys Gly Cys Leu Leu Asn Val Pro Ser Ser Ala Asn Pro
            115   120   125

Phe Asp Asn Ala Phe Glu Phe Gly Ser Glu Ser Gly Phe Leu Asn Gln
    130   135   140

Ile His Ala Pro Ile Ser Met Gly Phe Gly Ser Leu Thr Gln Leu Gly
145   150   155   160

Asn Arg Asp Leu Ser Ser Val Pro Asp Phe Leu Ser Ala Arg Ser Leu
                165   170   175

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Leu Ala Pro Glu Ser Asn Asn Asn Asn Thr Met Leu Cys Gly Gly Phe
        180                 185             190

Thr Ala Pro Leu Glu Leu Glu Gly Phe Gly Ser Pro Ala Asn Gly Gly
        195                 200             205

Phe Val Gly Asn Arg Ala Lys Val Leu Lys Pro Leu Glu Val Leu Ala
    210                 215             220

Ser Ser Gly Ala Gln Pro Thr Leu Phe Gln Lys Arg Ala Ala Met Arg
225                 230             235                 240

Gln Ser Ser Gly Ser Lys Met Gly Asn Ser Glu Ser Ser Gly Met Arg
                245                 250             255

Arg Phe Ser Asp Asp Gly Asp Met Asp Glu Thr Gly Ile Glu Val Ser
            260                 265             270

Gly Leu Asn Tyr Glu Ser Asp Glu Ile Asn Glu Ser Gly Lys Ala Ala
        275                 280             285

Glu Ser Val Gln Ile Gly Gly Gly Gly Lys Gly Lys Lys Lys Gly Met
    290                 295             300

Pro Ala Lys Asn Leu Met Ala Glu Arg Arg Arg Arg Lys Lys Leu Asn
305                 310             315                 320

Asp Arg Leu Tyr Met Leu Arg Ser Val Val Pro Lys Ile Ser Lys Met
            325                 330             335

Asp Arg Ala Ser Ile Leu Gly Asp Ala Ile Asp Tyr Leu Lys Glu Leu
            340                 345             350

Leu Gln Arg Ile Asn Asp Leu His Asn Glu Leu Glu Ser Thr Pro Pro
        355                 360             365

Gly Ser Leu Pro Pro Thr Ser Ser Ser Phe His Pro Leu Thr Pro Thr
    370                 375             380

Pro Gln Thr Leu Ser Cys Arg Val Lys Glu Glu Leu Cys Pro Ser Ser
385                 390             395                 400

Leu Pro Ser Pro Lys Gly Gln Gln Ala Arg Val Glu Val Arg Leu Arg
                405                 410             415
```

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Glu Gly Arg Ala Val Asn Ile His Met Phe Cys Gly Arg Arg Pro Gly
          420                 425                 430


Leu Leu Leu Ala Thr Met Lys Ala Leu Asp Asn Leu Gly Leu Asp Val
          435                 440                 445


Gln Gln Ala Val Ile Ser Cys Phe Asn Gly Phe Ala Leu Asp Val Phe
      450                 455                 460


Arg Ala Glu Gln Cys Gln Glu Gly Gln Glu Ile Leu Pro Asp Gln Ile
465                 470                 475                 480


Lys Ala Val Leu Phe Asp Thr Ala Gly Tyr Ala Gly Met Ile
                  485                 490
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aagactaccc atctattcag ttctttctct tatgatttaa gtttcattta gttttttttt
120

ctcatccgcc attttcgttg acttttgaa gcatttctcg aattgacttt gttcttcaca
180

ttgattcatt agaatgttct ttcataaagt ttggatcttt tcttcagggc ttgattaatt
240

tcatatctat gatcttctct gtattgtttt tgatccaatc acttctcaaa atttgatcct
300

tgtcattgga tttagattta gggttttttgt atccttgggg atttgaagat caaaaacaga
360

gtctttgagt gatacttctg gggaacaaa atg gct gca act gca ata gag cca
413
                                 Met Ala Ala Thr Ala Ile Glu Pro
                                 1                   5

tct tca tct ata agt ttc aca tct tct cac tta tca aac cct tct cct
461
Ser Ser Ser Ile Ser Phe Thr Ser Ser His Leu Ser Asn Pro Ser Pro
        10                  15                  20

gtt gtt act act tat cac tca gct gct aat ctt gaa gag ctc agc tct
509
Val Val Thr Thr Tyr His Ser Ala Ala Asn Leu Glu Glu Leu Ser Ser
25                  30                  35                  40

aac ttg gag cag ctt ctc act aat cca gat tgc gat tac act gac gca
557
Asn Leu Glu Gln Leu Leu Thr Asn Pro Asp Cys Asp Tyr Thr Asp Ala
```

                    45   50   55

gag atc atc att gaa gaa gaa gct aac cct cgg aag ctt cgt aac tat
605
Glu Ile Ile Ile Glu Glu Glu Ala Asn Pro Arg Lys Leu Arg Asn Tyr
            60   65   70

gtt gag aag tca cta gta gag aat gtt ctt cct atc ctc tta gtt gcg
653
Val Glu Lys Ser Leu Val Glu Asn Val Leu Pro Ile Leu Leu Val Ala
        75   80   85

ttt cat tgt gat ttg aca cag ctt ctt gat caa tgc att gag aga gtg
701
Phe His Cys Asp Leu Thr Gln Leu Leu Asp Gln Cys Ile Glu Arg Val
    90   95   100

gcg aga tca gac tta gac aga ttc tgt atc gaa aag gag ctt cct tta
749
Ala Arg Ser Asp Leu Asp Arg Phe Cys Ile Glu Lys Glu Leu Pro Leu
105   110   115   120

gaa gta ttg gaa aaa atc aaa cag ctt cga gtt aag tcg gtg aac ata
797
Glu Val Leu Glu Lys Ile Lys Gln Leu Arg Val Lys Ser Val Asn Ile
                125   130   135

ccc gag gtg gag gat aaa tcg ata gag aga aca ggg aaa gta ctc aag
845
Pro Glu Val Glu Asp Lys Ser Ile Glu Arg Thr Gly Lys Val Leu Lys
            140   145   150

gca ttg gat tca gat gat gta gaa ctc gtg aag ctt ctt ttg act gag
893
Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu Leu Leu Thr Glu
        155   160   165

tca gat ata act cta gac caa gcc aat ggt cta cat tat gca gtg gca
941
Ser Asp Ile Thr Leu Asp Gln Ala Asn Gly Leu His Tyr Ala Val Ala
    170   175   180

tac agt gat ccg aaa gtt gtg aca cag gtt ctt gat cta gat atg gct
989
Tyr Ser Asp Pro Lys Val Val Thr Gln Val Leu Asp Leu Asp Met Ala
185   190   195   200

gat gtt aat ttc aga aat tcc agg ggg tat acg gtt ctt cat att gct
1037
Asp Val Asn Phe Arg Asn Ser Arg Gly Tyr Thr Val Leu His Ile Ala
                205   210   215

gct atg cgt aga gag cca aca att atc ata cca ctt att caa aaa gga
1085
Ala Met Arg Arg Glu Pro Thr Ile Ile Ile Pro Leu Ile Gln Lys Gly
            220   225   230

gct aat gct tca gat ttc acg ttt gat gga cgc agt gcg gta aat ata
1133
Ala Asn Ala Ser Asp Phe Thr Phe Asp Gly Arg Ser Ala Val Asn Ile
        235   240   245

tgt agg aga ctc act agg ccg aaa gat tat cat acc aaa acc tca agg
1181
Cys Arg Arg Leu Thr Arg Pro Lys Asp Tyr His Thr Lys Thr Ser Arg
   250   255   260

aaa gaa cct agt aaa tac cgc tta tgc atc gat atc ttg gaa agg gaa
1229
Lys Glu Pro Ser Lys Tyr Arg Leu Cys Ile Asp Ile Leu Glu Arg Glu
265   270   275   280

att aga agg aat cca ttg gtt agt ggg gat aca ccc act tgt tcc cat
1277
Ile Arg Arg Asn Pro Leu Val Ser Gly Asp Thr Pro Thr Cys Ser His
           285   290   295

tcg atg ccc gag gat ctc caa atg agg ttg tta tac tta gaa aag cga
1325
Ser Met Pro Glu Asp Leu Gln Met Arg Leu Leu Tyr Leu Glu Lys Arg
      300   305   .   310

gtg gga ctt gct cag ttg ttc ttc cca gca gaa gcc aat gtg gct atg
1373
Val Gly Leu Ala Gln Leu Phe Phe Pro Ala Glu Ala Asn Val Ala Met
      315   320   325

gac gtt gct aat gtt gaa ggg aca agc gag tgc aca ggt ctt cta act
1421
Asp Val Ala Asn Val Glu Gly Thr Ser Glu Cys Thr Gly Leu Leu Thr
    330   335 ·   .   340

cca cct cca tca aat gat aca act gaa aac ttg ggt aaa gtc gat tta
1469
Pro Pro Pro Ser Asn Asp Thr Thr Glu Asn Leu Gly Lys Val Asp Leu
345   350   355   360

aat gaa acg cct tat gtg caa acg aaa aga atg ctt aca cgt atg aaa
1517
Asn Glu Thr Pro Tyr Val Gln Thr Lys Arg Met Leu Thr Arg Met Lys
         365   370   375

gcc ctc atg aaa aca gtt gag aca ggt cgg aga tac ttc cca tct tgt
1565
Ala Leu Met Lys Thr Val Glu Thr Gly Arg Arg Tyr Phe Pro Ser Cys
      380   385   390

tat gag gtt ctg gat aag tac atg gat cag tat atg gac gaa gaa atc
1613
Tyr Glu Val Leu Asp Lys Tyr Met Asp Gln Tyr Met Asp Glu Glu Ile
      395   400   405

cct gat atg tcg tat ccc gag aaa ggc act gtg aaa gag aga aga cag
1661
Pro Asp Met Ser Tyr Pro Glu Lys Gly Thr Val Lys Glu Arg Arg Gln
    410   415   420

aag agg atg aga tat aac gag ctg aag aac gac gtt aaa aaa gca tat
1709
Lys Arg Met Arg Tyr Asn Glu Leu Lys Asn Asp Val Lys Lys Ala Tyr
425   430   ·   435   440

agc aaa gac aaa gtc gcg cgg tct tgt ctt tct tct tca tca cca gct
1757
Ser Lys Asp Lys Val Ala Arg Ser Cys Leu Ser Ser Ser Ser Pro Ala
              445   450   455

tct tct ctt aga gaa gcc tta gag aat cca aca tga tcttgtccca
1803
Ser Ser Leu Arg Glu Ala Leu Glu Asn Pro Thr
              460   465

gataagtaat gctactagag atagttcctt ggaagaaatt agctatttta taggttttgg
1863

tttagaaaac agtggagatc ccattttggt attcaggttt attacatggt ttaggtttga
1923

tttttgtatta aaggagatgg atttttgaaa tgtataaagc aaaacctttc cttttttgctt
1983

tgcttctttc tttaaaaaaa aaattgtaat atatggaagt gaaatcgaag caacgattga
2043

gcaaaaaaaa a
2054

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28

Met Ala Ala Thr Ala Ile Glu Pro Ser Ser Ser Ile Ser Phe Thr Ser
1   5   10   15

Ser His Leu Ser Asn Pro Ser Pro Val Val Thr Thr Tyr His Ser Ala
              20   25   30

Ala Asn Leu Glu Glu Leu Ser Ser Asn Leu Glu Gln Leu Leu Thr Asn
              35   40   45

Pro Asp Cys Asp Tyr Thr Asp Ala Glu Ile Ile Ile Glu Glu Glu Ala
    50   55   60

Asn Pro Arg Lys Leu Arg Asn Tyr Val Glu Lys Ser Leu Val Glu Asn
65   70   75   80

Val Leu Pro Ile Leu Leu Val Ala Phe His Cys Asp Leu Thr Gln Leu
              85   90   95

Leu Asp Gln Cys Ile Glu Arg Val Ala Arg Ser Asp Leu Asp Arg Phe
              100   105   110

Cys Ile Glu Lys Glu Leu Pro Leu Glu Val Leu Glu Lys Ile Lys Gln
              115   120   125

59

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Leu Arg Val Lys Ser Val Asn Ile Pro Glu Val Glu Asp Lys Ser Ile
    130                 135                 140

Glu Arg Thr Gly Lys Val Leu Lys Ala Leu Asp Ser Asp Asp Val Glu
145                 150                 155                 160

Leu Val Lys Leu Leu Leu Thr Glu Ser Asp Ile Thr Leu Asp Gln Ala
                165                 170                 175

Asn Gly Leu His Tyr Ala Val Ala Tyr Ser Asp Pro Lys Val Val Thr
                180                 185                 190

Gln Val Leu Asp Leu Asp Met Ala Asp Val Asn Phe Arg Asn Ser Arg
            195                 200                 205

Gly Tyr Thr Val Leu His Ile Ala Ala Met Arg Arg Glu Pro Thr Ile
    210                 215                 220

Ile Ile Pro Leu Ile Gln Lys Gly Ala Asn Ala Ser Asp Phe Thr Phe
225                 230                 235                 240

Asp Gly Arg Ser Ala Val Asn Ile Cys Arg Arg Leu Thr Arg Pro Lys
                245                 250                 255

Asp Tyr His Thr Lys Thr Ser Arg Lys Glu Pro Ser Lys Tyr Arg Leu
            260                 265                 270

Cys Ile Asp Ile Leu Glu Arg Glu Ile Arg Arg Asn Pro Leu Val Ser
            275                 280                 285

Gly Asp Thr Pro Thr Cys Ser His Ser Met Pro Glu Asp Leu Gln Met
    290                 295                 300

Arg Leu Leu Tyr Leu Glu Lys Arg Val Gly Leu Ala Gln Leu Phe Phe
305                 310                 315                 320

Pro Ala Glu Ala Asn Val Ala Met Asp Val Ala Asn Val Glu Gly Thr
                325                 330                 335

Ser Glu Cys Thr Gly Leu Leu Thr Pro Pro Ser Asn Asp Thr Thr
            340                 345                 350

Glu Asn Leu Gly Lys Val Asp Leu Asn Glu Thr Pro Tyr Val Gln Thr
    355                 360                 365

Lys Arg Met Leu Thr Arg Met Lys Ala Leu Met Lys Thr Val Glu Thr
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60

            370   375   380

Gly Arg Arg Tyr Phe Pro Ser Cys Tyr Glu Val Leu Asp Lys Tyr Met
385   390   395   400

Asp Gln Tyr Met Asp Glu Glu Ile Pro Asp Met Ser Tyr Pro Glu Lys
                405   410   415

Gly Thr Val Lys Glu Arg Arg Gln Lys Arg Met Arg Tyr Asn Glu Leu
                420   425   430

Lys Asn Asp Val Lys Lys Ala Tyr Ser Lys Asp Lys Val Ala Arg Ser
                435   440   445

Cys Leu Ser Ser Ser Ser Pro Ala Ser Ser Leu Arg Glu Ala Leu Glu
        450   455   460

Asn Pro Thr
465

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59
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                                                               1

caa gag ttc cat agt agc aaa gat tca ttg cct tgt cct gca act tct
107
Gln Glu Phe His Ser Ser Lys Asp Ser Leu Pro Cys Pro Ala Thr Ser
            5   10   15

tgg gat aac tct gtc ttc acc aac tca aat gtc caa gga tca tca tcc
155
Trp Asp Asn Ser Val Phe Thr Asn Ser Asn Val Gln Gly Ser Ser Ser
        20   25   30

ttg acc gat aac aac act tta agc ttg aca atg gag atg aaa caa act
203
Leu Thr Asp Asn Asn Thr Leu Ser Leu Thr Met Glu Met Lys Gln Thr
    35   40   45

ggt ttt caa atg cag cac tat gat tcc tcc tct act caa tcc act gga
251
Gly Phe Gln Met Gln His Tyr Asp Ser Ser Ser Thr Gln Ser Thr Gly
50   55   60   65

gga gaa tca tat agt gaa gtt gct agc tta agt gaa cct act aat cgt
299
Gly Glu Ser Tyr Ser Glu Val Ala Ser Leu Ser Glu Pro Thr Asn Arg
                70   75   80

```
tat ggc cac aac att gtt gtc act cat ctc tca ggt tac aaa gaa aac
347
Tyr Gly His Asn Ile Val Val Thr His Leu Ser Gly Tyr Lys Glu Asn
             85                90                95

ccg gaa aat cct att gga agt cat tcg ata tca aag gtg tct caa gat
395
Pro Glu Asn Pro Ile Gly Ser His Ser Ile Ser Lys Val Ser Gln Asp
        100                105                110

tca gtg gtt ctt cct att gag gcg gct tct tgg cct tta cac ggc aat
443
Ser Val Val Leu Pro Ile Glu Ala Ala Ser Trp Pro Leu His Gly Asn
        115                120                125

gta acg cca cat ttc aat ggt ttc ttg tct ttt cct tat gca tca caa
491
Val Thr Pro His Phe Asn Gly Phe Leu Ser Phe Pro Tyr Ala Ser Gln
130                135                140                145

cac acg gtg cag cat cct caa atc aga ggg ttg gtt ccg tct aga atg
539
His Thr Val Gln His Pro Gln Ile Arg Gly Leu Val Pro Ser Arg Met
                150                155                160

cct ttg cct cac aac att cca gag aac gaa cca att ttc gtc aat gca
587
Pro Leu Pro His Asn Ile Pro Glu Asn Glu Pro Ile Phe Val Asn Ala
                165                170                175

aaa cag tac caa gcc att ctc cgc cgc aga gag cgc cgt gca aag ctt
635
Lys Gln Tyr Gln Ala Ile Leu Arg Arg Arg Glu Arg Arg Ala Lys Leu
        180                185                190

gaa gct cag aac aag ctc atc aaa gtc cgc aaa cca tat ctt cac gag
683
Glu Ala Gln Asn Lys Leu Ile Lys Val Arg Lys Pro Tyr Leu His Glu
        195                200                205

tcg cgg cac ctc cat gca cta aag aga gtt aga ggc tct ggt gga cgt
731
Ser Arg His Leu His Ala Leu Lys Arg Val Arg Gly Ser Gly Gly Arg
210                215                220                225

ttc ctc aac aca aag aag cat caa gaa tca aat tcc tca cta tct cct
779
Phe Leu Asn Thr Lys Lys His Gln Glu Ser Asn Ser Ser Leu Ser Pro
                230                235                240

cca ttc ttg att cca cct cat gtc ttc aag aac tct cca gga aag ttc
827
Pro Phe Leu Ile Pro Pro His Val Phe Lys Asn Ser Pro Gly Lys Phe
                245                250                255

cgg caa atg gac att tca agg ggt ggg gtt gtg tct agt gtc tcg aca
875
Arg Gln Met Asp Ile Ser Arg Gly Gly Val Val Ser Ser Val Ser Thr
        260                265                270
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62

```
aca tct tgc tcg gac ata acc ggg aac aac aac gac atg ttc cag caa
923
Thr Ser Cys Ser Asp Ile Thr Gly Asn Asn Asn Asp Met Phe Gln Gln
    275                 280                 285

aac cca caa ttc agg ttc tca ggt tat cca tca aac cac cat gtc tca
971
Asn Pro Gln Phe Arg Phe Ser Gly Tyr Pro Ser Asn His His Val Ser
290                 295                 300                 305

gtc ctc atg tga gagagctccc gcaagtggtg gatgaggc
1011
Val Leu Met
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Met Gln Glu Phe His Ser Ser Lys Asp Ser Leu Pro Cys Pro Ala Thr
1               5                   10                  15


Ser Trp Asp Asn Ser Val Phe Thr Asn Ser Asn Val Gln Gly Ser Ser
            20                  25                  30


Ser Leu Thr Asp Asn Asn Thr Leu Ser Leu Thr Met Glu Met Lys Gln
            35                  40                  45


Thr Gly Phe Gln Met Gln His Tyr Asp Ser Ser Ser Thr Gln Ser Thr
    50                  55                  60


Gly Gly Glu Ser Tyr Ser Glu Val Ala Ser Leu Ser Glu Pro Thr Asn
65                  70                  75                  80


Arg Tyr Gly His Asn Ile Val Val Thr His Leu Ser Gly Tyr Lys Glu
                85                  90                  95


Asn Pro Glu Asn Pro Ile Gly Ser His Ser Ile Ser Lys Val Ser Gln
            100                 105                 110


Asp Ser Val Val Leu Pro Ile Glu Ala Ala Ser Trp Pro Leu His Gly
            115                 120                 125


Asn Val Thr Pro His Phe Asn Gly Phe Leu Ser Phe Pro Tyr Ala Ser
            130                 135                 140


Gln His Thr Val Gln His Pro Gln Ile Arg Gly Leu Val Pro Ser Arg
145                 150                 155                 160


Met Pro Leu Pro His Asn Ile Pro Glu Asn Glu Pro Ile Phe Val Asn
                165                 170                 175
```

```
Ala Lys Gln Tyr Gln Ala Ile Leu Arg Arg Arg Glu Arg Arg Ala Lys
        180                     185                 190

Leu Glu Ala Gln Asn Lys Leu Ile Lys Val Arg Lys Pro Tyr Leu His
        195                     200                 205

Glu Ser Arg His Leu His Ala Leu Lys Arg Val Arg Gly Ser Gly Gly
        210                     215                 220

Arg Phe Leu Asn Thr Lys Lys His Gln Glu Ser Asn Ser Ser Leu Ser
225                     230                 235                 240

Pro Pro Phe Leu Ile Pro Pro His Val Phe Lys Asn Ser Pro Gly Lys
                245                     250                 255

Phe Arg Gln Met Asp Ile Ser Arg Gly Gly Val Val Ser Ser Val Ser
            260                     265                 270

Thr Thr Ser Cys Ser Asp Ile Thr Gly Asn Asn Asn Asp Met Phe Gln
        275                     280                 285

Gln Asn Pro Gln Phe Arg Phe Ser Gly Tyr Pro Ser Asn His His Val
    290                     295                 300

Ser Val Leu Met
305
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58
                                                    Met Gly Arg
                                                    1

ggg aag att gtg atc caa agg atc gat gat tca acg agt aga caa gtc
106
Gly Lys Ile Val Ile Gln Arg Ile Asp Asp Ser Thr Ser Arg Gln Val
    5                   10                  15

act ttc tcc aaa cga aga aag ggc ctt atc aag aaa gcc aaa gag cta
154
Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Lys Lys Ala Lys Glu Leu
20                  25                  30                  35

gct att ctc tgt gat gcc gag gtc ggt ctc atc atc ttc tct agc acc
202
Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Ile Ile Phe Ser Ser Thr
            40                  45                  50
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gga aag ctc tat gac ttt gca agc tcc agc atg aag tcg gtt att gat
250
Gly Lys Leu Tyr Asp Phe Ala Ser Ser Ser Met Lys Ser Val Ile Asp
            55              60              65

aga tac aac aag agc aag atc gag caa caa caa cta ttg aac ccc gca
298
Arg Tyr Asn Lys Ser Lys Ile Glu Gln Gln Gln Leu Leu Asn Pro Ala
        70              75              80

tca gaa gtc aag ttt tgg cag aga gaa gct gct gtt cta aga caa gaa
346
Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Ala Val Leu Arg Gln Glu
        85              90              95

ctg cat gct ttg caa gaa aat cat cgg caa atg atg gga gaa cag cta
394
Leu His Ala Leu Gln Glu Asn His Arg Gln Met Met Gly Glu Gln Leu
100             105             110             115

aat ggt tta agt gtt aac gag cta aac agt ctt gag aat caa att gag
442
Asn Gly Leu Ser Val Asn Glu Leu Asn Ser Leu Glu Asn Gln Ile Glu
            120             125             130

ata agt ttg cgt gga att cgt atg aga aag gaa caa ctg ttg act caa
490
Ile Ser Leu Arg Gly Ile Arg Met Arg Lys Glu Gln Leu Leu Thr Gln
            135             140             145

gaa atc caa gaa cta agc caa aag agg aat ctt att cat cag gaa aac
538
Glu Ile Gln Glu Leu Ser Gln Lys Arg Asn Leu Ile His Gln Glu Asn
            150             155             160

ctc gat tta tct agg aaa gta caa cgg att cat caa gaa aat gtg gag
586
Leu Asp Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu Asn Val Glu
            165             170             175

ctc tac aag aag gct tat atg gca aac aca aac ggg ttt aca cac cgt
634
Leu Tyr Lys Lys Ala Tyr Met Ala Asn Thr Asn Gly Phe Thr His Arg
180             185             190             195

gaa gta gct gtt gcg gat gat gaa tca cac act cag att cgg ctg caa
682
Glu Val Ala Val Ala Asp Asp Glu Ser His Thr Gln Ile Arg Leu Gln
            200             205             210

cta agc cag cct gaa cat tcc gat tat gac act cca cca aga gca aac
730
Leu Ser Gln Pro Glu His Ser Asp Tyr Asp Thr Pro Pro Arg Ala Asn
            215             220             225

gaa taa cagagagatt gaagttggaa gataccatga tgttgaagaa cactccaaag
786
Glu
```

gccttggttt gaataaggtt cttgaactgg aaacctctat acaccaagcc acgtacgata
846

agcagcatgg ttcttctaac atagtcatat tttcaatcct aaatataatt aaagcatata
906

taattaaaat ccggtgttgt tatactcatc ttgagtatta atattgtact tgtttataac
966

catagattcg tcaattaata gagaaaaatc atatgaatta ttatccaaaa aaaaaaaaaa
1026

aaaaaaaaaa aa
1038

<210> 32 <211> 228 <212> PRT <213> Arabidopsis thaliana <400>
32

Met Gly Arg Gly Lys Ile Val Ile Gln Arg Ile Asp Asp Ser Thr Ser
1   5   10   15

Arg Gln Val Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Lys Lys Ala
            20   25   30

Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Ile Ile Phe
        35   40   45

Ser Ser Thr Gly Lys Leu Tyr Asp Phe Ala Ser Ser Ser Met Lys Ser
    50   55   60

Val Ile Asp Arg Tyr Asn Lys Ser Lys Ile Glu Gln Gln Gln Leu Leu
65   70   75   80

Asn Pro Ala Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Ala Val Leu
                85   90   95

Arg Gln Glu Leu His Ala Leu Gln Glu Asn His Arg Gln Met Met Gly
            100   105   110

Glu Gln Leu Asn Gly Leu Ser Val Asn Glu Leu Asn Ser Leu Glu Asn
            115   120   125

Gln Ile Glu Ile Ser Leu Arg Gly Ile Arg Met Arg Lys Glu Gln Leu
        130   135   140

Leu Thr Gln Glu Ile Gln Glu Leu Ser Gln Lys Arg Asn Leu Ile His
145   150   155   160

Gln Glu Asn Leu Asp Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu
                165   170   175

```
Asn Val Glu Leu Tyr Lys Lys Ala Tyr Met Ala Asn Thr Asn Gly Phe
          180                 185             190


Thr His Arg Glu Val Ala Val Ala Asp Asp Glu Ser His Thr Gln Ile
          195                 200             205


Arg Leu Gln Leu Ser Gln Pro Glu His Ser Asp Tyr Asp Thr Pro Pro
    210                 215             220


Arg Ala Asn Glu
225


<210>  33 <211>  609 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (1)..(609) <223>  G1820

 <400>  33
atg gct gag aac aac aac aac aac ggc gac aac atg aac aac gac aac
48
Met Ala Glu Asn Asn Asn Asn Asn Gly Asp Asn Met Asn Asn Asp Asn
1                5                 10              15


cac cag caa cca ccg tcg tac tcg cag ctg ccg ccg atg gca tca tcc
96
His Gln Gln Pro Pro Ser Tyr Ser Gln Leu Pro Pro Met Ala Ser Ser
             20              25              30


aac cct cag tta cgt aat tac tgg att gag cag atg gaa acc gtc tcg
144
Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser
         35              40              45


gat ttc aaa aac cgt cag ctt cca ttg gct cga att aag aag atc atg
192
Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
     50              55              60


aag gct gat cca gat gtg cac atg gtc tcc gca gag gct ccg atc atc
240
Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile
65              70              75              80


ttc gca aag gct tgc gaa atg ttc atc gtt gat ctc acg atg cgg tcg
288
Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser
                85              90              95


tgg ctc aaa gcc gag gag aac aaa cgc cac acg ctt cag aaa tcg gat
336
Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp
             100             105             110


atc tcc aac gca gtg gct agc tct ttc acc tac gat ttc ctt ctt gat
384
Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp
         115             120             125
```

```
gtt gtc cct aag gac gag tct atc gcc acc gct gat cct ggc ttt gtg
432
Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val
    130             135             140

gct atg cca cat cct gac ggt gga gga gta ccg caa tat tat tat cca
480
Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro
145             150             155             160

ccg gga gtg gtg atg gga act cct atg gtt ggt agt gga atg tac gcg
528
Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala
                165             170             175

cca tcg cag gcg tgg cca gca gcg gct ggt gac ggg gag gat gat gct
576
Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala
            180             185             190

gag gat aat gga gga aac ggc ggc gga aat tga
609
Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn
        195             200
```

<210> 34 <211> 202 <212> PRT <213> Arabidopsis thaliana <400>
34

```
Met Ala Glu Asn Asn Asn Asn Gly Asp Asn Met Asn Asn Asp Asn
1               5               10              15

His Gln Gln Pro Pro Ser Tyr Ser Gln Leu Pro Pro Met Ala Ser Ser
        20              25              30

Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser
        35              40              45

Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
    50              55              60

Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile
65              70              75              80

Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser
            85              90              95

Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp
        100             105             110

Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp
        115             120             125
```

Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val
    130   135   140

Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro
145   150   155   160

Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala
                165   170   175

Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala
                180   185   190

Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn
        195   200

<210> 35 <211> 1155 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (76)..(1077) <223> G1930

<400> 35
attcacatta ctaatctctc aagatttcac aattttcttg tgattttctc tcagtttctt
60

atttcgtttc ataac atg gat gcc atg agt agc gta gac gag agc tct aca
111
           Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr
           1   5   10

act aca gat tcc att ccg gcg aga aag tca tcg tct ccg gcg agt tta
159
Thr Thr Asp Ser Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu
        15   20   25

cta tat aga atg gga agc gga aca agc gtg gta ctt gat tca gag aac
207
Leu Tyr Arg Met Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn
    30   35   40

ggt gtc gaa gtc gaa gtc gaa gcc gaa tca aga aag ctt cct tct tca
255
Gly Val Glu Val Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser
45   50   55   60

aga ttc aaa ggt gtt gtt cct caa cca aat gga aga tgg gga gct cag
303
Arg Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln
                65   70   75

att tac gag aaa cat caa cgc gtg tgg ctt ggt act ttc aac gag gaa
351
Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu
                80   85   90

gac gaa gca gct cgt gct tac gac gtc gcg gct cac cgt ttc cgt ggc
399
Asp Glu Ala Ala Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly

69

                    95   100   105

```
cgc gat gcc gtt act aat ttc aaa gac acg acg ttc gaa gaa gag gtt
447
Arg Asp Ala Val Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val
    110                 115                 120

gag ttc tta aac gcg cat tcg aaa tca gag atc gta gat atg ttg aga
495
Glu Phe Leu Asn Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg
125                 130                 135                 140

aaa cac act tac aaa gaa gag tta gac caa agg aaa cgt aac cgt gac
543
Lys His Thr Tyr Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp
                145                 150                 155

ggt aac gga aaa gag acg acg gcg ttt gct ttg gct tcg atg gtg gtt
591
Gly Asn Gly Lys Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val
            160                 165                 170

atg acg ggg ttt aaa acg gcg gag tta ctg ttt gag aaa acg gta acg
639
Met Thr Gly Phe Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr
            175                 180                 185

cca agt gac gtc ggg aaa cta aac cgt tta gtt ata cca aaa cac caa
687
Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln
    190                 195                 200

gcg gag aaa cat ttt ccg tta ccg tta ggt aat aat aac gtc tcc gtt
735
Ala Glu Lys His Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val
205                 210                 215                 220

aaa ggt atg ctg ttg aat ttc gaa gac gtt aac ggg aaa gtg tgg agg
783
Lys Gly Met Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg
                225                 230                 235

ttc cgt tac tct tat tgg aat agt agt caa agt tat gtg ttg acc aaa
831
Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
            240                 245                 250

ggt tgg agt aga ttc gtt aaa gag aag aga ctt tgt gct ggt gat ttg
879
Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu
            255                 260                 265

atc agt ttt aaa aga tcc aac gat caa gat caa aaa ttc ttt atc ggg
927
Ile Ser Phe Lys Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly
            270                 275                 280

tgg aaa tcg aaa tcc ggg ttg gat cta gag acg ggt cgg gtt atg aga
975
Trp Lys Ser Lys Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg
285                 290                 295                 300
```

                                    70

```
ttg ttt ggg gtt gat att tct tta aac gcc gtc gtt gta gtg aag gaa
1023
Leu Phe Gly Val Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu
            305             310                 315

aca acg gag gtg tta atg tcg tcg tta agg tgt aag aag caa cga gtt
1071
Thr Thr Glu Val Leu Met Ser Ser Leu Arg Cys Lys Lys Gln Arg Val
        320             325                 330

ttg taa taacaattta acaacttggg aaagaaaaaa aagcttttg attttaattt
1127
Leu


ctcttcaacg ttaatcttgc tgagatta
1155
```

<210> 36 <211> 333 <212> PRT <213> Arabidopsis thaliana <400> 36

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Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr Thr Thr Asp Ser
1               5               10                  15

Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met
            20              25                  30

Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val
        35              40                  45

Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly
    50              55                  60

Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
65              70                  75                  80

His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
            85              90                  95

Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val
            100             105                 110

Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn
            115             120                 125

Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
        130             135                 140

Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys
145             150                 155                 160
```

71

```
Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe
              165                 170                 175


Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val
              180                 185                 190


Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His
          195                 200                 205


Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu
    210                 215                 220


Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser
225                 230                 235                 240


Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg
                  245                 250                 255


Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys
              260                 265                 270


Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys
          275                 280                 285


Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val
    290                 295                 300


Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu Thr Thr Glu Val
305                 310                 315                 320


Leu Met Ser Ser Leu Arg Cys Lys Lys Gln Arg Val Leu
                  325                 330


<210> 37 <211> 525 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(525) <223> G2010

 <400> 37
atg gag ggt aag aga tca caa gga caa ggt tac atg aaa aag aag tct
48
Met Glu Gly Lys Arg Ser Gln Gly Gln Gly Tyr Met Lys Lys Lys Ser
1               5                   10                  15


tac ctt gtg gaa gaa gat atg gag act gat acg gat gaa gaa gag gaa
96
Tyr Leu Val Glu Glu Asp Met Glu Thr Asp Thr Asp Glu Glu Glu Glu
              20                  25                  30
```

```
gta ggt agg gat aga gtt aga ggg tct aga ggt agc atc aat cgt ggt
144
Val Gly Arg Asp Arg Val Arg Gly Ser Arg Gly Ser Ile Asn Arg Gly
         35                    40                   45

ggc tcg ttg cgg ctt tgc caa gta gat aga tgc aca gct gat atg aaa
192
Gly Ser Leu Arg Leu Cys Gln Val Asp Arg Cys Thr Ala Asp Met Lys
    50                    55                   60

gag gca aaa ctg tat cac cgg aga cac aaa gtg tgt gaa gtt cat gca
240
Glu Ala Lys Leu Tyr His Arg Arg His Lys Val Cys Glu Val His Ala
65                    70                   75                   80

aag gca tct tct gtc ttt ctc tca gga ctt aac caa cgc ttt tgt caa
288
Lys Ala Ser Ser Val Phe Leu Ser Gly Leu Asn Gln Arg Phe Cys Gln
                 85                    90                   95

caa tgc agt agg ttt cat gac ctc caa gag ttt gat gaa gct aag aga
336
Gln Cys Ser Arg Phe His Asp Leu Gln Glu Phe Asp Glu Ala Lys Arg
         100                   105                  110

agt tgc agg agg cgc tta gct gga cac aat gag cga aga agg aag agc
384
Ser Cys Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ser
         115                   120                  125

tct ggt gag agt act tat gga gaa gga tca ggt cgg aga gga atc aat
432
Ser Gly Glu Ser Thr Tyr Gly Glu Gly Ser Gly Arg Arg Gly Ile Asn
    130                   135                  140

ggt cag gtg gtg atg cag aat caa gaa aga tca agg gta gag atg aca
480
Gly Gln Val Val Met Gln Asn Gln Glu Arg Ser Arg Val Glu Met Thr
145                   150                  155                  160

ctt cct atg cca aac tca tca ttc aag cga cca cag att aga tag
525
Leu Pro Met Pro Asn Ser Ser Phe Lys Arg Pro Gln Ile Arg
                 165                   170
```

```
<210> 38 <211> 174 <212> PRT <213> Arabidopsis thaliana <400>
38

Met Glu Gly Lys Arg Ser Gln Gly Gln Gly Tyr Met Lys Lys Lys Ser
1             5                    10                   15

Tyr Leu Val Glu Glu Asp Met Glu Thr Asp Thr Asp Glu Glu Glu Glu
         20                    25                   30

Val Gly Arg Asp Arg Val Arg Gly Ser Arg Gly Ser Ile Asn Arg Gly
         35                    40                   45
```

Gly Ser Leu Arg Leu Cys Gln Val Asp Arg Cys Thr Ala Asp Met Lys
    50   55   60

Glu Ala Lys Leu Tyr His Arg Arg His Lys Val Cys Glu Val His Ala
65   70   75   80

Lys Ala Ser Ser Val Phe Leu Ser Gly Leu Asn Gln Arg Phe Cys Gln
            85   90   95

Gln Cys Ser Arg Phe His Asp Leu Gln Glu Phe Asp Glu Ala Lys Arg
        100   105   110

Ser Cys Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ser
        115   120   125

Ser Gly Glu Ser Thr Tyr Gly Glu Gly Ser Gly Arg Arg Gly Ile Asn
    130   135   140

Gly Gln Val Val Met Gln Asn Gln Glu Arg Ser Arg Val Glu Met Thr
145   150   155   160

Leu Pro Met Pro Asn Ser Ser Phe Lys Arg Pro Gln Ile Arg
            165   170

<210> 39 <211> 759 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (16)..(477) <223> G3

 <400> 39
gtttgtcttt tatca atg gaa aga gaa caa gaa gag tct acg atg aga aag
51
                 Met Glu Arg Glu Gln Glu Glu Ser Thr Met Arg Lys
                 1   5   10

aga agg cag cca cct caa gaa gaa gtg cct aac cac gtg gct aca agg
99
Arg Arg Gln Pro Pro Gln Glu Glu Val Pro Asn His Val Ala Thr Arg
        15   20   25

aag ccg tac aga ggg ata cgg agg agg aag tgg ggc aag tgg gtg gct
147
Lys Pro Tyr Arg Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ala
    30   35   40

gag att cgt gag cct aac aaa cgc tca cgg ctt tgg ctt ggc tct tac
195
Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser Tyr
45   50   55   60

aca acc gat atc gcc gcc gct aga gcc tac gac gtg gcc gtc ttc tac
243
Thr Thr Asp Ile Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe Tyr
            65   70   75

74

```
ctc cgt ggc ccc tcc gca cgt ctc aac ttc cct gat ctt ctc ttg caa
291
Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu Gln
        80                  85                  90

gaa gag gac cat ctc tca gcc gcc acc acc gct gac atg ccc gca gct
339
Glu Glu Asp His Leu Ser Ala Ala Thr Thr Ala Asp Met Pro Ala Ala
        95                  100                 105

ctt ata agg gaa aaa gcg gcg gag gtc ggc gcc aga gtc gac gct ctt
387
Leu Ile Arg Glu Lys Ala Ala Glu Val Gly Ala Arg Val Asp Ala Leu
    110                 115                 120

cta gct tct gcc gct cct tcg atg gct cac tcc act ccg ccg gta ata
435
Leu Ala Ser Ala Ala Pro Ser Met Ala His Ser Thr Pro Pro Val Ile
125                 130                 135                 140

aaa ccc gac ttg aat caa ata ccc gaa tcc gga gat ata tag
477
Lys Pro Asp Leu Asn Gln Ile Pro Glu Ser Gly Asp Ile
                145                 150

tcaatttata tacatgtagt ttgttttgtt tgattagaag attacattta catacaagat
537

acacatagat actggaaaat ataggtatgt atacattcat aaattatctt atgtatcaaa
597

gaattttata gattctgatt agctttttgt ttttgttttt gataagaact ctgattagtt
657

gtccggagac aaaaccggct aagagcaatc catgagaagc tagcgagtgt tttttagttc
717

aagttgtaat ataaatgcat attaattctt tagtaatttt gt
759
```

<210> 40 <211> 153 <212> PRT <213> Arabidopsis thaliana <400> 40

```
Met Glu Arg Glu Gln Glu Glu Ser Thr Met Arg Lys Arg Arg Gln Pro
1               5                   10                  15

Pro Gln Glu Glu Val Pro Asn His Val Ala Thr Arg Lys Pro Tyr Arg
            20                  25                  30

Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ala Glu Ile Arg Glu
        35                  40                  45

Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser Tyr Thr Thr Asp Ile
    50                  55                  60

Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe Tyr Leu Arg Gly Pro
```

75

```
       65                    70                    75                    80
```

Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu Gln Glu Glu Asp His
                85   90   95

Leu Ser Ala Ala Thr Thr Ala Asp Met Pro Ala Ala Leu Ile Arg Glu
            100   105   110

Lys Ala Ala Glu Val Gly Ala Arg Val Asp Ala Leu Leu Ala Ser Ala
            115   120   125

Ala Pro Ser Met Ala His Ser Thr Pro Pro Val Ile Lys Pro Asp Leu
        130   135   140

Asn Gln Ile Pro Glu Ser Gly Asp Ile
145   150

<210> 41 <211> 1650 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (107)..(1393) <223> G20

 <400> 41
ctctcactct ctttttctct ctctttactt ctactgtatc aagaagctcc gttttgctta
60

gccatagtgc gtctagggtt tggttggtgg gaagaaggtt ccgatc atg gcg tcg
115
                                                Met Ala Ser
                                                1

gtg tcg tcg tcg gat caa gga cct aag aca gaa gca gga tgt agc ggc
163
Val Ser Ser Ser Asp Gln Gly Pro Lys Thr Glu Ala Gly Cys Ser Gly
    5   10   15

gga gga gga gga gag agc tcg gag aca gtg gcg gcg agt gat cag atg
211
Gly Gly Gly Gly Glu Ser Ser Glu Thr Val Ala Ala Ser Asp Gln Met
20   25   30   35

ttg ttg tat aga ggt ttt aag aag gcg aag aag gag aga ggt tgt aca
259
Leu Leu Tyr Arg Gly Phe Lys Lys Ala Lys Lys Glu Arg Gly Cys Thr
                40   45   50

gct aag gag cgt att agt aaa atg cct ccg tgc act gct ggg aaa agg
307
Ala Lys Glu Arg Ile Ser Lys Met Pro Pro Cys Thr Ala Gly Lys Arg
            55   60   65

agt tcc ata tac cgg gga gtc acc aga cat aga tgg aca ggt cgt tat
355
Ser Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr
            70   75   80

```
gaa gct cac ctt tgg gat aag agt acc tgg aac caa aac cag aac aag
403
Glu Ala His Leu Trp Asp Lys Ser Thr Trp Asn Gln Asn Gln Asn Lys
     85              90              95


aag gga aaa caa gtt tat cta gga gca tat gat gat gaa gag gct gct
451
Lys Gly Lys Gln Val Tyr Leu Gly Ala Tyr Asp Asp Glu Glu Ala Ala
100             105             110             115


gct aga gct tac gac ctt gct gcc tta aaa tat tgg ggt cct ggg aca
499
Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Gly Thr
            120             125             130


ctt ata aat ttt ccg gtg act gat tat acc agg gat tta gaa gaa atg
547
Leu Ile Asn Phe Pro Val Thr Asp Tyr Thr Arg Asp Leu Glu Glu Met
            135             140             145


caa aat ctc tca agg gaa gaa tac ctt gca tct tta cgt aga tat ccc
595
Gln Asn Leu Ser Arg Glu Glu Tyr Leu Ala Ser Leu Arg Arg Tyr Pro
        150             155             160


ttt ggc aga aaa agc agc ggt ttc tct agg gga ata gcg aaa tat cgt
643
Phe Gly Arg Lys Ser Ser Gly Phe Ser Arg Gly Ile Ala Lys Tyr Arg
        165             170             175


gga ctt caa agc cga tgg gac gca tca gcc agt cgt atg cct gga cct
691
Gly Leu Gln Ser Arg Trp Asp Ala Ser Ala Ser Arg Met Pro Gly Pro
180             185             190             195


gaa tac ttc agt aac att cat tac ggg gca ggt gat gat cgt gga aca
739
Glu Tyr Phe Ser Asn Ile His Tyr Gly Ala Gly Asp Asp Arg Gly Thr
            200             205             210


gaa ggt gac ttt cta ggt agc ttt tgt ctg gaa aga aag att gat cta
787
Glu Gly Asp Phe Leu Gly Ser Phe Cys Leu Glu Arg Lys Ile Asp Leu
            215             220             225


aca gga tac ata aag tgg tgg gga gcc aac aag aac cgt caa cca gaa
835
Thr Gly Tyr Ile Lys Trp Trp Gly Ala Asn Lys Asn Arg Gln Pro Glu
            230             235             240


tct tca tca aaa gca tca gag gat gca aac gtc gaa gat gct ggt act
883
Ser Ser Ser Lys Ala Ser Glu Asp Ala Asn Val Glu Asp Ala Gly Thr
        245             250             255


gag ctt aaa aca ctg gaa cac aca tcc cat gca aca gaa cca tac aag
931
Glu Leu Lys Thr Leu Glu His Thr Ser His Ala Thr Glu Pro Tyr Lys
260             265             270             275
```

gcg cca aac ctt ggc gtc ctt tgt gga act cag aga aaa gaa aaa gaa
979
Ala Pro Asn Leu Gly Val Leu Cys Gly Thr Gln Arg Lys Glu Lys Glu
            280   285   290

ata tca tca cca tca agc tct tct gct tta agc atc ttg tct cag tcg
1027
Ile Ser Ser Pro Ser Ser Ser Ser Ala Leu Ser Ile Leu Ser Gln Ser
            295   300   305

cct gcc ttc aag agc cta gag gag aaa gtg ttg aag atc caa gaa agc
1075
Pro Ala Phe Lys Ser Leu Glu Glu Lys Val Leu Lys Ile Gln Glu Ser
            310   315   320

tgc aat aat gaa aac gat gag aat gca aac cgt aac atc atc aat atg
1123
Cys Asn Asn Glu Asn Asp Glu Asn Ala Asn Arg Asn Ile Ile Asn Met
            325   330   335

gag aag aat aac ggc aag gca ata gag aaa cca gtt gtg agt cat gga
1171
Glu Lys Asn Asn Gly Lys Ala Ile Glu Lys Pro Val Val Ser His Gly
340   345   -- 350   355

gtt gct tta ggc ggt gct gct gct ttg tct ctt cag aaa agc atg tac
1219
Val Ala Leu Gly Gly Ala Ala Ala Leu Ser Leu Gln Lys Ser Met Tyr
            360   365   370

cca ctt acc tct ctc tta acg gct cca ttg ctc acc aac tac aat aca
1267
Pro Leu Thr Ser Leu Leu Thr Ala Pro Leu Leu Thr Asn Tyr Asn Thr
            375   380   385

ttg gat cct ctt gca gac cct att ctc tgg aca cca ttt ctt cct tca
1315
Leu Asp Pro Leu Ala Asp Pro Ile Leu Trp Thr Pro Phe Leu Pro Ser
            390   395   400

gga tcc tct ctt act tca gag gtg aca aag aca gag acc agc tgt tcc
1363
Gly Ser Ser Leu Thr Ser Glu Val Thr Lys Thr Glu Thr Ser Cys Ser
            405   410   415

acg tac agc tac ctc cca caa gag aaa tga gccgttccct ttagacttta
1413
Thr Tyr Ser Tyr Leu Pro Gln Glu Lys
420   425

tgtatgtcag attctccttt tttgagatga attcgtcgac ttgacatctc tttgtctctt
1473

ttatggagaa aaagttggga aaagtgtgac aatggtctga agcaggaatg tacaggtttt
1533

gttagtggtt gtgttttttt ttttccagtg tggaatatag aatcatgata ttttgtgtaa
1593

aacagaaaaa agttatcatt atagtataga agtttgctct taaaaaaaaa aaaaaaa
1650

78

<210> 42 <211> 428 <212> PRT <213> Arabidopsis thaliana <400>
42

Met Ala Ser Val Ser Ser Ser Asp Gln Gly Pro Lys Thr Glu Ala Gly
1   5   10   15

Cys Ser Gly Gly Gly Gly Gly Glu Ser Ser Glu Thr Val Ala Ala Ser
            20   25   30

Asp Gln Met Leu Leu Tyr Arg Gly Phe Lys Lys Ala Lys Lys Glu Arg
        35   40   45

Gly Cys Thr Ala Lys Glu Arg Ile Ser Lys Met Pro Pro Cys Thr Ala
    50   55   60

Gly Lys Arg Ser Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr
65   70   75   80

Gly Arg Tyr Glu Ala His Leu Trp Asp Lys Ser Thr Trp Asn Gln Asn
            85   90   95

Gln Asn Lys Lys Gly Lys Gln Val Tyr Leu Gly Ala Tyr Asp Asp Glu
            100   105   110

Glu Ala Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly
        115   120   125

Pro Gly Thr Leu Ile Asn Phe Pro Val Thr Asp Tyr Thr Arg Asp Leu
    130   135   140

Glu Glu Met Gln Asn Leu Ser Arg Glu Glu Tyr Leu Ala Ser Leu Arg
145   150   155   160

Arg Tyr Pro Phe Gly Arg Lys Ser Ser Gly Phe Ser Arg Gly Ile Ala
            165   170   175

Lys Tyr Arg Gly Leu Gln Ser Arg Trp Asp Ala Ser Ala Ser Arg Met
            180   185   190

Pro Gly Pro Glu Tyr Phe Ser Asn Ile His Tyr Gly Ala Gly Asp Asp
        195   200   205

Arg Gly Thr Glu Gly Asp Phe Leu Gly Ser Phe Cys Leu Glu Arg Lys
    210   215   220

79

```
Ile Asp Leu Thr Gly Tyr Ile Lys Trp Trp Gly Ala Asn Lys Asn Arg
225             230             235             240

Gln Pro Glu Ser Ser Ser Lys Ala Ser Glu Asp Ala Asn Val Glu Asp
            245             250             255

Ala Gly Thr Glu Leu Lys Thr Leu Glu His Thr Ser His Ala Thr Glu
            260             265             270

Pro Tyr Lys Ala Pro Asn Leu Gly Val Leu Cys Gly Thr Gln Arg Lys
        275             280             285

Glu Lys Glu Ile Ser Ser Pro Ser Ser Ser Ser Ala Leu Ser Ile Leu
    290             295             300

Ser Gln Ser Pro Ala Phe Lys Ser Leu Glu Glu Lys Val Leu Lys Ile
305             310             315             320

Gln Glu Ser Cys Asn Asn Glu Asn Asp Glu Asn Ala Asn Arg Asn Ile
            325             330             335

Ile Asn Met Glu Lys Asn Asn Gly Lys Ala Ile Glu Lys Pro Val Val
        340             345             350

Ser His Gly Val Ala Leu Gly Gly Ala Ala Ala Leu Ser Leu Gln Lys
    355             360             365

Ser Met Tyr Pro Leu Thr Ser Leu Leu Thr Ala Pro Leu Leu Thr Asn
    370             375             380

Tyr Asn Thr Leu Asp Pro Leu Ala Asp Pro Ile Leu Trp Thr Pro Phe
385             390             395             400

Leu Pro Ser Gly Ser Ser Leu Thr Ser Glu Val Thr Lys Thr Glu Thr
            405             410             415

Ser Cys Ser Thr Tyr Ser Tyr Leu Pro Gln Glu Lys
            420             425
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<210>  43 <211>  933 <212>  DNA <213>  Arabidopsis thaliana <220>
<221>  CDS <222>  (20)..(757) <223>  G33

  <400>  43
attctcccccc aaccaaaat atg acc aca gaa aaa gag aat gtc act acg gcc
52
                    Met Thr Thr Glu Lys Glu Asn Val Thr Thr Ala
                    1               5                   10
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gtg gcc gtg aaa gac ggc gga gaa aag agt aag gaa gtg agt .gac aag
100
Val Ala Val Lys Asp Gly Gly Glu Lys Ser Lys Glu Val Ser Asp Lys
            15                  20                  25


ggc gta aag aag aga aag aat gta act aag gcc ctg gcc gtg aat gac
148
Gly Val Lys Lys Arg Lys Asn Val Thr Lys Ala Leu Ala Val Asn Asp
        30                  35                  40


ggc gga gaa aag agt aag gaa gtg cgt tac agg ggt gta agg agg aga
196
Gly Gly Glu Lys Ser Lys Glu Val Arg Tyr Arg Gly Val Arg Arg Arg
    45                  50                  55


cca tgg ggg aga tat gct gcg gag atc cgt gat ccg gta aag aaa aaa
244
Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Val Lys Lys Lys
60                  65                  70                  75


cgg gtc tgg ctc ggg tcc ttc aac acg ggg gag gaa gcc gcc aga gcc
292
Arg Val Trp Leu Gly Ser Phe Asn Thr Gly Glu Glu Ala Ala Arg Ala
                80                  85                  90


tac gac tcc gct gcc ata agg ttt cga gga tcg aaa gct act act aac
340
Tyr Asp Ser Ala Ala Ile Arg Phe Arg Gly Ser Lys Ala Thr Thr Asn
                95                  100                 105


ttc cct cta atc gga tac tat ggg att tct tcg gcg acg ccg gtg aac
388
Phe Pro Leu Ile Gly Tyr Tyr Gly Ile Ser Ser Ala Thr Pro Val Asn
            110                 115                 120


aac aac ctt tcc gag acg gtg agt gat gga aat gcc aac ctc cct ctc
436
Asn Asn Leu Ser Glu Thr Val Ser Asp Gly Asn Ala Asn Leu Pro Leu
    125                 130                 135


gtt gga gac gat ggg aat gct ttg gct tct ccg gtg aac aac acc ctt
484
Val Gly Asp Asp Gly Asn Ala Leu Ala Ser Pro Val Asn Asn Thr Leu
140                 145                 150                 155


tcc gaa acg gcg cgt gat gga aca ctt cca tcg gat tgt cac gac atg
532
Ser Glu Thr Ala Arg Asp Gly Thr Leu Pro Ser Asp Cys His Asp Met
                160                 165                 170


tta tct ccg ggg gtg gct gaa gcg gtt gct gga ttt ttc tta gat ctg
580
Leu Ser Pro Gly Val Ala Glu Ala Val Ala Gly Phe Phe Leu Asp Leu
                175                 180                 185


cct gaa gtt att gcg ttg aaa gag gag ctt gat cga gtt tgt cct gac
628
Pro Glu Val Ile Ala Leu Lys Glu Glu Leu Asp Arg Val Cys Pro Asp
                190                 195                 200
```

81

cag ttt gag tcc att gat atg ggg ttg act att ggt cct caa acc gcc
676
Gln Phe Glu Ser Ile Asp Met Gly Leu Thr Ile Gly Pro Gln Thr Ala
    205   210   215

gtg gaa gag cct gag act tcc tcc gcc gtg gat tgt aag ctg cga atg
724
Val Glu Glu Pro Glu Thr Ser Ser Ala Val Asp Cys Lys Leu Arg Met
220   225   230   235

gaa ccg gat ctt gac ctc aac gca agt ccc taa agattgatct gatgttgttg
777
Glu Pro Asp Leu Asp Leu Asn Ala Ser Pro
                240   245

tccttgaata agtttgttat cttgtcgctc ttctgattgt ctgtacttct attggttgat
837

tcgtgctttt ggaggacaaa acaaacattt ttttatgtat taaaaaaagg taattgaact
897

attatcgaaa aaaaaaaaaa aaaaaaaaaa aaaaaa
933

<210> 44 <211> 245 <212> PRT <213> Arabidopsis thaliana <400>
44

Met Thr Thr Glu Lys Glu Asn Val Thr Thr Ala Val Ala Val Lys Asp
1   5   10   15

Gly Gly Glu Lys Ser Lys Glu Val Ser Asp Lys Gly Val Lys Lys Arg
            20   25   30

Lys Asn Val Thr Lys Ala Leu Ala Val Asn Asp Gly Gly Glu Lys Ser
        35   40   45

Lys Glu Val Arg Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Arg Tyr
    50   55   60

Ala Ala Glu Ile Arg Asp Pro Val Lys Lys Lys Arg Val Trp Leu Gly
65   70   75   80

Ser Phe Asn Thr Gly Glu Glu Ala Ala Arg Ala Tyr Asp Ser Ala Ala
            85   90   95

Ile Arg Phe Arg Gly Ser Lys Ala Thr Thr Asn Phe Pro Leu Ile Gly
            100   105   110

Tyr Tyr Gly Ile Ser Ser Ala Thr Pro Val Asn Asn Asn Leu Ser Glu
        115   120   125

Thr Val Ser Asp Gly Asn Ala Asn Leu Pro Leu Val Gly Asp Asp Gly

```
         130                    135                    140

Asn Ala Leu Ala Ser Pro Val Asn Asn Thr Leu Ser Glu Thr Ala Arg
145                 150                 155                 160

Asp Gly Thr Leu Pro Ser Asp Cys His Asp Met Leu Ser Pro Gly Val
                165                 170                 175

Ala Glu Ala Val Ala Gly Phe Phe Leu Asp Leu Pro Glu Val Ile Ala
            180                 185                 190

Leu Lys Glu Glu Leu Asp Arg Val Cys Pro Asp Gln Phe Glu Ser Ile
        195                 200                 205

Asp Met Gly Leu Thr Ile Gly Pro Gln Thr Ala Val Glu Glu Pro Glu
    210                 215                 220

Thr Ser Ser Ala Val Asp Cys Lys Leu Arg Met Glu Pro Asp Leu Asp
225                 230                 235                 240

Leu Asn Ala Ser Pro
                245
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<210> 45 <211> 754 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (75)..(638) <223> G39

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 <400> 45
gtttccacag tccctgtact tgtgcataaa actgtaaaac actactctga aaattttgct
60

tctgttagga tata atg cca ccc tct cct cct aaa tct cct ttt att agc
110
               Met Pro Pro Ser Pro Pro Lys Ser Pro Phe Ile Ser
               1               5                   10

tct tca ctc aaa gga gct cat gaa gat cgc aaa ttt aaa tgc tat agg
158
Ser Ser Leu Lys Gly Ala His Glu Asp Arg Lys Phe Lys Cys Tyr Arg
        15              20                  25

ggt gtc cga aag agg tct tgg ggc aaa tgg gtg tct gaa atc aga gtt
206
Gly Val Arg Lys Arg Ser Trp Gly Lys Trp Val Ser Glu Ile Arg Val
    30              35                  40

cca aag act gga cga cga ata tgg cta ggt tca tac gat gct cca gag
254
Pro Lys Thr Gly Arg Arg Ile Trp Leu Gly Ser Tyr Asp Ala Pro Glu
45              50                  55                  60

aag gca gct aga gcc tat gat gct gct ttg ttc tgt att agg ggt gag
302
Lys Ala Ala Arg Ala Tyr Asp Ala Ala Leu Phe Cys Ile Arg Gly Glu
```

```
                    65                    70                    75

aag gga gtt tac aat ttt ccc act gat aaa aag ccg cag ctt cca gaa
350
Lys Gly Val Tyr Asn Phe Pro Thr Asp Lys Lys Pro Gln Leu Pro Glu
              80                    85                    90

ggt tct gtc cgg cct ctg tcc aag ctc gac ata cag aca ata gca aca
398
Gly Ser Val Arg Pro Leu Ser Lys Leu Asp Ile Gln Thr Ile Ala Thr
          95                    100                   105

aac tat gct tca tca gtt gtg cat gta cct tcc cat gcc acc aca ctc
446
Asn Tyr Ala Ser Ser Val Val His Val Pro Ser His Ala Thr Thr Leu
      110                   115                   120

ccg gca aca acc cag gtt ccc tct gaa gtt cct gct tcc tct gat gtt
494
Pro Ala Thr Thr Gln Val Pro Ser Glu Val Pro Ala Ser Ser Asp Val
125                   130                   135                   140

tct gct tct act gag att aca gag atg gtc gat gaa tat tat ctc cca
542
Ser Ala Ser Thr Glu Ile Thr Glu Met Val Asp Glu Tyr Tyr Leu Pro
              145                   150                   155

acc gat gca act gca gaa tca ata ttc tca gtt gaa gac tta caa ctg
590
Thr Asp Ala Thr Ala Glu Ser Ile Phe Ser Val Glu Asp Leu Gln Leu
              160                   165                   170

gac agt ttc ctc atg atg gac att gat tgg ata aac aat cta atc tga
638
Asp Ser Phe Leu Met Met Asp Ile Asp Trp Ile Asn Asn Leu Ile
          175                   180                   185

tgtgtaacgt cacttgcagt gacatttaat atggtttaac tatcagttac ctgtctgctt
698

cttgtaaggg tatacttgga tccttgtctt tgaacttgtt ttatttagca tgcaaa
754


<210> 46 <211> 187 <212> PRT <213> Arabidopsis thaliana <400>
46

Met Pro Pro Ser Pro Pro Lys Ser Pro Phe Ile Ser Ser Ser Leu Lys
1                   5                    10                   15


Gly Ala His Glu Asp Arg Lys Phe Lys Cys Tyr Arg Gly Val Arg Lys
              20                   25                   30


Arg Ser Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro Lys Thr Gly
          35                   40                   45


Arg Arg Ile Trp Leu Gly Ser Tyr Asp Ala Pro Glu Lys Ala Ala Arg
      50                   55                   60
```

84

Ala Tyr Asp Ala Ala Leu Phe Cys Ile Arg Gly Glu Lys Gly Val Tyr
65   70   75   80

Asn Phe Pro Thr Asp Lys Lys Pro Gln Leu Pro Glu Gly Ser Val Arg
                85   90   95

Pro Leu Ser Lys Leu Asp Ile Gln Thr Ile Ala Thr Asn Tyr Ala Ser
                100   105   110

Ser Val Val His Val Pro Ser His Ala Thr Thr Leu Pro Ala Thr Thr
            115   120   125

Gln Val Pro Ser Glu Val Pro Ala Ser Ser Asp Val Ser Ala Ser Thr
    130   135   140

Glu Ile Thr Glu Met Val Asp Glu Tyr Tyr Leu Pro Thr Asp Ala Thr
145   150   155   160

Ala Glu Ser Ile Phe Ser Val Glu Asp Leu Gln Leu Asp Ser Phe Leu
                165   170   175

Met Met Asp Ile Asp Trp Ile Asn Asn Leu Ile
            180   185

<210> 47 <211> 914 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (37)..(672) <223> G147

 <400> 47
aaatcatcag atagaaggaa atattctgat tgagag atg gct cgt gga aag att
54
                                      Met Ala Arg Gly Lys Ile
                                      1   5

cag ctt aag agg att gag aac ccg gtt cac aga caa gtg act ttt tgc
102
Gln Leu Lys Arg Ile Glu Asn Pro Val His Arg Gln Val Thr Phe Cys
        10   15   20

aag agg aga act ggt ctt ctc aag aag gct aag gag ctc tct gtg ctc
150
Lys Arg Arg Thr Gly Leu Leu Lys Lys Ala Lys Glu Leu Ser Val Leu
        25   30   35

tgt gat gcc gag atc ggt gtt gtg atc ttc tct cct cag ggc aag ctc
198
Cys Asp Ala Glu Ile Gly Val Val Ile Phe Ser Pro Gln Gly Lys Leu
    40   45   50

ttt gag ctc gct act aaa gga aca atg gag gga atg att gat aag tac
246
Phe Glu Leu Ala Thr Lys Gly Thr Met Glu Gly Met Ile Asp Lys Tyr

```
55                    60                   65                  70
atg aag tgt act ggt ggt ggt cgt ggt tct tct tct gct act ttt act
294
Met Lys Cys Thr Gly Gly Gly Arg Gly Ser Ser Ser Ala Thr Phe Thr
            75                    80                  85

gct caa gaa caa ctt caa cca cca aat ctt gat ccg aaa gat gag atc
342
Ala Gln Glu Gln Leu Gln Pro Pro Asn Leu Asp Pro Lys Asp Glu Ile
            90                    95                 100

aac gtg ctt aag caa gag att gag atg ctt cag aaa ggg ata agc tat
390
Asn Val Leu Lys Gln Glu Ile Glu Met Leu Gln Lys Gly Ile Ser Tyr
            105                   110                115

atg ttt gga gga gga gat ggg gct atg aat ctt gaa gaa ctt ctt ttg
438
Met Phe Gly Gly Gly Asp Gly Ala Met Asn Leu Glu Glu Leu Leu Leu
            120                   125                130

ctt gag aag cat ctt gag tat tgg att tct cag att cgc tct gct aag
486
Leu Glu Lys His Leu Glu Tyr Trp Ile Ser Gln Ile Arg Ser Ala Lys
135                   140                   145                150

atg gat gtt atg ctt caa gaa att cag tca ttg agg aac aag gaa gga
534
Met Asp Val Met Leu Gln Glu Ile Gln Ser Leu Arg Asn Lys Glu Gly
            155                   160                165

gtc ctc aaa aac acc aac aag tat ctc ctc gac aag ata gag gaa aac
582
Val Leu Lys Asn Thr Asn Lys Tyr Leu Leu Asp Lys Ile Glu Glu Asn
            170                   175                180

aac aat agc ata tta gat gct aac ttc gca gtc atg gag aca aac tat
630
Asn Asn Ser Ile Leu Asp Ala Asn Phe Ala Val Met Glu Thr Asn Tyr
            185                   190                195

tcc tat ccg cta aca atg cca agt gaa ata ttt cag ttc tag
672
Ser Tyr Pro Leu Thr Met Pro Ser Glu Ile Phe Gln Phe
            200                   205                210

accatagggt atttgaagac tatgtctcac gaatttaaat aaccttggta agtataatat
732

agtgttgtta aatcacacat aattaaaata aagcctgtgg aacttcgcta ggcagttgaa
792

aatctatccg tatgtttтat cctcttgttt tacatttgtt ggtgtgaaga tgaaatgact
852

gcaagtgtgg tgtgtactta taactctttc tactttctat ctatgttttg aatttatgga
912

tt
914
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<210> 48 <211> 211 <212> PRT <213> Arabidopsis thaliana <400>
48

Met Ala Arg Gly Lys Ile Gln Leu Lys Arg Ile Glu Asn Pro Val His
1   5   10   15

Arg Gln Val Thr Phe Cys Lys Arg Arg Thr Gly Leu Leu Lys Lys Ala
            20   ·25   30

Lys Glu Leu Ser Val Leu Cys Asp Ala Glu Ile Gly Val Val Ile Phe
            35   40   45

Ser Pro Gln Gly Lys Leu Phe Glu Leu Ala Thr Lys Gly Thr Met Glu
    50   55   60

Gly Met Ile Asp Lys Tyr Met Lys Cys Thr Gly Gly Gly Arg Gly Ser
65   70   75   80

Ser Ser Ala Thr Phe Thr Ala Gln Glu Gln Leu Gln Pro Pro Asn Leu
            85   90   95

Asp Pro Lys Asp Glu Ile Asn Val Leu Lys Gln Glu Ile Glu Met Leu
            100   105   110

Gln Lys Gly Ile Ser Tyr Met Phe Gly Gly Gly Asp Gly Ala Met Asn
            115   120   125

Leu Glu Glu Leu Leu Leu Leu Glu Lys His Leu Glu Tyr Trp Ile Ser
    130   135   140

Gln Ile Arg Ser Ala Lys Met Asp Val Met Leu Gln Glu Ile Gln Ser
145   150   155   160

Leu Arg Asn Lys Glu Gly Val Leu Lys Asn Thr Asn Lys Tyr Leu Leu
                165   170   175

Asp Lys Ile Glu Glu Asn Asn Asn Ser Ile Leu Asp Ala Asn Phe Ala·
            180   185   190

Val Met Glu Thr Asn Tyr Ser Tyr Pro Leu Thr Met Pro Ser Glu Ile
            195   200   205

Phe Gln Phe
    210

<210> 49 <211> 1414 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (171)..(1169) <223> G158

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60

tttttgatttt ttgtgttgga ttgaagagaa gaatagttta ttgatgtttt gtgaagaaga
120

agaagaagag atttttgattt tggtttaata tatagttggg gattaacagg atg gga
176
                                                               Met Gly
                                                               1

agg gta aaa ttg aag ata aag aag tta gag aac aca aat gga cgc caa
224
Arg Val Lys Leu Lys Ile Lys Lys Leu Glu Asn Thr Asn Gly Arg Gln
        5   10   15

tct aca ttt gct aaa agg aaa aat ggg atc ttg aaa aag gct aat gag
272
Ser Thr Phe Ala Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala Asn Glu
    20   25   30

cta tct att ctt tgt gac att gat att gtt ctt ctt atg ttc tct cct
320
Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe Ser Pro
35   40   45   50

act ggc aag gct gca ata tgt tgc ggt aca cga aga tgt ttc tct ttc
368
Thr Gly Lys Ala Ala Ile Cys Cys Gly Thr Arg Arg Cys Phe Ser Phe
                55   60   65

gaa agc tca gaa ctt gaa gaa aac ttt cca aaa gtt gga tca cga tgt
416
Glu Ser Ser Glu Leu Glu Glu Asn Phe Pro Lys Val Gly Ser Arg Cys
            70   75   80

aaa tat acg cga att tat agc ctc aag gac ttg agt act caa gca agg
464
Lys Tyr Thr Arg Ile Tyr Ser Leu Lys Asp Leu Ser Thr Gln Ala Arg
        85   90   95

att ctg cag gct cgg att tct gag ata cat gga aga tta agt tat tgg
512
Ile Leu Gln Ala Arg Ile Ser Glu Ile His Gly Arg Leu Ser Tyr Trp
    100   105   110

acg gaa cca gat aag att aac aat gtt gaa cac ttg gga cag ctc gaa
560
Thr Glu Pro Asp Lys Ile Asn Asn Val Glu His Leu Gly Gln Leu Glu
115   120   125   130

att tcg att agg caa tcc ctt gat caa ttg cgt gca cac aag atg caa
608
Ile Ser Ile Arg Gln Ser Leu Asp Gln Leu Arg Ala His Lys Met Gln
                135   140   145

```
gat ggg att cag att cct tta gaa caa cag ctt caa tct atg tca tgg
656
Asp Gly Ile Gln Ile Pro Leu Glu Gln Gln Leu Gln Ser Met Ser Trp
            150             155             160

att ctt aat agc aac acc acc aac att gtc acc gag gaa cac aat tca
704
Ile Leu Asn Ser Asn Thr Thr Asn Ile Val Thr Glu Glu His Asn Ser
            165             170             175

atc ccg cag agg gaa gtc gag tgc tca gcg agt tct tca ttc ggg agc
752
Ile Pro Gln Arg Glu Val Glu Cys Ser Ala Ser Ser Ser Phe Gly Ser
        180             185             190

tat cca ggc tac ttt gga aca ggg aaa tct cct gaa atg aca att ccg
800
Tyr Pro Gly Tyr Phe Gly Thr Gly Lys Ser Pro Glu Met Thr Ile Pro
195             200             205             210

ggt caa gaa aca agc ttt ctt gat gaa cta aac acc gga cag ctg aaa
848
Gly Gln Glu Thr Ser Phe Leu Asp Glu Leu Asn Thr Gly Gln Leu Lys
            215             220             225

cag gac aca agc tcg cag cag cag ttc act aat aat aat aat atc aca
896
Gln Asp Thr Ser Ser Gln Gln Gln Phe Thr Asn Asn Asn Asn Ile Thr
            230             235             240

gca tac aat ccc aat ctt cac aat gat atg aat cat cac caa acg ttg
944
Ala Tyr Asn Pro Asn Leu His Asn Asp Met Asn His His Gln Thr Leu
            245             250             255

cct cct cct cct ctt cct ctt act ctt ccg cat gct cag gtg tat att
992
Pro Pro Pro Pro Leu Pro Leu Thr Leu Pro His Ala Gln Val Tyr Ile
        260             265             270

cca atg aat cag aga gag tat cat atg aat gga ttc ttt gaa gca cca
1040
Pro Met Asn Gln Arg Glu Tyr His Met Asn Gly Phe Phe Glu Ala Pro
275             280             285             290

cca cct gat tct tct gct tac aac gac aac acc aac caa acc agg ttt
1088
Pro Pro Asp Ser Ser Ala Tyr Asn Asp Asn Thr Asn Gln Thr Arg Phe
            295             300             305

ggt tct agc agc agc tcc ttg cct tgc tca atc tca atg ttc gac gaa
1136
Gly Ser Ser Ser Ser Ser Leu Pro Cys Ser Ile Ser Met Phe Asp Glu
            310             315             320

tac ttg ttt tcc cag atg cag cag ccg aac tga gagagatttg atgaatgatg
1189
Tyr Leu Phe Ser Gln Met Gln Gln Pro Asn
        325             330
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ataaaacatc tcactgaaga aactcaaacc aatatttttt ttcagaaaca gcaagaaagc
1249

taaaactctg ccgatttctg aattggttcc aagaagaaaa aaaccagtgg taatccctgg
1309

tagattgtgc aaccaaacca cacacaatac gtgttcattt atttttttcta tatcttcaat
1369

agatgtcact taattctttt ctatacataa tttctcagtc agaat
1414

<210> 50 <211> 332 <212> PRT <213> Arabidopsis thaliana <400>
50

Met Gly Arg Val Lys Leu Lys Ile Lys Lys Leu Glu Asn Thr Asn Gly
1   5   10   15

Arg Gln Ser Thr Phe Ala Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala
            20   25   30

Asn Glu Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe
            35   40   45

Ser Pro Thr Gly Lys Ala Ala Ile Cys Cys Gly Thr Arg Arg Cys Phe
        50   55   60

Ser Phe Glu Ser Ser Glu Leu Glu Glu Asn Phe Pro Lys Val Gly Ser
65   70   75   80

Arg Cys Lys Tyr Thr Arg Ile Tyr Ser Leu Lys Asp Leu Ser Thr Gln
                85   90   95

Ala Arg Ile Leu Gln Ala Arg Ile Ser Glu Ile His Gly Arg Leu Ser
            100   105   110

Tyr Trp Thr Glu Pro Asp Lys Ile Asn Asn Val Glu His Leu Gly Gln
        115   120   125

Leu Glu Ile Ser Ile Arg Gln Ser Leu Asp Gln Leu Arg Ala His Lys
        130   135   140

Met Gln Asp Gly Ile Gln Ile Pro Leu Glu Gln Gln Leu Gln Ser Met
145   150   155   160

Ser Trp Ile Leu Asn Ser Asn Thr Thr Asn Ile Val Thr Glu Glu His
                165   170   175

Asn Ser Ile Pro Gln Arg Glu Val Glu Cys Ser Ala Ser Ser Ser Phe

```
            180                    185                    190


Gly Ser Tyr Pro Gly Tyr Phe Gly Thr Gly Lys Ser Pro Glu Met Thr
        195                 200                 205


Ile Pro Gly Gln Glu Thr Ser Phe Leu Asp Glu Leu Asn Thr Gly Gln
    210                 215                 220


Leu Lys Gln Asp Thr Ser Ser Gln Gln Gln Phe Thr Asn Asn Asn Asn
225                 230                 235                 240


Ile Thr Ala Tyr Asn Pro Asn Leu His Asn Asp Met Asn His His Gln
            245                 250                 255


Thr Leu Pro Pro Pro Pro Leu Pro Leu Thr Leu Pro His Ala Gln Val
            260                 265                 270


Tyr Ile Pro Met Asn Gln Arg Glu Tyr His Met Asn Gly Phe Phe Glu
        275                 280                 285


Ala Pro Pro Pro Asp Ser Ser Ala Tyr Asn Asp Asn Thr Asn Gln Thr
    290                 295                 300


Arg Phe Gly Ser Ser Ser Ser Ser Leu Pro Cys Ser Ile Ser Met Phe
305                 310                 315                 320


Asp Glu Tyr Leu Phe Ser Gln Met Gln Gln Pro Asn
            325                 330
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<210>  51 <211>  991 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (38)..(784) <223>  G160

 <400>  51
tcaaatttgt catttgttta ttcaaatttt tgagaaa atg gtg aga agt acc aaa
55
                                        Met Val Arg Ser Thr Lys
                                        1                   5


ggt cgt cag aaa ata gag atg aaa aaa atg gaa aac gaa agc aac ctt
103
Gly Arg Gln Lys Ile Glu Met Lys Lys Met Glu Asn Glu Ser Asn Leu
            10                  15                  20


cag gtt act ttc tca aaa aga aga ttc ggt ctt ttc aaa aaa gct agt
151
Gln Val Thr Phe Ser Lys Arg Arg Phe Gly Leu Phe Lys Lys Ala Ser
        25                  30                  35


gaa ctt tgc aca tta agt ggt gca gag att ctg ttg att gtg ttc tct
199
Glu Leu Cys Thr Leu Ser Gly Ala Glu Ile Leu Leu Ile Val Phe Ser
```

```
          40                        45                        50

cct ggt ggg aaa gtg ttt tct ttt ggc cat cca agt gtt caa gaa ctc
247
Pro Gly Gly Lys Val Phe Ser Phe Gly His Pro Ser Val Gln Glu Leu
55                       60                  65                  70

att cat cgc ttt tcg aat cct aac cat aat tct gcc att gtc cat cat
295
Ile His Arg Phe Ser Asn Pro Asn His Asn Ser Ala Ile Val His His
                        75                  80                  85

cag aac aac aat ctc caa ctt gtt gaa acc cgt ccg gat aga aat atc
343
Gln Asn Asn Asn Leu Gln Leu Val Glu Thr Arg Pro Asp Arg Asn Ile
                90                  95                  100

caa tat ctc aac aat ata ctc act gag gtg ctg gca aac cag gaa aag
391
Gln Tyr Leu Asn Asn Ile Leu Thr Glu Val Leu Ala Asn Gln Glu Lys
            105                 110                 115

gag aaa cag aag aga atg gtt ttg gac cta ttg aaa gaa tcc aga gaa
439
Glu Lys Gln Lys Arg Met Val Leu Asp Leu Leu Lys Glu Ser Arg Glu
        120                 125                 130

caa gta gga aac tgg tat gaa aaa gat gtg aaa gat ctc gac atg aat
487
Gln Val Gly Asn Trp Tyr Glu Lys Asp Val Lys Asp Leu Asp Met Asn
135                 140                 145                 150

gaa acc aac cag ctg ata tct gct ctt caa gat gtg aaa aag aaa ctg
535
Glu Thr Asn Gln Leu Ile Ser Ala Leu Gln Asp Val Lys Lys Lys Leu
                155                 160                 165

gta aga gaa atg tct caa tat tct caa gta aat gtt tcg cag aat tac
583
Val Arg Glu Met Ser Gln Tyr Ser Gln Val Asn Val Ser Gln Asn Tyr
                170                 175                 180

ttt ggt caa agt tct ggc gtg att ggt ggt ggt aat gtt ggc att gat
631
Phe Gly Gln Ser Ser Gly Val Ile Gly Gly Gly Asn Val Gly Ile Asp
            185                 190                 195

ctt ttt gat caa aga aga aat gca ttc aac tat aat cca aac atg gtg
679
Leu Phe Asp Gln Arg Arg Asn Ala Phe Asn Tyr Asn Pro Asn Met Val
            200                 205                 210

ttt ccc aat cat aca cca cca atg ttt gga tac aac aat gat gga gtt
727
Phe Pro Asn His Thr Pro Pro Met Phe Gly Tyr Asn Asn Asp Gly Val
215                 220                 225                 230

ctc gtt ccg ata tcc aac atg aac tac atg tca agt tac aac ttc aac
775
Leu Val Pro Ile Ser Asn Met Asn Tyr Met Ser Ser Tyr Asn Phe Asn
                235                 240                 245
```

cag agc tag agtctgaagc tagaagaaca tcctaatcaa tatttgcgtt
824
Gln Ser

attttggcta tggttactgt taggattgtt cttgtattgt gagacttaag tttgtttttt
884

cttttaattt gtttcagttg gttggttttt catttattc gtcgtttgtt ttcctttgtt
944

tttggatatt tttgtatccc agaataaatt tatttatcct ttaaaaa
991

<210> 52 <211> 248 <212> PRT <213> Arabidopsis thaliana <400>
52

Met Val Arg Ser Thr Lys Gly Arg Gln Lys Ile Glu Met Lys Lys Met
1   5   10   15

Glu Asn Glu Ser Asn Leu Gln Val Thr Phe Ser Lys Arg Arg Phe Gly
            20   25   30

Leu Phe Lys Lys Ala Ser Glu Leu Cys Thr Leu Ser Gly Ala Glu Ile
            35   40   45

Leu Leu Ile Val Phe Ser Pro Gly Gly Lys Val Phe Ser Phe Gly His
    50   55   60

Pro Ser Val Gln Glu Leu Ile His Arg Phe Ser Asn Pro Asn His Asn
65   70   75   80

Ser Ala Ile Val His His Gln Asn Asn Asn Leu Gln Leu Val Glu Thr
                85   90   95

Arg Pro Asp Arg Asn Ile Gln Tyr Leu Asn Asn Ile Leu Thr Glu Val
            100   105   110

Leu Ala Asn Gln Glu Lys Glu Lys Gln Lys Arg Met Val Leu Asp Leu
            115   120   125

Leu Lys Glu Ser Arg Glu Gln Val Gly Asn Trp Tyr Glu Lys Asp Val
    130   135   140

Lys Asp Leu Asp Met Asn Glu Thr Asn Gln Leu Ile Ser Ala Leu Gln
145   150   155   160

Asp Val Lys Lys Lys Leu Val Arg Glu Met Ser Gln Tyr Ser Gln Val
                165   170   175

```
Asn Val Ser Gln Asn Tyr Phe Gly Gln Ser Ser Gly Val Ile Gly Gly
        180                 185                 190


Gly Asn Val Gly Ile Asp Leu Phe Asp Gln Arg Arg Asn Ala Phe Asn
        195                 200                 205


Tyr Asn Pro Asn Met Val Phe Pro Asn His Thr Pro Pro Met Phe Gly
    210                 215                 220


Tyr Asn Asn Asp Gly Val Leu Val Pro Ile Ser Asn Met Asn Tyr Met
225                 230                 235                 240


Ser Ser Tyr Asn Phe Asn Gln Ser
                245
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<210> 53 <211> 837 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (54)..(629) <223> G180

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<400> 53
gtaattacga tctacaacaa gtgacatcgt cgtcgacgac gattcaagag aat atg
56
                                                        Met
                                                         1


aac ttc ctc gtt cct ttt gaa gaa acc aat gtc tta acc ttt ttc tct
104
Asn Phe Leu Val Pro Phe Glu Glu Thr Asn Val Leu Thr Phe Phe Ser
            5                  10                  15


tct tct tct tcc tct tct ctt tct tct cct tct ttc ccc att cac aac
152
Ser Ser Ser Ser Ser Ser Leu Ser Ser Pro Ser Phe Pro Ile His Asn
        20                  25                  30


tct tcc tcc act act act act cat gca cct cta ggg ttt tct aat aat
200
Ser Ser Ser Thr Thr Thr Thr His Ala Pro Leu Gly Phe Ser Asn Asn
    35                  40                  45


ctt cag ggt gga gga ccc ttg gga tca aag gtg gtt aat gat gat cag
248
Leu Gln Gly Gly Gly Pro Leu Gly Ser Lys Val Val Asn Asp Asp Gln
50                  55                  60                  65


gag aat ttt gga ggt gga act aac aat gat gct cat tct aat tct tgg
296
Glu Asn Phe Gly Gly Gly Thr Asn Asn Asp Ala His Ser Asn Ser Trp
                70                  75                  80


tgg aga tca aat agt gga agt gga gat atg aag aac aaa gtg aag ata
344
Trp Arg Ser Asn Ser Gly Ser Gly Asp Met Lys Asn Lys Val Lys Ile
            85                  90                  95
```

```
agg agg aaa cta aga gag cca aga ttc tgt ttc caa acc aaa agc gat
392
Arg Arg Lys Leu Arg Glu Pro Arg Phe Cys Phe Gln Thr Lys Ser Asp
        100                 105                 110

gtt gat gtt ctt gac gat ggc tac aaa tgg cgt aaa tat ggt cag aaa
440
Val Asp Val Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Gln Lys
    115                 120                 125

gtc gtc aag aac agc ctt cac ccc agg agt tat tac aga tgc aca cac
488
Val Val Lys Asn Ser Leu His Pro Arg Ser Tyr Tyr Arg Cys Thr His
130             135                 140                     145

aac aac tgt agg gtg aaa aag aga gtg gag cga cta tcg gaa gat tgt
536
Asn Asn Cys Arg Val Lys Lys Arg Val Glu Arg Leu Ser Glu Asp Cys
            150                 155                 160

aga atg gtg att act act tac gaa ggt cgt cac aac cac att ccc tct
584
Arg Met Val Ile Thr Thr Tyr Glu Gly Arg His Asn His Ile Pro Ser
            165                 170                 175

gat gac tcc act tct cct gac cat gat tgt ctc tct tcc ttt taa
629
Asp Asp Ser Thr Ser Pro Asp His Asp Cys Leu Ser Ser Phe
        180                 185                 190

catctctttc tatatatcta tatatagaca gttatatgtg cacatataga tgtgtgatat
689

attgcatatt tgatattgca tgtgtttttc aagagtatgt catcagatgt tatgcatata
749

ttcttgactt gttgcttata gtatacatat gtaataatat atattgacat tggtagttca
809

tttctgttca aacaaaaaaa aaaaaaaa
837


<210> 54 <211> 191 <212> PRT <213> Arabidopsis thaliana <400>
54

Met Asn Phe Leu Val Pro Phe Glu Glu Thr Asn Val Leu Thr Phe Phe
1               5                   10                  15

Ser Ser Ser Ser Ser Ser Ser Leu Ser Ser Pro Ser Phe Pro Ile His
            20                  25                  30

Asn Ser Ser Ser Thr Thr Thr Thr His Ala Pro Leu Gly Phe Ser Asn
        35                  40                  45

Asn Leu Gln Gly Gly Gly Pro Leu Gly Ser Lys Val Val Asn Asp Asp
    50                  55                  60
```

95

```
Gln Glu Asn Phe Gly Gly Gly Thr Asn Asn Asp Ala His Ser Asn Ser
65                  70                  75                  80


Trp Trp Arg Ser Asn Ser Gly Ser Gly Asp Met Lys Asn Lys Val Lys
                85                  90                  95


Ile Arg Arg Lys Leu Arg Glu Pro Arg Phe Cys Phe Gln Thr Lys Ser
            100                 105                 110


Asp Val Asp Val Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Gln
            115                 120                 125


Lys Val Val Lys Asn Ser Leu His Pro Arg Ser Tyr Tyr Arg Cys Thr
        130                 135                 140


His Asn Asn Cys Arg Val Lys Lys Arg Val Glu Arg Leu Ser Glu Asp
145                 150                 155                 160


Cys Arg Met Val Ile Thr Thr Tyr Glu Gly Arg His Asn His Ile Pro
                165                 170                 175


Ser Asp Asp Ser Thr Ser Pro Asp His Asp Cys Leu Ser Ser Phe
            180                 185                 190


<210> 55 <211> 844 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (5)..(544) <223> G181

 <400> 55
aaca atg gac aga gaa gac ata aat cct atg tta agc cgc cta gat gtc
49
     Met Asp Arg Glu Asp Ile Asn Pro Met Leu Ser Arg Leu Asp Val
     1               5                   10                  15


gaa aac aac aac acc ttc tct tcc ttt gta gac aaa acc cta atg atg
97
Glu Asn Asn Asn Thr Phe Ser Ser Phe Val Asp Lys Thr Leu Met Met
                20                  25                  30


atg cct cca tca aca ttt tcc ggt gaa gtg gaa cct tca tct tct tct
145
Met Pro Pro Ser Thr Phe Ser Gly Glu Val Glu Pro Ser Ser Ser Ser
            35                  40                  45


tct tgg tat cca gaa agc ttt cat gtg cat gcg ccg cca tta cca cct
193
Ser Trp Tyr Pro Glu Ser Phe His Val His Ala Pro Pro Leu Pro Pro
            50                  55                  60


gag aat gat caa ata ggt gag aaa ggg aag gag ctg aaa gag aag aga
241
Glu Asn Asp Gln Ile Gly Glu Lys Gly Lys Glu Leu Lys Glu Lys Arg
        65                  70                  75
```

```
tcg agg aaa gtt cca agg att gcg ttt cat acg agg agc gat gat gat
289
Ser Arg Lys Val Pro Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp
80              85              90              95

gtt ctt gat gat ggt tat cgt tgg cga aaa tat ggg cag aaa tct gtc
337
Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val
                100             105             110

aag cac aat gct cat ccc agg agc tat tac aga tgt acg tac cac aca
385
Lys His Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr
            115             120             125

tgc aac gtg aag aaa caa gtg cag aga ttg gca aaa gat cca aac gtc
433
Cys Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val
            130             135             140

gtc gta acg acc tac gaa ggc gtt cat aac cat cct tgt gag aag ctc
481
Val Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu
        145             150             155

atg gag act ctt aat cct ctt ctc agg caa ctc cag ttc ctc tcc agt
529
Met Glu Thr Leu Asn Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Ser
160             165             170             175

ttc tct aat ctt tga atatataatg gcttaattaa tggtgtaatt acttaaaggt
584
Phe Ser Asn Leu


gattaaggtg ttaatcaccc cactgaccgt ttgacgaccc acatctccca agtgacaagt
644

cacaagtgtg tagatcagat tttaaaccaa tgtaacagtt acgacttttt acaaatgttt
704

ctgaatttta tcccctgatt tctggttaat gatcggttta cgccgatgat ttgacaaata
764

ccagacaaaa caagtttagt tacatatgta agtatgaaaa ggtagtttcc tctaacttca
824

ttaaaaaaaa aaaaaaaaaa
844


<210>   56 <211>   179 <212>   PRT <213>   Arabidopsis thaliana   <400>
56


Met Asp Arg Glu Asp Ile Asn Pro Met Leu Ser Arg Leu Asp Val Glu
1               5               10              15


Asn Asn Asn Thr Phe Ser Ser Phe Val Asp Lys Thr Leu Met Met Met
            20              25              30
```

Pro Pro Ser Thr Phe Ser Gly Glu Val Glu Pro Ser Ser Ser Ser Ser
        35   40   45

Trp Tyr Pro Glu Ser Phe His Val His Ala Pro Pro Leu Pro Pro Glu
    50   55   60

Asn Asp Gln Ile Gly Glu Lys Gly Lys Glu Leu Lys Glu Lys Arg Ser
65   70   75   80

Arg Lys Val Pro Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp Val
                85   90   95

Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys
            100   105   110

His Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr Cys
        115   120   125

Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val Val
    130   135   140

Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu Met
145   150   155   160

Glu Thr Leu Asn Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Ser Phe
                165   170   175

Ser Asn Leu

<210> 57 <211> 1974 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (327)..(1937) <223> G184

 <400> 57
tgaattctag cctttttgta ggcgaatcat ctggaccggt aagagactct ctcatcgata
60

ataaccacat aatttaatca aactctttct ctctctttct aagatctttt gctttgctct
120

tttccttttt gatcttccta tatatggaga agcaccaaaa cggtacttac tatacgatac
180

tgtacggatc catcaaactg gattaattat caaaacgtac atttttatct tacctggcaa
240

gttacattcc tagggttttg gagaatccaa tcaacaacaa agaaaataat catcgttaca
300

98

ataatcagta tcacgcacag acttag atg ttc cgg ttt cca gtg agt cta ggc
353
                                    Met Phe Arg Phe Pro Val Ser Leu Gly
                                    1   5

ggt tca cgt gac gaa gac cgt cac gat cag atc aca ccg ttg gat gac
401
Gly Ser Arg Asp Glu Asp Arg His Asp Gln Ile Thr Pro Leu Asp Asp
10   15   20   25

cat cgt gtg gtg gtt gat gag gtt gac ttc ttc tca gag aag aga gat
449
His Arg Val Val Val Asp Glu Val Asp Phe Phe Ser Glu Lys Arg Asp
            30   35   40

agg gtt tca cgt gag aac atc aac gac gac gac gac gaa ggc aat aag
497
Arg Val Ser Arg Glu Asn Ile Asn Asp Asp Asp Asp Glu Gly Asn Lys
        45   50   55

gtt ctc atc aaa atg gag ggt tca cga gtt gaa gaa aac gat cgt tcc
545
Val Leu Ile Lys Met Glu Gly Ser Arg Val Glu Glu Asn Asp Arg Ser
        60   65   70

aga gat gtc aat atc ggt ctg aat ctt ctg acc gcg aat acg gga agc
593
Arg Asp Val Asn Ile Gly Leu Asn Leu Leu Thr Ala Asn Thr Gly Ser
    75   80   85

gat gag tca acg gtg gat gat gga cta tca atg gat atg gaa gat aaa
641
Asp Glu Ser Thr Val Asp Asp Gly Leu Ser Met Asp Met Glu Asp Lys
90   95   100   105

cgt gca aag att gag aac gca caa cta caa gaa gag ctc aag aag atg
689
Arg Ala Lys Ile Glu Asn Ala Gln Leu Gln Glu Glu Leu Lys Lys Met
            110   115   120

aaa ata gag aat caa agg cta aga gat atg ttg agc caa gcg acg acc
737
Lys Ile Glu Asn Gln Arg Leu Arg Asp Met Leu Ser Gln Ala Thr Thr
            125   130   135

aac ttc aat gcc tta caa atg caa ctt gtt gcc gtc atg agg caa caa
785
Asn Phe Asn Ala Leu Gln Met Gln Leu Val Ala Val Met Arg Gln Gln
            140   145   150

gaa caa cgt aac tct tca caa gat cat ctc ctg gag agc aaa gca gaa
833
Glu Gln Arg Asn Ser Ser Gln Asp His Leu Leu Glu Ser Lys Ala Glu
        155   160   165

gga agg aaa cgg cag gaa ctg caa atc atg gtg cca agg cag ttc atg
881
Gly Arg Lys Arg Gln Glu Leu Gln Ile Met Val Pro Arg Gln Phe Met
170   175   180   185

99

```
gac ctt ggg ccg tcg tct gga gca gca gag cat gga gcc gaa gtg tca
929
Asp Leu Gly Pro Ser Ser Gly Ala Ala Glu His Gly Ala Glu Val Ser
            190             195             200


tct gaa gag agg aca acg gtt cgt tca ggt tct cct cct tcg ctt cta
977
Ser Glu Glu Arg Thr Thr Val Arg Ser Gly Ser Pro Pro Ser Leu Leu
            205             210             215


gaa agt tcc aat ccc cga gag aac gga aag agg ttg ctt gga aga gaa
1025
Glu Ser Ser Asn Pro Arg Glu Asn Gly Lys Arg Leu Leu Gly Arg Glu
            220             225             230


gaa agc tca gag gaa tca gag tct aac gcc tgg gga aac cct aac aaa
1073
Glu Ser Ser Glu Glu Ser Glu Ser Asn Ala Trp Gly Asn Pro Asn Lys
        235             240             245


gtc ccc aaa cat aat cca tcc tct agc aat agc aat gga aac aga aac
1121
Val Pro Lys His Asn Pro Ser Ser Ser Asn Ser Asn Gly Asn Arg Asn
250             255             260             265


gga aat gtt att gat cag tcg gcc gca gaa gcc acc atg cgg aaa gcc
1169
Gly Asn Val Ile Asp Gln Ser Ala Ala Glu Ala Thr Met Arg Lys Ala
            270             275             280


cgt gtc tca gtt cgt gcc cga tct gaa gct gcc atg ata agc gat gga
1217
Arg Val Ser Val Arg Ala Arg Ser Glu Ala Ala Met Ile Ser Asp Gly
            285             290             295


tgt caa tgg aga aag tac gga caa aaa atg gct aaa gga aac ccg tgt
1265
Cys Gln Trp Arg Lys Tyr Gly Gln Lys Met Ala Lys Gly Asn Pro Cys
            300             305             310


ccg cgg gct tat tat cgt tgc aca atg gcc ggt gga tgt cca gtt cgc
1313
Pro Arg Ala Tyr Tyr Arg Cys Thr Met Ala Gly Gly Cys Pro Val Arg
        315             320             325


aag caa gtg cag cgt tgc gca gaa gac aga tct att ctc ata acc acc
1361
Lys Gln Val Gln Arg Cys Ala Glu Asp Arg Ser Ile Leu Ile Thr Thr
330             335             340             345


tac gaa gga aac cac aac cat cca ctc cca cca gcc gct acg gcc atg
1409
Tyr Glu Gly Asn His Asn His Pro Leu Pro Pro Ala Ala Thr Ala Met
            350             355             360


gcc tca aca acc acc gca gct gca agc atg ctc ctc tcg ggc tca atg
1457
Ala Ser Thr Thr Thr Ala Ala Ala Ser Met Leu Leu Ser Gly Ser Met
            365             370             375
```

tcg agt caa gac ggt tta atg aac cca aca aac ctc cta gct cga gct
1505
Ser Ser Gln Asp Gly Leu Met Asn Pro Thr Asn Leu Leu Ala Arg Ala
        380   385   390

atc ttg cct tgc tcc tca agc atg gct aca atc tca gcc tcc gca cca
1553
Ile Leu Pro Cys Ser Ser Ser Met Ala Thr Ile Ser Ala Ser Ala Pro
        395   400   405

ttc cca acc atc aca ttg gac ctc acc aat tca ccc aac ggt aac aac
1601
Phe Pro Thr Ile Thr Leu Asp Leu Thr Asn Ser Pro Asn Gly Asn Asn
410   415   420   425

cct aat atg acc act aat aac ccg ttg atg cag ttc gct caa cgg ccc
1649
Pro Asn Met Thr Thr Asn Asn Pro Leu Met Gln Phe Ala Gln Arg Pro
            430   435   440

ggt ttc aac ccg gca gtt ttg cct caa gtg gtt ggt caa gct atg tac
1697
Gly Phe Asn Pro Ala Val Leu Pro Gln Val Val Gly Gln Ala Met Tyr
            445   450   455

aat aac caa caa cag tcc aag ttt tct ggt tta cag tta ccg gct cag
1745
Asn Asn Gln Gln Gln Ser Lys Phe Ser Gly Leu Gln Leu Pro Ala Gln
        460   465   470

cca ctg cag atc gcg gcc act tcc tcg gtg gcc gag agc gtt agt gct
1793
Pro Leu Gln Ile Ala Ala Thr Ser Ser Val Ala Glu Ser Val Ser Ala
        475   480   485

gcc agt gca gca att gcg tcc gat cca aac ttt gcg gcg gct cta gcg
1841
Ala Ser Ala Ala Ile Ala Ser Asp Pro Asn Phe Ala Ala Ala Leu Ala
490   495   500   505

gca gcg atc acg tcc att atg aac ggt tcc agt cat caa aat aat aac
1889
Ala Ala Ile Thr Ser Ile Met Asn Gly Ser Ser His Gln Asn Asn Asn
            510   515   520

acc aat aat aat aat gtg gct acg agc aac aat gac agt agg caa taa
1937
Thr Asn Asn Asn Asn Val Ala Thr Ser Asn Asn Asp Ser Arg Gln
        525   530   535

gagttttcat tttgatggtc gatttttttt tttggggg
1974

<210> 58 <211> 536 <212> PRT <213> Arabidopsis thaliana <400>
58

Met Phe Arg Phe Pro Val Ser Leu Gly Gly Ser Arg Asp Glu Asp Arg
1   5   10   15

His Asp Gln Ile Thr Pro Leu Asp Asp His Arg Val Val Val Asp Glu
            20   25   30

Val Asp Phe Phe Ser Glu Lys Arg Asp Arg Val Ser Arg Glu Asn Ile
            35   40   45

Asn Asp Asp Asp Asp Glu Gly Asn Lys Val Leu Ile Lys Met Glu Gly
    50   55   60

Ser Arg Val Glu Glu Asn Asp Arg Ser Arg Asp Val Asn Ile Gly Leu
65   70   75   80

Asn Leu Leu Thr Ala Asn Thr Gly Ser Asp Glu Ser Thr Val Asp Asp
                85   90   95

Gly Leu Ser Met Asp Met Glu Asp Lys Arg Ala Lys Ile Glu Asn Ala
                100   105   110

Gln Leu Gln Glu Glu Leu Lys Lys Met Lys Ile Glu Asn Gln Arg Leu
            115   120   125

Arg Asp Met Leu Ser Gln Ala Thr Thr Asn Phe Asn Ala Leu Gln Met
    130   135   140

Gln Leu Val Ala Val Met Arg Gln Gln Glu Gln Arg Asn Ser Ser Gln
145   150   155   160

Asp His Leu Leu Glu Ser Lys Ala Glu Gly Arg Lys Arg Gln Glu Leu
                165   170   175

Gln Ile Met Val Pro Arg Gln Phe Met Asp Leu Gly Pro Ser Ser Gly
                180   185   190

Ala Ala Glu His Gly Ala Glu Val Ser Ser Glu Glu Arg Thr Thr Val
                195   200   205

Arg Ser Gly Ser Pro Pro Ser Leu Leu Glu Ser Ser Asn Pro Arg Glu
    210   215   220

Asn Gly Lys Arg Leu Leu Gly Arg Glu Glu Ser Ser Glu Glu Ser Glu
225   230   235   240

Ser Asn Ala Trp Gly Asn Pro Asn Lys Val Pro Lys His Asn Pro Ser
                245   250   255

Ser Ser Asn Ser Asn Gly Asn Arg Asn Gly Asn Val Ile Asp Gln Ser

                260   265   270

    Ala Ala Glu Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala Arg
            275   280   285

    Ser Glu Ala Ala Met Ile Ser Asp Gly Cys Gln Trp Arg Lys Tyr Gly
            290   295   300

    Gln Lys Met Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg Cys
    305   310   315   320

    Thr Met Ala Gly Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala
                    325   330   335

    Glu Asp Arg Ser Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His
                340   345   350

    Pro Leu Pro Pro Ala Ala Thr Ala Met Ala Ser Thr Thr Thr Ala Ala
            355   360   365

    Ala Ser Met Leu Leu Ser Gly Ser Met Ser Ser Gln Asp Gly Leu Met
        370   375   380

    Asn Pro Thr Asn Leu Leu Ala Arg Ala Ile Leu Pro Cys Ser Ser Ser
    385   390   395   400

    Met Ala Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Ile Thr Leu Asp
                    405   410   415

    Leu Thr Asn Ser Pro Asn Gly Asn Asn Pro Asn Met Thr Thr Asn Asn
                420   425   430

    Pro Leu Met Gln Phe Ala Gln Arg Pro Gly Phe Asn Pro Ala Val Leu
            435   440   445

    Pro Gln Val Val Gly Gln Ala Met Tyr Asn Asn Gln Gln Gln Ser Lys
        450   455   460

    Phe Ser Gly Leu Gln Leu Pro Ala Gln Pro Leu Gln Ile Ala Ala Thr
    465   470   475   480

    Ser Ser Val Ala Glu Ser Val Ser Ala Ala Ser Ala Ala Ile Ala Ser
                    485   490   495

    Asp Pro Asn Phe Ala Ala Ala Leu Ala Ala Ala Ile Thr Ser Ile Met
                500   505   510

                            103

Asn Gly Ser Ser His Gln Asn Asn Asn Thr Asn Asn Asn Asn Val Ala
        515   520   525

Thr Ser Asn Asn Asp Ser Arg Gln
    530   535

<210> 59 <211> 1205 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (77)..(988) <223> G185

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atgcaaaaat aaacatagta acaatacttt aaactattta caccacttta atcttattct
60

ccactctttg aacgta atg gag aag aac cat agt agt gga gag tgg gag aag
112
               Met Glu Lys Asn His Ser Ser Gly Glu Trp Glu Lys
               1   5   10

atg aag aac gag atc aac gag cta atg ata gaa gga aga gac tat gca
160
Met Lys Asn Glu Ile Asn Glu Leu Met Ile Glu Gly Arg Asp Tyr Ala
        15   20   25

cac cag ttt gga tca gct tca tct caa gaa aca cgt gaa cat tta gcc
208
His Gln Phe Gly Ser Ala Ser Ser Gln Glu Thr Arg Glu His Leu Ala
    30   35   40

aaa aag att ctt caa tct tac cac aag tct ctc acc atc atg aac tac
256
Lys Lys Ile Leu Gln Ser Tyr His Lys Ser Leu Thr Ile Met Asn Tyr
45   50   55   60

tcc ggc gaa ctt gac caa gtt tct cag ggt gga gga agc ccc aag agc
304
Ser Gly Glu Leu Asp Gln Val Ser Gln Gly Gly Gly Ser Pro Lys Ser
                65   70   75

gat gat tcc gat caa gaa cca ctt gtc atc aag agt tcg aag aag tca
352
Asp Asp Ser Asp Gln Glu Pro Leu Val Ile Lys Ser Ser Lys Lys Ser
                80   85   90

atg cca agg tgg agt tca aaa gtc aga att gcc cct gga gct ggt gtt
400
Met Pro Arg Trp Ser Ser Lys Val Arg Ile Ala Pro Gly Ala Gly Val
            95   100   105

gat aga acg ctg gac gat gga ttc agt tgg aga aag tac ggc cag aag
448
Asp Arg Thr Leu Asp Asp Gly Phe Ser Trp Arg Lys Tyr Gly Gln Lys
        110   115   120

gat att ctc gga gcc aaa ttt cca aga gga tac tat aga tgc acg tat
496
Asp Ile Leu Gly Ala Lys Phe Pro Arg Gly Tyr Tyr Arg Cys Thr Tyr
125   130   135   140

104

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aga aag tct caa gga tgt gaa gcc act aaa caa gtc caa aga tct gat
544
Arg Lys Ser Gln Gly Cys Glu Ala Thr Lys Gln Val Gln Arg Ser Asp
            145             150             155

gaa aat cag atg ctc ctt gag atc agt tac cga gga ata cat tct tgc
592
Glu Asn Gln Met Leu Leu Glu Ile Ser Tyr Arg Gly Ile His Ser Cys
            160             165             170

tct caa gct gca aat gtc ggt aca aca atg ccg ata caa aac ctc gaa
640
Ser Gln Ala Ala Asn Val Gly Thr Thr Met Pro Ile Gln Asn Leu Glu
        175             180             185

ccg aac cag acc caa gaa cac gga aat ctt gac atg gta aag gaa agt
688
Pro Asn Gln Thr Gln Glu His Gly Asn Leu Asp Met Val Lys Glu Ser
        190             195             200

gta gac aac tac aat cac caa gca cat ttg cat cac aac ctt cac tat
736
Val Asp Asn Tyr Asn His Gln Ala His Leu His His Asn Leu His Tyr
205             210             215             220

cca ttg tca tct acc cca aat cta gag aat aac aat gcc tat atg ctt
784
Pro Leu Ser Ser Thr Pro Asn Leu Glu Asn Asn Asn Ala Tyr Met Leu
            225             230             235

caa atg cga gat caa aac atc gaa tat ttt gga tct acg agc ttc tct
832
Gln Met Arg Asp Gln Asn Ile Glu Tyr Phe Gly Ser Thr Ser Phe Ser
            240             245             250

agt gat cta gga act agt atc aac tac aat ttt cca gca tct ggc tcg
880
Ser Asp Leu Gly Thr Ser Ile Asn Tyr Asn Phe Pro Ala Ser Gly Ser
        255             260             265

gct tct cac tca gca tca aac tct ccg tcc acc gtc cct ttg gaa tcc
928
Ala Ser His Ser Ala Ser Asn Ser Pro Ser Thr Val Pro Leu Glu Ser
        270             275             280

ccg ttt gaa agc tat gat cca aat cat cca tat gga gga ttt ggt ggg
976
Pro Phe Glu Ser Tyr Asp Pro Asn His Pro Tyr Gly Gly Phe Gly Gly
285             290             295             300

ttc tat tct tag ttatctactt aagggaggga cggaactttt tacatgacct
1028
Phe Tyr Ser

cttgattaaa gagagagttt tcataatagc taatcaattt cctattcaaa tatccgagtt
1088

ttttttctaa tcatgtttat caattgtctt attacagaag gcttattttc aggtctatgt
1148
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105

tgaaataaat ggatttgtac tcgtaggtat gatccttgtt atctaaaaaa aaaaaaa
1205

<210> 60 <211> 303 <212> PRT <213> Arabidopsis thaliana <400>
60

Met Glu Lys Asn His Ser Ser Gly Glu Trp Glu Lys Met Lys Asn Glu
1   5   10   15

Ile Asn Glu Leu Met Ile Glu Gly Arg Asp Tyr Ala His Gln Phe Gly
            20   25   30

Ser Ala Ser Ser Gln Glu Thr Arg Glu His Leu Ala Lys Lys Ile Leu
        35   40   45

Gln Ser Tyr His Lys Ser Leu Thr Ile Met Asn Tyr Ser Gly Glu Leu
    50   55   60

Asp Gln Val Ser Gln Gly Gly Ser Pro Lys Ser Asp Asp Ser Asp
65   70   75   80

Gln Glu Pro Leu Val Ile Lys Ser Ser Lys Lys Ser Met Pro Arg Trp
            85   90   95

Ser Ser Lys Val Arg Ile Ala Pro Gly Ala Gly Val Asp Arg Thr Leu
            100   105   110

Asp Asp Gly Phe Ser Trp Arg Lys Tyr Gly Gln Lys Asp Ile Leu Gly
        115   120   125

Ala Lys Phe Pro Arg Gly Tyr Tyr Arg Cys Thr Tyr Arg Lys Ser Gln
    130   135   140

Gly Cys Glu Ala Thr Lys Gln Val Gln Arg Ser Asp Glu Asn Gln Met
145   150   155   160

Leu Leu Glu Ile Ser Tyr Arg Gly Ile His Ser Cys Ser Gln Ala Ala
            165   170   175

Asn Val Gly Thr Thr Met Pro Ile Gln Asn Leu Glu Pro Asn Gln Thr
            180   185   190

Gln Glu His Gly Asn Leu Asp Met Val Lys Glu Ser Val Asp Asn Tyr
    195   200   205

Asn His Gln Ala His Leu His His Asn Leu His Tyr Pro Leu Ser Ser

106

        210   215   220

Thr Pro Asn Leu Glu Asn Asn Asn Ala Tyr Met Leu Gln Met Arg Asp
225   230   235   240

Gln Asn Ile Glu Tyr Phe Gly Ser Thr Ser Phe Ser Ser Asp Leu Gly
            245   250   255

Thr Ser Ile Asn Tyr Asn Phe Pro Ala Ser Gly Ser Ala Ser His Ser
        260   265   270

Ala Ser Asn Ser Pro Ser Thr Val Pro Leu Glu Ser Pro Phe Glu Ser
        275   280   285

Tyr Asp Pro Asn His Pro Tyr Gly Gly Phe Gly Gly Phe Tyr Ser
    290   295   300

<210> 61 <211> 1241 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (51)..(1031) <223> G195

<400> 61
ttttctttt ctttctttt ggtttaagtt ttttctcttt gttcttcgtc atg tct
56
                                                        Met Ser
                                                         1

cat gaa atc aaa gat ctt aac aac tat cac tac act tca tcg tat aat
104
His Glu Ile Lys Asp Leu Asn Asn Tyr His Tyr Thr Ser Ser Tyr Asn
        5   10   15

cat tac aat atc aac aac caa aat atg att aat ctc cct tac gtt tct
152
His Tyr Asn Ile Asn Asn Gln Asn Met Ile Asn Leu Pro Tyr Val Ser
    20   25   30

ggt cca tct gct tat aat gca aac atg atc tca tca tca caa gta ggt
200
Gly Pro Ser Ala Tyr Asn Ala Asn Met Ile Ser Ser Ser Gln Val Gly
35   40   45   50

ttt gat cta ccc tcg aag aac ttg agt cct caa gga gcc ttc gag ttg
248
Phe Asp Leu Pro Ser Lys Asn Leu Ser Pro Gln Gly Ala Phe Glu Leu
                55   60   65

ggt ttc gag ctt tct cca tct tct tct gac ttt ttt aat cct tcc ctc
296
Gly Phe Glu Leu Ser Pro Ser Ser Ser Asp Phe Phe Asn Pro Ser Leu
            70   75   80

gat caa gag aac ggt ttg tat aat gct tat aat tat aat agt agt caa
344
Asp Gln Glu Asn Gly Leu Tyr Asn Ala Tyr Asn Tyr Asn Ser Ser Gln
            85   90   95

107

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aag agt cat gaa gtt gtc ggt gat ggt tgt gca acc att aag agt gaa
392
Lys Ser His Glu Val Val Gly Asp Gly Cys Ala Thr Ile Lys Ser Glu
    100                 105                 110

gtt agg gtt tca gca tct cct tct tca agt gag gcc gat cat cat cca
440
Val Arg Val Ser Ala Ser Pro Ser Ser Ser Glu Ala Asp His His Pro
115                 120                 125                 130

gga gaa gat tcc ggc aag atc cgg aag aaa aga gaa gtt cgc gat gga
488
Gly Glu Asp Ser Gly Lys Ile Arg Lys Lys Arg Glu Val Arg Asp Gly
                135                 140                 145

gga gaa gat gat caa cgc tct cag aaa gta gtt aaa aca aag aag aaa
536
Gly Glu Asp Asp Gln Arg Ser Gln Lys Val Val Lys Thr Lys Lys Lys
            150                 155                 160

gag gag aag aaa aaa gag cca cga gtc tcg ttc atg act aag acc gaa
584
Glu Glu Lys Lys Lys Glu Pro Arg Val Ser Phe Met Thr Lys Thr Glu
        165                 170                 175

gtt gat cat ctc gaa gac ggc tat cgt tgg aga aag tat ggc caa aaa
632
Val Asp His Leu Glu Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys
    180                 185                 190

gca gtc aaa aac agt cct tat ccg agg agt tac tat aga tgc acg act
680
Ala Val Lys Asn Ser Pro Tyr Pro Arg Ser Tyr Tyr Arg Cys Thr Thr
195                 200                 205                 210

cag aag tgc aac gtg aag aag aga gtg gag aga tct tac caa gac cca
728
Gln Lys Cys Asn Val Lys Lys Arg Val Glu Arg Ser Tyr Gln Asp Pro
                215                 220                 225

acg gtc gtc atc aca acc tac gag agt caa cac aac cat ccg atc ccg
776
Thr Val Val Ile Thr Thr Tyr Glu Ser Gln His Asn His Pro Ile Pro
                230                 235                 240

acc aat cgt cgg aca gca atg ttc tct gga acc acc gca tct gat tat
824
Thr Asn Arg Arg Thr Ala Met Phe Ser Gly Thr Thr Ala Ser Asp Tyr
            245                 250                 255

aac cca tca tcg tct cca ata ttc tcc gat ctc atc atc aat act cca
872
Asn Pro Ser Ser Ser Pro Ile Phe Ser Asp Leu Ile Ile Asn Thr Pro
        260                 265                 270

aga agc ttc tca aat gat gat ctc ttc cgt gtg cca tac gct agt gtg
920
Arg Ser Phe Ser Asn Asp Asp Leu Phe Arg Val Pro Tyr Ala Ser Val
275                 280                 285                 290
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aac gtg aac cct agt tat cat caa cag caa cat gga ttt cat caa cag
968
Asn Val Asn Pro Ser Tyr His Gln Gln Gln His Gly Phe His Gln Gln
            295   300   305

gag agt gag ttc gag ctc ttg aag gag atg ttt cct tcg gtt ttc ttc
1016
Glu Ser Glu Phe Glu Leu Leu Lys Glu Met Phe Pro Ser Val Phe Phe
            310   315   320

aaa caa gag cct tga tgatataata taatatagaa acaatttttt ttctgctaag
1071
Lys Gln Glu Pro
        325

aaatatagaa caaaacttgg atgcataata agtgatgata gtgttattta ttttttgcat
1131

gtatatatta tacatgtttt gttaactagc tataggatat actggtagta attaagcata
1191

aatatggagc ccttcgactt attacaataa tttttggtat ggaaaaaatt
1241

<210> 62 <211> 326 <212> PRT <213> Arabidopsis thaliana <400>
62

Met Ser His Glu Ile Lys Asp Leu Asn Asn Tyr His Tyr Thr Ser Ser
1   5   10   15

Tyr Asn His Tyr Asn Ile Asn Asn Gln Asn Met Ile Asn Leu Pro Tyr
            20   25   30

Val Ser Gly Pro Ser Ala Tyr Asn Ala Asn Met Ile Ser Ser Ser Gln
        35   40   45

Val Gly Phe Asp Leu Pro Ser Lys Asn Leu Ser Pro Gln Gly Ala Phe
    50   55   60

Glu Leu Gly Phe Glu Leu Ser Pro Ser Ser Ser Asp Phe Phe Asn Pro
65   70   75   80

Ser Leu Asp Gln Glu Asn Gly Leu Tyr Asn Ala Tyr Asn Tyr Asn Ser
                85   90   95

Ser Gln Lys Ser His Glu Val Val Gly Asp Gly Cys Ala Thr Ile Lys
            100   105   110

Ser Glu Val Arg Val Ser Ala Ser Pro Ser Ser Ser Glu Ala Asp His
            115   120   125

His Pro Gly Glu Asp Ser Gly Lys Ile Arg Lys Lys Arg Glu Val Arg

109

        130   135   140

Asp Gly Gly Glu Asp Asp Gln Arg Ser Gln Lys Val Val Lys Thr Lys
145   150   155   160

Lys Lys Glu Glu Lys Lys Lys Glu Pro Arg Val Ser Phe Met Thr Lys
                165   170   175

Thr Glu Val Asp His Leu Glu Asp Gly Tyr Arg Trp Arg Lys Tyr Gly
            180   185   190

Gln Lys Ala Val Lys Asn Ser Pro Tyr Pro Arg Ser Tyr Tyr Arg Cys
        195   200   205

Thr Thr Gln Lys Cys Asn Val Lys Lys Arg Val Glu Arg Ser Tyr Gln
    210   215   220

Asp Pro Thr Val Val Ile Thr Thr Tyr Glu Ser Gln His Asn His Pro
225   230   235   240

Ile Pro Thr Asn Arg Arg Thr Ala Met Phe Ser Gly Thr Thr Ala Ser
            245   250   255

Asp Tyr Asn Pro Ser Ser Ser Pro Ile Phe Ser Asp Leu Ile Ile Asn
        260   265   270

Thr Pro Arg Ser Phe Ser Asn Asp Asp Leu Phe Arg Val Pro Tyr Ala
        275   280   285

Ser Val Asn Val Asn Pro Ser Tyr His Gln Gln Gln His Gly Phe His
    290   295   300

Gln Gln Glu Ser Glu Phe Glu Leu Leu Lys Glu Met Phe Pro Ser Val
305   310   315   320

Phe Phe Lys Gln Glu Pro
                325

<210> 63 <211> 1107 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (16)..(930) <223> G207

 <400> 63
aaaagatctg tttca atg gcg gat cgt gtt aaa ggt cca tgg agt caa gaa
51
                  Met Ala Asp Arg Val Lys Gly Pro Trp Ser Gln Glu
                  1   5   10

gaa gat gag cag cta cga agg atg gtt gag aaa tac gga ccg agg aat
99
Glu Asp Glu Gln Leu Arg Arg Met Val Glu Lys Tyr Gly Pro Arg Asn
            15   20   25

tgg tct gcg att agc aaa tcg att cca ggt cga tct ggt aaa tcg tgt
147
Trp Ser Ala Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys
    30   35   40

aga tta cgt tgg tgt aat cag tta tct ccg gag gtt gag cat cgt cct
195
Arg Leu Arg Trp Cys Asn Gln Leu Ser Pro Glu Val Glu His Arg Pro
45   50   55   60

ttc tcg ccg gag gaa gat gag act att gta acc gcc cgt gct cag ttt
243
Phe Ser Pro Glu Glu Asp Glu Thr Ile Val Thr Ala Arg Ala Gln Phe
                65   70   75

ggt aac aag tgg gcg acg att gct cgt ctt ctt aac ggt cgt acg gat
291
Gly Asn Lys Trp Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp
            80   85   90

aac gcc gtt aaa aat cac tgg aac tct acg ctt aag agg aaa tgc agc
339
Asn Ala Val Lys Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Ser
        95   100   105

gga ggt gtg gcg gtt acg acg gtg acg gag acg gag gaa gat cag gat
387
Gly Gly Val Ala Val Thr Thr Val Thr Glu Thr Glu Glu Asp Gln Asp
    110   115   120

cgg ccg aag aag agg aga tct gtt agc ttt gat cct gct ttt gct ccg
435
Arg Pro Lys Lys Arg Arg Ser Val Ser Phe Asp Pro Ala Phe Ala Pro
125   130   135   140

gtg gat act gga ttg tac atg agt cct gag agt cct aac gga atc gat
483
Val Asp Thr Gly Leu Tyr Met Ser Pro Glu Ser Pro Asn Gly Ile Asp
            145   150   155

gtt agt gat tct agc acg att ccg tca ccg tcg tct cct gtt gct cag
531
Val Ser Asp Ser Ser Thr Ile Pro Ser Pro Ser Ser Pro Val Ala Gln
            160   165   170

ctg ttt aaa cca atg ccg att tcc ggc ggt ttt acg gtg gtt ccg cag
579
Leu Phe Lys Pro Met Pro Ile Ser Gly Gly Phe Thr Val Val Pro Gln
        175   180   185

ccg tta ccg gtt gaa atg tct tcg tct tcg gag gat cca cct act tcg
627
Pro Leu Pro Val Glu Met Ser Ser Ser Ser Glu Asp Pro Pro Thr Ser
        190   195   200

111

ttg agt ttg tca cta cct gga gct gag aac acg agt tcg agc cat aac
675
Leu Ser Leu Ser Leu Pro Gly Ala Glu Asn Thr Ser Ser Ser His Asn
205   210   215   220

aat aac aac aac gcg ttg atg ttt ccg aga ttt gag agt cag atg aag
723
Asn Asn Asn Asn Ala Leu Met Phe Pro Arg Phe Glu Ser Gln Met Lys
                    225   230   235

att aat gta gag gag aga gga gga gga gga gaa gga cgt aga ggt gag
771
Ile Asn Val Glu Glu Arg Gly Gly Gly Gly Glu Gly Arg Arg Gly Glu
                240   245   250

ttt atg acg gtg gtg cag gag atg ata aaa gct gaa gtg agg agt tac
819
Phe Met Thr Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr
            255   260   265

atg gcg gaa atg cag aaa aca agt ggt gga ttc gtc gtc gga ggt tta
867
Met Ala Glu Met Gln Lys Thr Ser Gly Gly Phe Val Val Gly Gly Leu
        270   275   280

tac gaa tcc ggc ggc aat ggt ggt ttt agg gat tgt gga gta ata aca
915
Tyr Glu Ser Gly Gly Asn Gly Gly Phe Arg Asp Cys Gly Val Ile Thr
285   290   295   300

cct aag gtt gag tag ttttggttta gggttaaaac ttgaatcgat tggggatttt
970
Pro Lys Val Glu

caagagcatt catttttggg gtttatggta aaattaaaaa caaaaacaaa atgtacagag
1030

gaattaaaat ttctatggaa taatcttaaa tctcaaatat ttgttacttg ttttggtgat
1090

tcataaccaa aatcaaa
1107

<210>   64 <211>   304 <212>   PRT <213>   Arabidopsis thaliana   <400>
64

Met Ala Asp Arg Val Lys Gly Pro Trp Ser Gln Glu Glu Asp Glu Gln
1   5   10   15

Leu Arg Arg Met Val Glu Lys Tyr Gly Pro Arg Asn Trp Ser Ala Ile
            20   25   30

Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp
        35   40   45

Cys Asn Gln Leu Ser Pro Glu Val Glu His Arg Pro Phe Ser Pro Glu

112

```
        50                    55                         60


Glu Asp Glu Thr Ile Val Thr Ala Arg Ala Gln Phe Gly Asn Lys Trp
65                70              75                        80


Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val Lys
                85              90                    95


Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Ser Gly Gly Val Ala
            100             105               110


Val Thr Thr Val Thr Glu Thr Glu Glu Asp Gln Asp Arg Pro Lys Lys
        115             120             125


Arg Arg Ser Val Ser Phe Asp Pro Ala Phe Ala Pro Val Asp Thr Gly
    130             135             140


Leu Tyr Met Ser Pro Glu Ser Pro Asn Gly Ile Asp Val Ser Asp Ser
145             150             155               160


Ser Thr Ile Pro Ser Pro Ser Ser Pro Val Ala Gln Leu Phe Lys Pro
            165             170             175


Met Pro Ile Ser Gly Gly Phe Thr Val Val Pro Gln Pro Leu Pro Val
            180             185             190


Glu Met Ser Ser Ser Ser Glu Asp Pro Pro Thr Ser Leu Ser Leu Ser
        195             200             205


Leu Pro Gly Ala Glu Asn Thr Ser Ser Ser His Asn Asn Asn Asn Asn
    210             215             220


Ala Leu Met Phe Pro Arg Phe Glu Ser Gln Met Lys Ile Asn Val Glu
225             230             235               240


Glu Arg Gly Gly Gly Gly Glu Gly Arg Arg Gly Glu Phe Met Thr Val
            245             250             255


Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr Met Ala Glu Met
        260             265             270


Gln Lys Thr Ser Gly Gly Phe Val Val Gly Gly Leu Tyr Glu Ser Gly
    275             280             285


Gly Asn Gly Gly Phe Arg Asp Cys Gly Val Ile Thr Pro Lys Val Glu
    290             295             300
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<210> 65 <211> 1209 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (41)..(1156) <223> G229

<400> 65
ttgtggtcag tggaataaac acatataacc gccggagaaa atg gga aga gcg cca
55

                                                           Met Gly Arg Ala Pro
                                                           1   5

tgt tgc gag aag gtc ggt atc aag aga ggg cgg tgg acg gcg gag gag
103
Cys Cys Glu Lys Val Gly Ile Lys Arg Gly Arg Trp Thr Ala Glu Glu
               10   15   20

gac cag att ctc tcc aac tac att caa tcc aat ggt gaa ggt tct tgg
151
Asp Gln Ile Leu Ser Asn Tyr Ile Gln Ser Asn Gly Glu Gly Ser Trp
               25   30   35

aga tct ctc ccc aaa aat gcc gga tta aaa agg tgt gga aag agc tgt
199
Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys
           40   45   50

aga ttg aga tgg ata aac tat cta aga tca gac ctc aag cgt gga aac
247
Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp Leu Lys Arg Gly Asn
       55   60   65

ata act cca gaa gaa gaa gaa ctc gtt gtt aaa ttg cat tcc act ttg
295
Ile Thr Pro Glu Glu Glu Glu Leu Val Val Lys Leu His Ser Thr Leu
70   75   80   85

gga aac agg tgg tca cta atc gcg ggt cat cta cca ggg aga aca gac
343
Gly Asn Arg Trp Ser Leu Ile Ala Gly His Leu Pro Gly Arg Thr Asp
               90   95   100

aac gaa ata aaa aat tat tgg aac tct cat ctc agc cgt aaa ctc cac
391
Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu Ser Arg Lys Leu His
           105   110   115

aac ttc att agg aag cca tcc atc tct caa gac gtc tcc gcc gta atc
439
Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp Val Ser Ala Val Ile
           120   125   130

atg gcg aac gct tct tca gcg cca ccg ccg ccg cag gca aaa cgc aga
487
Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro Gln Ala Lys Arg Arg
           135   140   145

ctt ggg aga acg agt agg tcc gct atg aaa cca aaa atc cgc aga aca
535
Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro Lys Ile Arg Arg Thr
150   155   160   165

114

aaa act cgt aaa acg aag aaa acg tct gca cca ccg gag cct aac gcc
583
Lys Thr Arg Lys Thr Lys Lys Thr Ser Ala Pro Pro Glu Pro Asn Ala
          170   175   180

gat gta gct ggg gct gat aaa gaa gca tta atg gtg gag tca agt gga
631
Asp Val Ala Gly Ala Asp Lys Glu Ala Leu Met Val Glu Ser Ser Gly
              185   190   195

gcc gag gct gag cta gga cga cca tgt gac tac tat gga gat gat tgt
679
Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr Tyr Gly Asp Asp Cys
          200   205   210

aac aaa aat ctc atg agc att aat ggc gat aat gga gtt tta acg ttt
727
Asn Lys Asn Leu Met Ser Ile Asn Gly Asp Asn Gly Val Leu Thr Phe
          215   220   225

gat gat gat atc atc gat ctt ttg ttg gac gag tca gat cct ggc cac
775
Asp Asp Asp Ile Ile Asp Leu Leu Leu Asp Glu Ser Asp Pro Gly His
230   235   240   245

ttg tac aca aac aca acg tgc ggt ggt ggt ggg gag ttg cat aac ata
823
Leu Tyr Thr Asn Thr Thr Cys Gly Gly Gly Gly Glu Leu His Asn Ile
              250   255   260

aga gac tct gaa gga gcc aga ggg ttc tcg gat act tgg aac caa ggg
871
Arg Asp Ser Glu Gly Ala Arg Gly Phe Ser Asp Thr Trp Asn Gln Gly
              265   270   275

aat ctc gac tgt ctt ctt cag tct tgt cca tct gtg gag tcg ttt ctc
919
Asn Leu Asp Cys Leu Leu Gln Ser Cys Pro Ser Val Glu Ser Phe Leu
          280   285   290

aac tac gac cac caa gtt aac gac gcg tcg acg gat gag ttt atc gat
967
Asn Tyr Asp His Gln Val Asn Asp Ala Ser Thr Asp Glu Phe Ile Asp
          295   300   305

tgg gat tgt gtt tgg caa gaa ggt agt gat aat aat ctt tgg cat gag
1015
Trp Asp Cys Val Trp Gln Glu Gly Ser Asp Asn Asn Leu Trp His Glu
310   315   320   325

aaa gag aat ccc gac tca atg gtc tcg tgg ctt tta gac ggt gat gat
1063
Lys Glu Asn Pro Asp Ser Met Val Ser Trp Leu Leu Asp Gly Asp Asp
              330   335   340

gag gcc acg atc ggg aat agt aat tgt gag aac ttt gga gaa ccg tta
1111
Glu Ala Thr Ile Gly Asn Ser Asn Cys Glu Asn Phe Gly Glu Pro Leu
              345   350   355

115

```
gat cat gac gac gaa agc gct ttg gtc gct tgg ctt ctg tca tga
1156
Asp His Asp Asp Glu Ser Ala Leu Val Ala Trp Leu Leu Ser
        360                 365             370

tgatattgat tgatccgtta tgtaatcttt tttgtgcatt cacagtttga atc
1209
```

<210> 66 <211> 371 <212> PRT <213> Arabidopsis thaliana <400>
66

```
Met Gly Arg Ala Pro Cys Cys Glu Lys Val Gly Ile Lys Arg Gly Arg
1               5               10              15

Trp Thr Ala Glu Glu Asp Gln Ile Leu Ser Asn Tyr Ile Gln Ser Asn
            20              25              30

Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg
        35              40              45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp
    50              55              60

Leu Lys Arg Gly Asn Ile Thr Pro Glu Glu Glu Leu Val Val Lys
65              70              75              80

Leu His Ser Thr Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly His Leu
            85              90              95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu
            100             105             110

Ser Arg Lys Leu His Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp
        115             120             125

Val Ser Ala Val Ile Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro
    130             135             140

Gln Ala Lys Arg Arg Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro
145             150             155             160

Lys Ile Arg Arg Thr Lys Thr Arg Lys Thr Lys Lys Thr Ser Ala Pro
            165             170             175

Pro Glu Pro Asn Ala Asp Val Ala Gly Ala Asp Lys Glu Ala Leu Met
            180             185             190

Val Glu Ser Ser Gly Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr
```

```
           195                  200                  205


Tyr Gly Asp Asp Cys Asn Lys Asn Leu Met Ser Ile Asn Gly Asp Asn
    210                  215                  220


Gly Val Leu Thr Phe Asp Asp Asp Ile Ile Asp Leu Leu Leu Asp Glu
225                  230                  235                  240


Ser Asp Pro Gly His Leu Tyr Thr Asn Thr Thr Cys Gly Gly Gly Gly
             245                  250                  255


Glu Leu His Asn Ile Arg Asp Ser Glu Gly Ala Arg Gly Phe Ser Asp
         260                  265                  270


Thr Trp Asn Gln Gly Asn Leu Asp Cys Leu Leu Gln Ser Cys Pro Ser
         275                  280                  285


Val Glu Ser Phe Leu Asn Tyr Asp His Gln Val Asn Asp Ala Ser Thr
    290                  295                  300


Asp Glu Phe Ile Asp Trp Asp Cys Val Trp Gln Glu Gly Ser Asp Asn
305                  310                  315                  320


Asn Leu Trp His Glu Lys Glu Asn Pro Asp Ser Met Val Ser Trp Leu
             325                  330                  335


Leu Asp Gly Asp Asp Glu Ala Thr Ile Gly Asn Ser Asn Cys Glu Asn
         340                  345                  350


Phe Gly Glu Pro Leu Asp His Asp Asp Glu Ser Ala Leu Val Ala Trp
         355                  360                  365


Leu Leu Ser
    370
```

<210> 67 <211> 1195 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (66)..(983) <223> G242

 <400> 67
ctctcaaaac caaaatcact aaagaggaga agattgctaa agtttgataa aacattccaa
60

```
aatca atg gct gat agg atc aaa ggt cca tgg agt cct gaa gaa gac gag
110
      Met Ala Asp Arg Ile Lys Gly Pro Trp Ser Pro Glu Glu Asp Glu
      1           5           10                  15

cag ctt cgt agg ctt gtt gtt aaa tac ggt cca aga aac tgg aca gtg
158
```

117

```
Gln Leu Arg Arg Leu Val Val Lys Tyr Gly Pro Arg Asn Trp Thr Val
            20                  25                  30

att agc aaa tct att ccc ggt aga tcg ggg aaa tcg tgt cgt tta cgg
206
Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg
            35                  40                  45

tgg tgc aac cag ctt tcg ccg caa gtt gag cat cgg ccg ttt tcg gct
254
Trp Cys Asn Gln Leu Ser Pro Gln Val Glu His Arg Pro Phe Ser Ala
            50                  55                  60

gag gaa gac gag acg atc gca cgt gct cac gct cag ttc ggg aat aaa
302
Glu Glu Asp Glu Thr Ile Ala Arg Ala His Ala Gln Phe Gly Asn Lys
            65                  70                  75

tgg gcg acg att gct cgt ctt ctc aac ggt cgt acg gac aac gcc gtg
350
Trp Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val
80                  85                  90                  95

aag aat cac tgg aac tcg acg ctc aag agg aaa tgc ggc ggt tac gac
398
Lys Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Gly Gly Tyr Asp
            100                 105                 110

cat cgg ggt tac gat ggt tcg gag gat cat cgg ccg gtt aag aga tcg
446
His Arg Gly Tyr Asp Gly Ser Glu Asp His Arg Pro Val Lys Arg Ser
            115                 120                 125

gtg agt gcg gga tct cca cct gtt gtt act ggg ctt tac atg agc cca
494
Val Ser Ala Gly Ser Pro Pro Val Val Thr Gly Leu Tyr Met Ser Pro
            130                 135                 140

gga agc cca act gga tct gat gtc agt gat tca agt act atc ccg ata
542
Gly Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr Ile Pro Ile
            145                 150                 155

tta cct tcc gtt gag ctt ttc aag cct gtg cct aga cct ggt gct gtt
590
Leu Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro Gly Ala Val
160                 165                 170                 175

gtg cta ccg ctt cct atc gaa acg tcg tct ttt tcc gat gat cca ccg
638
Val Leu Pro Leu Pro Ile Glu Thr Ser Ser Phe Ser Asp Asp Pro Pro
            180                 185                 190

act tcg tta agc ttg tca ctt cct ggt gcc gac gta agc gag gag tca
686
Thr Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser Glu Glu Ser
            195                 200                 205

aac cgt agc cac gag tca acg aat atc aac aac acc act tcg agc cgc
734
Asn Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr Ser Ser Arg
```

118

              210   215   220

cac aac cac aac aat acg gtg tcg ttt atg ccg ttt agt ggt ggg ttt
782
His Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser Gly Gly Phe
    225   230   235

aga ggt gcg att gag gaa atg ggg aag tct ttt ccc ggt aac gga ggc
830
Arg Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly Asn Gly Gly
240   245   250   255

gag ttt atg gcg gtg gtg caa gag atg att aag gcg gaa gtg agg agt
878
Glu Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser
              260   265   270

tac atg acg gag atg caa cgg aac aat ggt ggc gga ttc gtc gga gga
926
Tyr Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe Val Gly Gly
              275   280   285

ttc att gat aat ggc atg att ccg atg agt caa att gga gtt ggg aga
974
Phe Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly Val Gly Arg
          290   295   300

atc gag tag acaaagtgag attattagga aactgtttaa attggagaag
1023
Ile Glu
    305

aagaaaaatg ctctgttttt ttctcctttg gattaggctt aagaattttg ggttttaagg
1083

aaatgtatag aggaaatcga gtgaacaaag ctcgagagct ggggacgtag tgacgaagac
1143

gaagatcaaa tttctcttaa gctattcagg aaaataaaat aaatttttat tt
1195

<210> 68 <211> 305 <212> PRT <213> Arabidopsis thaliana <400>
68

Met Ala Asp Arg Ile Lys Gly Pro Trp Ser Pro Glu Glu Asp Glu Gln
1   5   10   15

Leu Arg Arg Leu Val Val Lys Tyr Gly Pro Arg Asn Trp Thr Val Ile
              20   25   30

Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp
          35   40   45

Cys Asn Gln Leu Ser Pro Gln Val Glu His Arg Pro Phe Ser Ala Glu
    50   55   60

Glu Asp Glu Thr Ile Ala Arg Ala His Ala Gln Phe Gly Asn Lys Trp
65   70   75   80

Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val Lys
                85   90   95

Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Gly Gly Tyr Asp His
            100   105   110

Arg Gly Tyr Asp Gly Ser Glu Asp His Arg Pro Val Lys Arg Ser Val
        115   120   125

Ser Ala Gly Ser Pro Pro Val Val Thr Gly Leu Tyr Met Ser Pro Gly
    130   135   140

Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr Ile Pro Ile Leu
145   150   155   160

Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro Gly Ala Val Val
            165   170   175

Leu Pro Leu Pro Ile Glu Thr Ser Ser Phe Ser Asp Asp Pro Pro Thr
        180   185   190

Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser Glu Glu Ser Asn
    195   200   205

Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr Ser Ser Arg His
    210   215   220

Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser Gly Gly Phe Arg
225   230   235   240

Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly Asn Gly Gly Glu
            245   250   255

Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr
            260   265   270

Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe Val Gly Gly Phe
        275   280   285

Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly Val Gly Arg Ile
        290   295   300

Glu

120

305

<210> 69 <211> 660 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(660) <223> G247

<400> 69
atg aga atg aca aga gat gga aaa gaa cat gaa tac aag aaa ggt tta
48
Met Arg Met Thr Arg Asp Gly Lys Glu His Glu Tyr Lys Lys Gly Leu
1   5   10   15

tgg aca gtg gaa gaa gac aag atc ctc atg gat tat gtc cga act cat
96
Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr Val Arg Thr His
            20   25   30

ggc cag ggc cac tgg aac cgc atc gcc aag aaa act ggg ctc aag aga
144
Gly Gln Gly His Trp Asn Arg Ile Ala Lys Lys Thr Gly Leu Lys Arg
        35   40   45

tgt ggg aaa agc tgt agg ttg aga tgg atg aac tac tta agc cct aat
192
Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn
    50   55   60

gtt aac aga ggc aat ttt act gac caa gaa gaa gat ctc atc atc aga
240
Val Asn Arg Gly Asn Phe Thr Asp Gln Glu Glu Asp Leu Ile Ile Arg
65   70   75   80

ctc cac aag ctc ctc ggc aac aga tgg tcg ttg ata gcg aaa aga gtt
288
Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val
                85   90   95

ccg gga aga aca gac aac caa gta aag aat tac tgg aac aca cat ctc
336
Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Thr His Leu
            100   105   110

agc aag aaa ctt ggt ctc gga gat cat tca act gcc gtc aaa gcc gca
384
Ser Lys Lys Leu Gly Leu Gly Asp His Ser Thr Ala Val Lys Ala Ala
        115   120   125

tgc ggt gta gag tct cca ccg tct atg gcc ctt ata acc aca acg tcc
432
Cys Gly Val Glu Ser Pro Pro Ser Met Ala Leu Ile Thr Thr Thr Ser
    130   135   140

tcc tct cat caa gag atc tcc ggt gga aaa aat tca act cta agg ttc
480
Ser Ser His Gln Glu Ile Ser Gly Gly Lys Asn Ser Thr Leu Arg Phe
145   150   155   160

gac act tta gtt gac gaa tcc aaa ctc aaa cca aaa tcc aaa cta gtc
528
Asp Thr Leu Val Asp Glu Ser Lys Leu Lys Pro Lys Ser Lys Leu Val
                165   170   175

cac gca aca cca act gac gta gaa gtt gca gct acg gtt cca aat ctg
576
His Ala Thr Pro Thr Asp Val Glu Val Ala Ala Thr Val Pro Asn Leu
        180   185   190

ttc gat acc ttt tgg gtt ctt gaa gac gac ttc gag ctt agt tca ctc
624
Phe Asp Thr Phe Trp Val Leu Glu Asp Asp Phe Glu Leu Ser Ser Leu
        195   200   205

act atg atg gat ttt act aat ggg tat tgc ctt tga
660
Thr Met Met Asp Phe Thr Asn Gly Tyr Cys Leu
    210   215

<210> 70 <211> 219 <212> PRT <213> Arabidopsis thaliana <400>
70

Met Arg Met Thr Arg Asp Gly Lys Glu His Glu Tyr Lys Lys Gly Leu
1   5   10   15

Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr Val Arg Thr His
            20   25   30

Gly Gln Gly His Trp Asn Arg Ile Ala Lys Lys Thr Gly Leu Lys Arg
        35   40   45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn
    50   55   60

Val Asn Arg Gly Asn Phe Thr Asp Gln Glu Glu Asp Leu Ile Ile Arg
65   70   75   80

Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val
            85   90   95

Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Thr His Leu
            100   105   110

Ser Lys Lys Leu Gly Leu Gly Asp His Ser Thr Ala Val Lys Ala Ala
        115   120   125

Cys Gly Val Glu Ser Pro Pro Ser Met Ala Leu Ile Thr Thr Thr Ser
    130   135   140

Ser Ser His Gln Glu Ile Ser Gly Gly Lys Asn Ser Thr Leu Arg Phe
145   150   155   160

Asp Thr Leu Val Asp Glu Ser Lys Leu Lys Pro Lys Ser Lys Leu Val

122

```
              165                    170                    175
```

```
His Ala Thr Pro Thr Asp Val Glu Val Ala Ala Thr Val Pro Asn Leu
        180                    185                    190
```

```
Phe Asp Thr Phe Trp Val Leu Glu Asp Asp Phe Glu Leu Ser Ser Leu
        195                    200                    205
```

```
Thr Met Met Asp Phe Thr Asn Gly Tyr Cys Leu
        210                    215
```

<210> 71 <211> 1613 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (30)..(1430) <223> G264

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 <400> 71
cttgtaccag tttctgatta gattcaaca atg aac ggc gca tta ggt aac tcc
53
                                  Met Asn Gly Ala Leu Gly Asn Ser
                                  1               5
```

```
tcc gcc tcc gtt agc ggc gga gaa gga gcc gga gga cca gcg cct ttc
101
Ser Ala Ser Val Ser Gly Gly Glu Gly Ala Gly Gly Pro Ala Pro Phe
    10                  15                  20
```

```
ttg gtg aaa acc tac gag atg gtc gac gat tca tca acg gac cag atc
149
Leu Val Lys Thr Tyr Glu Met Val Asp Asp Ser Ser Thr Asp Gln Ile
25                  30                  35                  40
```

```
gta tcg tgg agc gct aac aac aac agc ttc atc gtt tgg aat cat gcc
197
Val Ser Trp Ser Ala Asn Asn Asn Ser Phe Ile Val Trp Asn His Ala
                45                  50                  55
```

```
gaa ttt tca cgc ctc ctt ctt cca acc tac ttc aaa cac aat aac ttc
245
Glu Phe Ser Arg Leu Leu Leu Pro Thr Tyr Phe Lys His Asn Asn Phe
            60                  65                  70
```

```
tct tcc ttc att cgt cag ctc aat acc tat ggg ttt agg aag att gat
293
Ser Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Asp
        75                  80                  85
```

```
cca gag agg tgg gag ttt ttg aat gat gat ttt att aag gat cag aag
341
Pro Glu Arg Trp Glu Phe Leu Asn Asp Asp Phe Ile Lys Asp Gln Lys
    90                  95                  100
```

```
cat ctt ctc aag aat ata cat aga agg aaa cct ata cac agc cac agt
389
His Leu Leu Lys Asn Ile His Arg Arg Lys Pro Ile His Ser His Ser
105                 110                 115                 120
```

```
cat cca cct gct tcg tcg act gat caa gaa aga gca gtg ttg caa gag
437
```

```
His Pro Pro Ala Ser Ser Thr Asp Gln Glu Arg Ala Val Leu Gln Glu
                125             130             135


caa atg gac aag ctt tca cgt gag aaa gct gca att gaa gct aag ctt
485
Gln Met Asp Lys Leu Ser Arg Glu Lys Ala Ala Ile Glu Ala Lys Leu
            140             145             150


tta aag ttc aaa caa cag aag gtt gta gca aag cat cag ttt gaa gaa
533
Leu Lys Phe Lys Gln Gln Lys Val Val Ala Lys His Gln Phe Glu Glu
        155             160             165


atg act gag cat gtt gat gat atg gag aat agg cag aag aag ctg ctg
581
Met Thr Glu His Val Asp Asp Met Glu Asn Arg Gln Lys Lys Leu Leu
    170             175             180


aat ttt ttg gaa act gcg att cgg aat cct act ttt gtt aag aat ttt
629
Asn Phe Leu Glu Thr Ala Ile Arg Asn Pro Thr Phe Val Lys Asn Phe
185             190             195             200


ggt aag aaa gtc gag cag ttg gat att tca gct tac aac aaa aag cga
677
Gly Lys Lys Val Glu Gln Leu Asp Ile Ser Ala Tyr Asn Lys Lys Arg
            205             210             215


agg ctc cct gaa gtt gag caa tca aag cca cct tca gaa gat tct cat
725
Arg Leu Pro Glu Val Glu Gln Ser Lys Pro Pro Ser Glu Asp Ser His
            220             225             230


ctg gat aat agt agt ggt agc tcg aga cgc gag tct gga aac att ttt
773
Leu Asp Asn Ser Ser Gly Ser Ser Arg Arg Glu Ser Gly Asn Ile Phe
            235             240             245


cat caa aat ttc tct aat aaa ttg cga cta gag ctt tct cca gct gat
821
His Gln Asn Phe Ser Asn Lys Leu Arg Leu Glu Leu Ser Pro Ala Asp
    250             255             260


tca gat atg aac atg gtt tca cac agt ata caa agt tcc aat gaa gaa
869
Ser Asp Met Asn Met Val Ser His Ser Ile Gln Ser Ser Asn Glu Glu
265             270             275             280


ggt gcg agt ccc aaa ggg ata ctg tca gga ggt gat cca aat act aca
917
Gly Ala Ser Pro Lys Gly Ile Leu Ser Gly Gly Asp Pro Asn Thr Thr
            285             290             295


cta aca aaa aga gaa ggc cta cca ttt gca cct gaa gct cta gag ctt
965
Leu Thr Lys Arg Glu Gly Leu Pro Phe Ala Pro Glu Ala Leu Glu Leu
            300             305             310


gcg gat acc ggg aca tgc ccg agg aga tta ctg tta aat gat aat aca
1013
Ala Asp Thr Gly Thr Cys Pro Arg Arg Leu Leu Leu Asn Asp Asn Thr
```

```
          315                   320                   325

agg gtg gag acc ttg cag cag agg cta act tct tca gag gag act gat
1061
Arg Val Glu Thr Leu Gln Gln Arg Leu Thr Ser Ser Glu Glu Thr Asp
    330                   335                   340


ggt agc ttt tca tgt cat tta aat cta acc ctg gct tct gct ccg tta
1109
Gly Ser Phe Ser Cys His Leu Asn Leu Thr Leu Ala Ser Ala Pro Leu
345                   350                   355                   360


ccg gac aaa aca gct tca cag ata gct aag acg act ctt aaa agt cag
1157
Pro Asp Lys Thr Ala Ser Gln Ile Ala Lys Thr Thr Leu Lys Ser Gln
                365                   370                   375


gag tta aac ttt aac tca ata gaa aca agt gca agt gag aaa aat cgg
1205
Glu Leu Asn Phe Asn Ser Ile Glu Thr Ser Ala Ser Glu Lys Asn Arg
                380                   385                   390


ggt aga caa gag att gca gtt gga ggt agc caa gca aat gca gct cct
1253
Gly Arg Gln Glu Ile Ala Val Gly Gly Ser Gln Ala Asn Ala Ala Pro
                395                   400                   405


cca gca aga gtg aat gat gta ttc tgg gaa cag ttc cta aca gaa agg
1301
Pro Ala Arg Val Asn Asp Val Phe Trp Glu Gln Phe Leu Thr Glu Arg
    410                   415                   420


cca ggg tct tca gat aat gag gag gca agt tcg act tat aga ggt aac
1349
Pro Gly Ser Ser Asp Asn Glu Glu Ala Ser Ser Thr Tyr Arg Gly Asn
425                   430                   435                   440


cca tac gaa gag caa gag gag aaa aga aac ggg agt atg atg tta cgt
1397
Pro Tyr Glu Glu Gln Glu Glu Lys Arg Asn Gly Ser Met Met Leu Arg
                445                   450                   455


aat aca aag aat atc gag cag ctg acc tta taa actatttgga cggttacatc
1450
Asn Thr Lys Asn Ile Glu Gln Leu Thr Leu
                460                   465


aacgagagta cgaactgagg ttttggtaag aagtatgggt gagtaagtaa tgaaacattg
1510


gactgaaaaa gcgtaagtag ctttgttgta aacacttgcg tctctgtcta cacaagtaat
1570


ttgactgtaa atgtaagtgt acaggattta aattgaataa gca
1613


<210> 72 <211> 466 <212> PRT <213> Arabidopsis thaliana <400>
72


Met Asn Gly Ala Leu Gly Asn Ser Ser Ala Ser Val Ser Gly Gly Glu
```

```
1                    5                      10                     15


Gly Ala Gly Gly Pro Ala Pro Phe Leu Val Lys Thr Tyr Glu Met Val
             20                  25                  30


Asp Asp Ser Ser Thr Asp Gln Ile Val Ser Trp Ser Ala Asn Asn Asn
             35                  40                  45


Ser Phe Ile Val Trp Asn His Ala Glu Phe Ser Arg Leu Leu Leu Pro
    50                  55                  60


Thr Tyr Phe Lys His Asn Asn Phe Ser Ser Phe Ile Arg Gln Leu Asn
65                  70                  75                  80


Thr Tyr Gly Phe Arg Lys Ile Asp Pro Glu Arg Trp Glu Phe Leu Asn
             85                  90                  95


Asp Asp Phe Ile Lys Asp Gln Lys His Leu Leu Lys Asn Ile His Arg
             100                 105                 110


Arg Lys Pro Ile His Ser His Ser His Pro Pro Ala Ser Ser Thr Asp
             115                 120                 125


Gln Glu Arg Ala Val Leu Gln Glu Gln Met Asp Lys Leu Ser Arg Glu
    130                 135                 140


Lys Ala Ala Ile Glu Ala Lys Leu Leu Lys Phe Lys Gln Gln Lys Val
145                 150                 155                 160


Val Ala Lys His Gln Phe Glu Glu Met Thr Glu His Val Asp Asp Met
                165                 170                 175


Glu Asn Arg Gln Lys Lys Leu Leu Asn Phe Leu Glu Thr Ala Ile Arg
             180                 185                 190


Asn Pro Thr Phe Val Lys Asn Phe Gly Lys Lys Val Glu Gln Leu Asp
             195                 200                 205


Ile Ser Ala Tyr Asn Lys Lys Arg Arg Leu Pro Glu Val Glu Gln Ser
    210                 215                 220


Lys Pro Pro Ser Glu Asp Ser His Leu Asp Asn Ser Ser Gly Ser Ser
225                 230                 235                 240


Arg Arg Glu Ser Gly Asn Ile Phe His Gln Asn Phe Ser Asn Lys Leu
             245                 250                 255
```

Arg Leu Glu Leu Ser Pro Ala Asp Ser Asp Met Asn Met Val Ser His
            260   265   270

Ser Ile Gln Ser Ser Asn Glu Glu Gly Ala Ser Pro Lys Gly Ile Leu
            275   280   285

Ser Gly Gly Asp Pro Asn Thr Thr Leu Thr Lys Arg Glu Gly Leu Pro
            290   295   300

Phe Ala Pro Glu Ala Leu Glu Leu Ala Asp Thr Gly Thr Cys Pro Arg
305   310   315   320

Arg Leu Leu Leu Asn Asp Asn Thr Arg Val Glu Thr Leu Gln Gln Arg
            325   330   335

Leu Thr Ser Ser Glu Glu Thr Asp Gly Ser Phe Ser Cys His Leu Asn
            340   345   350

Leu Thr Leu Ala Ser Ala Pro Leu Pro Asp Lys Thr Ala Ser Gln Ile
            355   360   365

Ala Lys Thr Thr Leu Lys Ser Gln Glu Leu Asn Phe Asn Ser Ile Glu
            370   375   380

Thr Ser Ala Ser Glu Lys Asn Arg Gly Arg Gln Glu Ile Ala Val Gly
385   390   395   400

Gly Ser Gln Ala Asn Ala Ala Pro Pro Ala Arg Val Asn Asp Val Phe
            405   410   415

Trp Glu Gln Phe Leu Thr Glu Arg Pro Gly Ser Ser Asp Asn Glu Glu
            420   425   430

Ala Ser Ser Thr Tyr Arg Gly Asn Pro Tyr Glu Glu Gln Glu Glu Lys
            435   440   445

Arg Asn Gly Ser Met Met Leu Arg Asn Thr Lys Asn Ile Glu Gln Leu
            450   455   460

Thr Leu
465

<210> 73 <211> 2104 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (93)..(1874) <223> G278

127

<400> 73

tcgatcttta accaaatcca gttgataagg tctcttcgtt gattagcaga gatctcttta
60

atttgtgaat ttcaattcat cggaacctgt tg atg gac acc acc att gat gga
113
                                         Met Asp Thr Thr Ile Asp Gly
                                        1　　　　　　　5

ttc gcc gat tct tat gaa atc agc agc act agt ttc gtc gct acc gat
161
Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp
       10　　　　　　　　　　　 15　　　　　　　　　　　 20

aac acc gac tcc tct att gtt tat ctg gcc gcc gaa caa gta ctc acc
209
Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr
    25　　　　　　　　　　　 30　　　　　　　　　　　 35

gga cct gat gta tct gct ctg caa ttg ctc tcc aac agc ttc gaa tcc
257
Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser
40　　　　　　　　　　　 45　　　　　　　　　　　 50　　　　　　　　　　　 55

gtc ttt gac tcg ccg gat gat ttc tac agc gac gct aag ctt gtt ctc
305
Val Phe Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys Leu Val Leu
           60　　　　　　　　　　　 65　　　　　　　　　　　 70

tcc gac ggc cgg gaa gtt tct ttc cac cgg tgc gtt ttg tca gcg aga
353
Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg
            75　　　　　　　　　　　 80　　　　　　　　　　　 85

agc tct ttc ttc aag agc gct tta gcc gcc gct aag aag gag aaa gac
401
Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys Glu Lys Asp
          90　　　　　　　　　　　 95　　　　　　　　　　　 100

tcc aac aac acc gcc gcc gtg aag ctc gag ctt aag gag att gcc aag
449
Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys
       105　　　　　　　　　　　 110　　　　　　　　　　　 115

gat tac gaa gtc ggt ttc gat tcg gtt gtg act gtt ttg gct tat gtt
497
Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val
120　　　　　　　　　　　 125　　　　　　　　　　　 130　　　　　　　　　　　 135

tac agc agc aga gtg aga ccg ccg cct aaa gga gtt tct gaa tgc gca
545
Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala
            140　　　　　　　　　　　 145　　　　　　　　　　　 150

gac gag aat tgc tgc cac gtg gct tgc cgg ccg gcg gtg gat ttc atg
593
Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met
          155　　　　　　　　　　　 160　　　　　　　　　　　 165

ttg gag gtt ctc tat ttg gct ttc atc ttc aag atc cct gaa tta att
641

128

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Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile
    170             175                 180

act ctc tat cag agg cac tta ttg gac gtt gta gac aaa gtt gtt ata
689
Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys Val Val Ile
    185             190                 195

gag gac aca ttg gtt ata ctc aag ctt gct aat ata tgt ggt aaa gct
737
Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly Lys Ala
200             205                 210                 215

tgt atg aag cta ttg gat aga tgt aaa gag att att gtc aag tct aat
785
Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn
            220                 225                 230

gta gat atg gtt agt ctt gaa aag tca ttg ccg gaa gag ctt gtt aaa
833
Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu Val Lys
            235                 240                 245

gag ata att gat aga cgt aaa gag ctt ggt ttg gag gta cct aaa gta
881
Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val
        250                 255                 260

aag aaa cat gtc tcg aat gta cat aag gca ctt gac tcg gat gat att
929
Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile
        265                 270                 275

gag tta gtc aag ttg ctt ttg aaa gag gat cac acc aat cta gat gat
977
Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp
280             285                 290                 295

gcg tgt gct ctt cat ttc gct gtt gca tat tgc aat gtg aag acc gca
1025
Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala
            300                 305                 310

aca gat ctt tta aaa ctt gat ctt gcc gat gtc aac cat agg aat ccg
1073
Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His Arg Asn Pro
            315                 320                 325

agg gga tat acg gtg ctt cat gtt gct gcg atg cgg aag gag cca caa
1121
Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys Glu Pro Gln
        330                 335                 340

ttg ata cta tct cta ttg gaa aaa ggt gca agt gca tca gaa gca act
1169
Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr
        345                 350                 355

ttg gaa ggt aga acc gca ctc atg atc gca aaa caa gcc act atg gcg
1217
Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala
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129

360   365   370   375

gtt gaa tgt aat aat atc ccg gag caa tgc aag cat tct ctc aaa ggc
1265
Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly
          380   385   390

cga cta tgt gta gaa ata cta gag caa gaa gac aaa cga gaa caa att
1313
Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile
          395   400   405

cct aga gat gtt cct ccc tct ttt gca gtg gcg gcc gat gaa ttg aag
1361
Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys
          410   415   420

atg acg ctg ctc gat ctt gaa aat aga gtt gca ctt gct caa cgt ctt
1409
Met Thr Leu Leu Asp Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu
      425   430   435

ttt cca acg gaa gca caa gct gca atg gag atc gcc gaa atg aag gga
1457
Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly
440   445   450   455

aca tgt gag ttc ata gtg act agc ctc gag cct gac cgt ctc act ggt
1505
Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly
              460   465   470

acg aag aga aca tca ccg ggt gta aag ata gca cct ttc aga atc cta
1553
Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu
          475   480   485

gaa gag cat caa agt aga cta aaa gcg ctt tct aaa acc gtg gaa ctc
1601
Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu
          490   495   500

ggg aaa cga ttc ttc ccg cgc tgt tcg gca gtg ctc gac cag att atg
1649
Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met
      505   510   515

aac tgt gag gac ttg act caa ctg gct tgc gga gaa gac gac act gct
1697
Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu Asp Asp Thr Ala
520   525   530   535

gag aaa cga cta caa aag aag caa agg tac atg gaa ata caa gag aca
1745
Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu Ile Gln Glu Thr
              540   545   550

cta aag aag gcc ttt agt gag gac aat ttg gaa tta gga aat tcg tcc
1793
Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu Gly Asn Ser Ser
          555   560   565

130

ctg aca gat tcg act tct tcc aca tcg aaa tca acc ggt gga aag agg
1841
Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr Gly Gly Lys Arg
        570   575   580

tct aac cgt aaa ctc tct cat cgt cgt cgg tga gactcttgcc tcttagtgta
1894
Ser Asn Arg Lys Leu Ser His Arg Arg Arg
    585   590

atttttgctg taccatataa ttctgttttc atgatgactg taactgttta tgtctatcgt
1954

tggcgtcata tagtttcgct cttcgttttg catcctgtgt attattgctg caggtgtgct
2014

tcaaacaaat gttgtaacaa tttgaaccaa tggtatacag atttgtaata tatatttatg
2074

tacatcaaca ataaaaaaaa aaaaaaaaaa
2104

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Met Asp Thr Thr Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser
1   5   10   15

Thr Ser Phe Val Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu
            20   25   30

Ala Ala Glu Gln Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu
        35   40   45

Leu Ser Asn Ser Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr
    50   55   60

Ser Asp Ala Lys Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His
65   70   75   80

Arg Cys Val Leu Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala
            85   90   95

Ala Ala Lys Lys Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu
        100   105   110

Glu Leu Lys Glu Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val
        115   120   125

Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro
        130   135   140

131

Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys
145   150   155   160

Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile
                165   170   175

Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp
            180   185   190

Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu
        195   200   205

Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys
    210   215   220

Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser
225   230   - 235   240

Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu
            245   250   255

Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys
            260   265   270

Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu
        275   280   285

Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala
    290   295   300

Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala
305   310   315   320

Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala
            325   330   335

Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly
            340   345   350

Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile
        355   360   365

Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln
        370   375   380

132

Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln
385   390   395   400

Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala
                405   410   415

Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg
                420   425   430

Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met
                435   440   445

Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu
        450   455   460

Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys
465   470   475   480

Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala
                485   490   495

Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser
                500   505   510

Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala
                515   520   525

Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg
        530   535   540

Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn
545   550   555   560

Leu Glu Leu Gly Asn Ser Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser
                565   570   575

Lys Ser Thr Gly Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg
                580   585   590

Arg

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tcaaatcaat tctcgcgatt aagcaaaacc ctagatttat tctactcttc gaagtcgatt
120

tca atg gaa ggt tcc tcg tca gcc atc gcg agg aag aca tgg gag cta
168
    Met Glu Gly Ser Ser Ser Ala Ile Ala Arg Lys Thr Trp Glu Leu
    1   5   10   15

gag aac aac att ctc cca gtg gaa cca acc gat tca gcc tcc gac agt
216
Glu Asn Asn Ile Leu Pro Val Glu Pro Thr Asp Ser Ala Ser Asp Ser
            20   25   30

ata ttc cac tac gac gac gct tca caa gcc aaa atc cag cag gag aag
264
Ile Phe His Tyr Asp Asp Ala Ser Gln Ala Lys Ile Gln Gln Glu Lys
            35   40   45

cca tgg gcc tcc gat cct aac tac ttc aag cgc gtt cac atc tca gcc
312
Pro Trp Ala Ser Asp Pro Asn Tyr Phe Lys Arg Val His Ile Ser Ala
            50   55   60

ctt gct ctt ctc aag atg gtg gtt cac gct cgc tcc ggt ggc aca atc
360
Leu Ala Leu Leu Lys Met Val Val His Ala Arg Ser Gly Gly Thr Ile
            65   70   75

gag atc atg ggt ctt atg cag ggt aaa acc gag ggt gat aca atc atc
408
Glu Ile Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile
80   85   90   95

gtt atg gat gct ttt gct ttg cct gtt gaa ggt act gag act agg gtt
456
Val Met Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val
            100   105   110

aat gct cag tct gat gcc tat gag tat atg gtt gaa tac tct cag acc
504
Asn Ala Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr
            115   120   125

agc aag ctg gct ggg agg ttg gag aac gtt gtt gga tgg tat cac tct
552
Ser Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser
            130   135   140

cac cct ggg tat gga tgt tgg ctc tcg ggt att gat gtt tcg aca cag
600
His Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln
            145   150   155

atg ctt aac caa cag tat cag gag cca ttc tta gct gtt gtt att gat
648
Met Leu Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp
160   165   170   175

cca aca agg act gtt tcg gct ggt aag gtt gag att ggg gca ttc aga
696
Pro Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg
            180   185   190

aca tat cca gag gga cat aag atc tcg gat gat cat gtt tct gag tat
744
Thr Tyr Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr
            195   200   205

cag act atc cct ctt aac aag att gag gac ttt ggt gta cat tgc aaa
792
Gln Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys
        210   215   220

cag tac tac tca ttg gac atc act tat ttc aag tca tct ctc gat agt
840
Gln Tyr Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser
    225   230   235

cac ctt ctg gat ctc ctt tgg aac aag tac tgg gtg aac act ctt tct
888
His Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser
240   245   250   255

tct tcc cca ctg ttg ggc aat gga gac tat gtt gcc ggg caa ata tca
936
Ser Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser
                260   265   270

gac ttg gct gag aag ctc gag caa gcg gag agt cag ctc gct aac tcc
984
Asp Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser
            275   280   285

cgg tat gga gga att gcg cca gcc ggt cac caa agg agg aaa gag gat
1032
Arg Tyr Gly Gly Ile Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp
            290   295   300

gag cct caa ctc gcg aag ata act cgg gat agt gca aag ata act gtc
1080
Glu Pro Gln Leu Ala Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val
    305   310   315

gag cag gtc cat gga cta atg tca cag gtt atc aaa gac atc ttg ttc
1128
Glu Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe
320   325   330   335

aat tcc gct cgt cag tcc aag aag tct gct gac gac tca tca gat cca
1176
Asn Ser Ala Arg Gln Ser Lys Lys Ser Ala Asp Asp Ser Ser Asp Pro
                340   345   350

gag ccc atg att aca tcg tga agttggtcta ttcttttgtt ttttggctgc
1227
Glu Pro Met Ile Thr Ser
                355

ggaaattgac tatcggtttg acccggttta tgaggcaatg cccattgttc cctatatctc
1287

tagtgtagta tctgcttcag acaaagatct ttgggttatt aaatgacatt aacataaaaa
1347

aaa
1350

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76

Met Glu Gly Ser Ser Ser Ala Ile Ala Arg Lys Thr Trp Glu Leu Glu
1   5   10   15

Asn Asn Ile Leu Pro Val Glu Pro Thr Asp Ser Ala Ser Asp Ser Ile
                20   25   30

Phe His Tyr Asp Asp Ala Ser Gln Ala Lys Ile Gln Gln Glu Lys Pro
            35   40   45

Trp Ala Ser Asp Pro Asn Tyr Phe Lys Arg Val His Ile Ser Ala Leu
        50   55   60

Ala Leu Leu Lys Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu
65   70   75   80

Ile Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val
                85   90   95

Met Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn
            100   105   110

Ala Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser
            115   120   125

Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His
        130   135   140

Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met
145   150   155   160

Leu Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro
                165   170   175

Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr
                180   185   190

136

```
Tyr Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln
        195                 200                 205

Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln
        210                 215                 220

Tyr Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His
225                 230                 235                 240

Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser
                245                 250                 255

Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp
            260                 265                 270

Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg
            275                 280                 285

Tyr Gly Gly Ile Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp Glu
        290                 295                 300

Pro Gln Leu Ala Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu
305                 310                 315                 320

Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe Asn
                325                 330                 335

Ser Ala Arg Gln Ser Lys Lys Ser Ala Asp Asp Ser Ser Asp Pro Glu
            340                 345                 350

Pro Met Ile Thr Ser
        355
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48
Met Asp Val Tyr Gly Leu Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp
1               5                   10                  15

ctt ctt gat ttc tcc aac gaa gac atc ttc tcc gct tct tct tcc ggt
96
Leu Leu Asp Phe Ser Asn Glu Asp Ile Phe Ser Ala Ser Ser Ser Gly
                20                  25                  30

ggt tcc acc gcc gct act tcc tct tct tct ttc cct cct cct caa aac
144
Gly Ser Thr Ala Ala Thr Ser Ser Ser Ser Phe Pro Pro Pro Gln Asn
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137

```
              35                    40                    45

cct agt ttc cac cac cac cat ctc cct tcc tcc gcc gat cat cac tcc
192
Pro Ser Phe His His His His Leu Pro Ser Ser Ala Asp His His Ser
    50                    55                    60

ttc ctc cac gac att tgc gtt ccc agt gat gac gca gct cat ctt gaa
240
Phe Leu His Asp Ile Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu
65                    70                    75                    80

tgg ctt tcg caa ttc gtg gac gat tct ttc gct gat ttt ccg gcg aat
288
Trp Leu Ser Gln Phe Val Asp Asp Ser Phe Ala Asp Phe Pro Ala Asn
                  85                    90                    95

cca tta gga gga act atg act tct gtc aaa act gaa act tcc ttt ccg
336
Pro Leu Gly Gly Thr Met Thr Ser Val Lys Thr Glu Thr Ser Phe Pro
              100                   105                   110

ggg aaa cca aga agc aaa cga tca aga gct cct gct cct ttc gcc gga
384
Gly Lys Pro Arg Ser Lys Arg Ser Arg Ala Pro Ala Pro Phe Ala Gly
          115                   120                   125

aca tgg tct ccg atg cca ctg gaa tcc gag cat cag cag ctt cac tcc
432
Thr Trp Ser Pro Met Pro Leu Glu Ser Glu His Gln Gln Leu His Ser
    130                   135                   140

gcc gcc aaa ttc aag cca aag aaa gaa caa tcc ggc gga gga gga gga
480
Ala Ala Lys Phe Lys Pro Lys Lys Glu Gln Ser Gly Gly Gly Gly Gly
145                   150                   155                   160

gga gga gga aga cat cag tca tcg tca tcg gag act acg gaa gga gga
528
Gly Gly Gly Arg His Gln Ser Ser Ser Ser Glu Thr Thr Glu Gly Gly
                  165                   170                   175

gga atg agg aga tgt act cac tgt gca tcg gag aaa acg cca cag tgg
576
Gly Met Arg Arg Cys Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp
                  180                   185                   190

agg aca gga cca ctt gga cct aaa aca cta tgt aac gct tgt gga gtc
624
Arg Thr Gly Pro Leu Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val
          195                   200                   205

cgg ttt aaa tcc ggt aga ctt gta ccg gaa tat aga ccg gct tcg agt
672
Arg Phe Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser
          210                   215                   220

cct act ttt gtt ttg act cag cat tca aac tct cac cgg aaa gtg atg
720
Pro Thr Phe Val Leu Thr Gln His Ser Asn Ser His Arg Lys Val Met
225                   230                   235                   240
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138

gag ctt cga cgg cag aaa gaa gtt atg aga caa cca caa caa gtt caa
768
Glu Leu Arg Arg Gln Lys Glu Val Met Arg Gln Pro Gln Gln Val Gln
                245   250   255

ctt cat cac cac cac cac ccg ttt tag
795
Leu His His His His His Pro Phe
                260

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78

Met Asp Val Tyr Gly Leu Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp
1   5   10   15

Leu Leu Asp Phe Ser Asn Glu Asp Ile Phe Ser Ala Ser Ser Ser Gly
            20   25   30

Gly Ser Thr Ala Ala Thr Ser Ser Ser Ser Phe Pro Pro Pro Gln Asn
        35   40   45

Pro Ser Phe His His His His Leu Pro Ser Ser Ala Asp His His Ser
    50   ,   55   60

Phe Leu His Asp Ile Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu
65   70   75   80

Trp Leu Ser Gln Phe Val Asp Asp Ser Phe Ala Asp Phe Pro Ala Asn
                85   90   95

Pro Leu Gly Gly Thr Met Thr Ser Val Lys Thr Glu Thr Ser Phe Pro
            100   105   110

Gly Lys Pro Arg Ser Lys Arg Ser Arg Ala Pro Ala Pro Phe Ala Gly
        115   120   125

Thr Trp Ser Pro Met Pro Leu Glu Ser Glu His Gln Gln Leu His Ser
    130   135   140

Ala Ala Lys Phe Lys Pro Lys Lys Glu Gln Ser Gly Gly Gly Gly Gly
145   150   155   160

Gly Gly Gly Arg His Gln Ser Ser Ser Glu Thr Thr Glu Gly Gly
            165   170   175

Gly Met Arg Arg Cys Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp
            180   185   190

```
Arg Thr Gly Pro Leu Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val
        195             200             205

Arg Phe Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser
    210             215             220

Pro Thr Phe Val Leu Thr Gln His Ser Asn Ser His Arg Lys Val Met
·225             230             235             240

Glu Leu Arg Arg Gln Lys Glu Val Met Arg Gln Pro Gln Gln Val Gln
            245             250             255

Leu His His His His His Pro Phe
            260
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<221> CDS <222> (82)..(570) <223> G353
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60

atcatcatca tcagaagaaa a atg gtt gcg ata tcg gag atc aag tcg acg
111                     Met Val Ala Ile Ser Glu Ile Lys Ser Thr
                         1               5                   10

gtg gat gtc acg gcg gcg aat tgt ttg atg ctt tta tct aga gtt gga
159
Val Asp Val Thr Ala Ala Asn Cys Leu Met Leu Leu Ser Arg Val Gly
            15              20              25

caa gaa aac gtt gac ggt ggc gat caa aaa cgc gtt ttc aca tgt aaa
207
Gln Glu Asn Val Asp Gly Gly Asp Gln Lys Arg Val Phe Thr Cys Lys
            30              35              40

acg tgt ttg aag cag ttt cat tcg ttc caa gcc tta gga ggt cac cgt
255
Thr Cys Leu Lys Gln Phe His Ser Phe Gln Ala Leu Gly Gly His Arg
            45              50              55

gcg agt cac aag aag cct aac aac gac gct ttg tcg tct gga ttg atg
303
Ala Ser His Lys Lys Pro Asn Asn Asp Ala Leu Ser Ser Gly Leu Met
        60              65              70

aag aag gtg aaa acg tcg tcg cat cct tgt ccc ata tgt gga gtg gag
351
Lys Lys Val Lys Thr Ser Ser His Pro Cys Pro Ile Cys Gly Val Glu
75              80              85              90

ttt ccg atg gga caa gct ttg gga gga cac atg agg aga cac agg aac
399
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140

```
Phe Pro Met Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Asn
                 95                 100             105

gag agt ggg gct gct ggt ggc gcg ttg gtt aca cgc gct ttg ttg ccg
447
Glu Ser Gly Ala Ala Gly Gly Ala Leu Val Thr Arg Ala Leu Leu Pro
             110             115             120

gag ccc acg gtg act acg ttg aag aaa tct agc agt ggg aag aga gtg
495
Glu Pro Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val
             125             130             135

gct tgt ttg gat ctg agt cta ggg atg gtg gac aat ttg aat ctc aag
543
Ala Cys Leu Asp Leu Ser Leu Gly Met Val Asp Asn Leu Asn Leu Lys
    140             145             150

ttg gag ctt gga aga aca gtt tat tga ttttatttat tttccttaaa
590
Leu Glu Leu Gly Arg Thr Val Tyr
155                 160

ttttctgaat atatttgttt ctctcattct ttgaattttt cttaatattc tagattatac
650

atacatccgc agatttagga aactttcata gagtgtaatc ttttctttct gtaaaaatat
710

attttacttg tagcaaa
727


<210>  80 <211>  162 <212>    PRT <213>    Arabidopsis thaliana   <400>
80

Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala Ala
1               5               10              15

Asn Cys Leu Met Leu Leu Ser Arg Val Gly Gln Glu Asn Val Asp Gly
             20              25              30

Gly Asp Gln Lys Arg Val Phe Thr Cys Lys Thr Cys Leu Lys Gln Phe
         35              40              45

His Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Pro
    50              55              60

Asn Asn Asp Ala Leu Ser Ser Gly Leu Met Lys Lys Val Lys Thr Ser
65              70              75              80

Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln Ala
                 85              90              95

Leu Gly Gly His Met Arg Arg His Arg Asn Glu Ser Gly Ala Ala Gly
```

            100   105   110

Gly Ala Leu Val Thr Arg Ala Leu Leu Pro Glu Pro Thr Val Thr Thr
        115   120   125

Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu Asp Leu Ser
    130   135   140

Leu Gly Met Val Asp Asn Leu Asn Leu Lys Leu Glu Leu Gly Arg Thr
145   150   155   160

Val Tyr

<210> 81 <211> 628 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (27)..(533) <223> G354

 <400> 81
cctagaagtc actaagtcga ttcaaa atg gtt gcg aga agt gag gaa att gtg
53
                          Met Val Ala Arg Ser Glu Glu Ile Val
                          1   5

ata gtg gaa gaa gat acg act gcg aaa tgt ttg atg ttg tta tca aga
101
Ile Val Glu Glu Asp Thr Thr Ala Lys Cys Leu Met Leu Leu Ser Arg
10   15   20   25

gtc gga gaa tgc ggc ggc ggc tgc ggg gga gat gaa cgt gtt ttc cga
149
Val Gly Glu Cys Gly Gly Gly Cys Gly Gly Asp Glu Arg Val Phe Arg
                30   35   40

tgc aag act tgt ctt aaa gag ttc tca tcg ttt caa gct ttg gga ggt
197
Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser Phe Gln Ala Leu Gly Gly
                45   50   55

cat cgt gca agc cac aag aaa ctt atc aac agt gac aat cca tca ctt
245
His Arg Ala Ser His Lys Lys Leu Ile Asn Ser Asp Asn Pro Ser Leu
        60   65   70

ctt gga tcc ttg tcc aac aag aaa act aaa acg tct cat cct tgt ccg
293
Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys Thr Ser His Pro Cys Pro
    75   80   85

ata tgt gga gtg aag ttt ccg atg gga caa gct ctt ggt ggt cac atg
341
Ile Cys Gly Val Lys Phe Pro Met Gly Gln Ala Leu Gly Gly His Met
90   95   100   105

agg aga cat agg aac gag aaa gtc tca ggc tcg ttg gtt aca cgt tct
389
Arg Arg His Arg Asn Glu Lys Val Ser Gly Ser Leu Val Thr Arg Ser

```
                    110                    115                    120
ttt cta ccg gag acg acg acg gtg acg gct ttg aag aaa ttt agt agt
437
Phe Leu Pro Glu Thr Thr Thr Val Thr Ala Leu Lys Lys Phe Ser Ser
        125                    130                    135

ggg aag aga gtg gct tgt ttg gat ttg gac tta gat tcg atg gag agt
485
Gly Lys Arg Val Ala Cys Leu Asp Leu Asp Leu Asp Ser Met Glu Ser
        140                    145                    150

ttg gtc aat tgg aag ttg gag ttg gga aga acg att tct tgg agt taa
533
Leu Val Asn Trp Lys Leu Glu Leu Gly Arg Thr Ile Ser Trp Ser
    155                    160                    165

gttttgggt tgtatacagt ttcacatgat tttgtaatct ttgttgatcc aattatcgta
593

ccgatcgatg tgaatattat tttgatacaa taaaa
628


<210> 82 <211> 168 <212> PRT <213> Arabidopsis thaliana <400>
82

Met Val Ala Arg Ser Glu Glu Ile Val Ile Val Glu Glu Asp Thr Thr
1               5                    10                    15


Ala Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly
            20                    25                    30


Cys Gly Gly Asp Glu Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu
        35                    40                    45


Phe Ser Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys
    50                    55                    60


Leu Ile Asn Ser Asp Asn Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys
65                    70                    75                    80


Lys Thr Lys Thr Ser His Pro Cys Pro Ile Cys Gly Val Lys Phe Pro
                85                    90                    95


Met Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Asn Glu Lys
            100                    105                    110


Val Ser Gly Ser Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr
        115                    120                    125


Val Thr Ala Leu Lys Lys Phe Ser Ser Gly Lys Arg Val Ala Cys Leu
    130                    135                    140
```

Asp Leu Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu
145   150   155   160

Leu Gly Arg Thr Ile Ser Trp Ser
                165

<210> 83 <211> 615 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(615) <223> G357

<400> 83
atg cag aac aaa cac aaa tgc aag ctc tgt tcc aag agt ttc tgt aat   48
Met Gln Asn Lys His Lys Cys Lys Leu Cys Ser Lys Ser Phe Cys Asn
1   5   10   15

ggc aga gca ctt ggt ggt cac atg aag tct cac ttg gtc tca tct cag   96
Gly Arg Ala Leu Gly Gly His Met Lys Ser His Leu Val Ser Ser Gln
            20   25   30

tct tca gct cgg aag aaa cta ggt gac tcg gtc tat tct tct tct tcc   144
Ser Ser Ala Arg Lys Lys Leu Gly Asp Ser Val Tyr Ser Ser Ser Ser
        35   40   45

tct tcc tcc gat ggt aaa gcg ctc gcc tac ggg tta cga gag aac ccg   192
Ser Ser Ser Asp Gly Lys Ala Leu Ala Tyr Gly Leu Arg Glu Asn Pro
    50   55   60

agg aag agt ttc cgg gtc ttt aat ccg gat cct gag tca tcc aca att   240
Arg Lys Ser Phe Arg Val Phe Asn Pro Asp Pro Glu Ser Ser Thr Ile
65   70   75   80

tac aac agt gag aca gag acc gaa cct gaa tcc gga gac ccg gtt aag   288
Tyr Asn Ser Glu Thr Glu Thr Glu Pro Glu Ser Gly Asp Pro Val Lys
                85   90   95

aaa cgg gtc aga gga gat gtt tca aag aag aag aag aag aag gca aag   336
Lys Arg Val Arg Gly Asp Val Ser Lys Lys Lys Lys Lys Lys Ala Lys
            100   105   110

agt aag aga gtg ttt gag aac tcg aag aag caa aag aca att cac gag   384
Ser Lys Arg Val Phe Glu Asn Ser Lys Lys Gln Lys Thr Ile His Glu
            115   120   125

tca cca gaa cca gcg agt tct gtc tct gat ggt tct cct gaa caa gat   432
Ser Pro Glu Pro Ala Ser Ser Val Ser Asp Gly Ser Pro Glu Gln Asp
            130   135   140

tta gct atg tgc ttg atg atg ctg tca aga gat tca agg gag ctc gag   480

```
Leu Ala Met Cys Leu Met Met Leu Ser Arg Asp Ser Arg Glu Leu Glu
145                 150             155                 160

att aaa ctg aaa aaa ccg gag gaa gag agg aag ccg gaa aaa aga cat
528
Ile Lys Leu Lys Lys Pro Glu Glu Glu Arg Lys Pro Glu Lys Arg His
                165             170                 175

ttc cct gag ctc cgt cgc tgt atg ata gat ctg aat ctt cct ccg ccg
576
Phe Pro Glu Leu Arg Arg Cys Met Ile Asp Leu Asn Leu Pro Pro Pro
            180             185                 190

caa gaa gct gaa gct gtc acc gtc gtt tca gcc ata taa
615
Gln Glu Ala Glu Ala Val Thr Val Val Ser Ala Ile
        195             200
```

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<210>  84 <211>  204 <212>  PRT <213>  Arabidopsis thaliana  <400>
84
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Met Gln Asn Lys His Lys Cys Lys Leu Cys Ser Lys Ser Phe Cys Asn
1               5               10              15


Gly Arg Ala Leu Gly Gly His Met Lys Ser His Leu Val Ser Ser Gln
            20              25              30


Ser Ser Ala Arg Lys Lys Leu Gly Asp Ser Val Tyr Ser Ser Ser Ser
        35              40              45


Ser Ser Ser Asp Gly Lys Ala Leu Ala Tyr Gly Leu Arg Glu Asn Pro
    50              55              60


Arg Lys Ser Phe Arg Val Phe Asn Pro Asp Pro Glu Ser Ser Thr Ile
65              70              75              80


Tyr Asn Ser Glu Thr Glu Thr Glu Pro Glu Ser Gly Asp Pro Val Lys
            85              90              95


Lys Arg Val Arg Gly Asp Val Ser Lys Lys Lys Lys Lys Lys Ala Lys
            100             105             110


Ser Lys Arg Val Phe Glu Asn Ser Lys Lys Gln Lys Thr Ile His Glu
        115             120             125


Ser Pro Glu Pro Ala Ser Ser Val Ser Asp Gly Ser Pro Glu Gln Asp
        130             135             140


Leu Ala Met Cys Leu Met Met Leu Ser Arg Asp Ser Arg Glu Leu Glu
145             150             155             160
```

145

```
Ile Lys Leu Lys Lys Pro Glu Glu Glu Arg Lys Pro Glu Lys Arg His
                165                 170                 175


Phe Pro Glu Leu Arg Arg Cys Met Ile Asp Leu Asn Leu Pro Pro Pro
            180                 185                 190


Gln Glu Ala Glu Ala Val Thr Val Val Ser Ala Ile
        195                 200
```

<210> 85 <211> 728 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (64)..(516) <223> G364

<400> 85
aagcttgata tcgcctctct ctaatctctc tttctctctc tatctctaag aatatataaa
60

```
ggt atg gac tac cag cca aac aca tcc cta cgt cta agc cta cca agt
108
    Met Asp Tyr Gln Pro Asn Thr Ser Leu Arg Leu Ser Leu Pro Ser
    1               5                   10                  15


tac aag aac cac caa cta aac cta gaa ctt gtt ctc gag cct tct tcc
156
Tyr Lys Asn His Gln Leu Asn Leu Glu Leu Val Leu Glu Pro Ser Ser
                20                  25                  30


atg tct tct tct tca tct tct tcc acg aac tca tca tca tgt ttg gag
204
Met Ser Ser Ser Ser Ser Ser Thr Asn Ser Ser Ser Cys Leu Glu
            35                  40                  45


cag cct agg gta ttc tca tgt aac tat tgt caa aga aag ttt tac agc
252
Gln Pro Arg Val Phe Ser Cys Asn Tyr Cys Gln Arg Lys Phe Tyr Ser
        50                  55                  60


tct caa gct ctt ggt ggt cat caa aac gct cat aag ctt gag aga acc
300
Ser Gln Ala Leu Gly Gly His Gln Asn Ala His Lys Leu Glu Arg Thr
        65                  70                  75


tta gcc aag aag agt cga gaa ctc ttt aga tcc tca aac act gtt gat
348
Leu Ala Lys Lys Ser Arg Glu Leu Phe Arg Ser Ser Asn Thr Val Asp
80                  85                  90                  95


tct gat cag cct tac ccg ttc tcc ggt cgc ttt gag ctt tac ggc cgt
396
Ser Asp Gln Pro Tyr Pro Phe Ser Gly Arg Phe Glu Leu Tyr Gly Arg
                100                 105                 110


ggc tac caa gga ttt ctc gaa agt ggc ggc tcg agg gac ttc tcc gcc
444
Gly Tyr Gln Gly Phe Leu Glu Ser Gly Gly Ser Arg Asp Phe Ser Ala
            115                 120                 125
```

146

```
cgc cgt gtg ccg gag agt ggt ctt gat cag gat cag gag aag agt cac
492
Arg Arg Val Pro Glu Ser Gly Leu Asp Gln Asp Gln Glu Lys Ser His
        130                 135                 140

ctt gac tta tcc tta agg ctc taa aagaatctta tattttgtta gtctatatat
546
Leu Asp Leu Ser Leu Arg Leu
        145                 150

tatcatatca attgttaatc ttaaaattga ttgttttact tattagtcat ttcctattat
606

ctgaaagttt tctttgtaag ttgtaactat ggtcctaaat tcaaatccaa atttgatttt
666

ggaagatggt acctaatgca gtagttaaat aagttaaaaa aatgaaggat ctataattct
726

ct
728


<210>  86 <211>  150 <212>  PRT <213>  Arabidopsis thaliana  <400>
86

Met Asp Tyr Gln Pro Asn Thr Ser Leu Arg Leu Ser Leu Pro Ser Tyr
1                5                  10                  15


Lys Asn His Gln Leu Asn Leu Glu Leu Val Leu Glu Pro Ser Ser Met
            20                  25                  30


Ser Ser Ser Ser Ser Ser Ser Thr Asn Ser Ser Ser Cys Leu Glu Gln
            35                  40                  45


Pro Arg Val Phe Ser Cys Asn Tyr Cys Gln Arg Lys Phe Tyr Ser Ser
    50                  55                  60


Gln Ala Leu Gly Gly His Gln Asn Ala His Lys Leu Glu Arg Thr Leu
65                  70                  75                  80


Ala Lys Lys Ser Arg Glu Leu Phe Arg Ser Ser Asn Thr Val Asp Ser
            85                  90                  95


Asp Gln Pro Tyr Pro Phe Ser Gly Arg Phe Glu Leu Tyr Gly Arg Gly
            100                 105                 110


Tyr Gln Gly Phe Leu Glu Ser Gly Gly Ser Arg Asp Phe Ser Ala Arg
            115                 120                 125


Arg Val Pro Glu Ser Gly Leu Asp Gln Asp Gln Glu Lys Ser His Leu
        130                 135                 140
```

147

Asp Leu Ser Leu Arg Leu
145   150

<210> 87 <211> 2217 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (37)..(2202) <223> G385

<400> 87
tagggtttgc tttcagtttc cggagtataa gaaaag atg ttc gag cca aat atg
54
                                       Met Phe Glu Pro Asn Met
                                       1   5

ctg ctt gcg gct atg aac aac gca gac agc aat aac cac aac tac aac
102
Leu Leu Ala Ala Met Asn Asn Ala Asp Ser Asn Asn His Asn Tyr Asn
            10   15   20

cac gaa gac aac aat aat gaa gga ttt ctt cgg gac gat gaa ttc gac
150
His Glu Asp Asn Asn Asn Glu Gly Phe Leu Arg Asp Asp Glu Phe Asp
        25   30   35

agt ccg aat act aaa tcg gga agt gag aat caa gaa gga gga tca gga
198
Ser Pro Asn Thr Lys Ser Gly Ser Glu Asn Gln Glu Gly Gly Ser Gly
   40   45   50

aac gac caa gat cct ctt cat cct aac aag aag aaa cga tat cat cga
246
Asn Asp Gln Asp Pro Leu His Pro Asn Lys Lys Lys Arg Tyr His Arg
55   60   65   70

cac acc caa ctt cag atc cag gag atg gaa gcg ttc ttc aaa gag tgt
294
His Thr Gln Leu Gln Ile Gln Glu Met Glu Ala Phe Phe Lys Glu Cys
            75   80   85

cct cac cca gat gac aag caa agg aaa cag cta agc cgt gaa ttg aat
342
Pro His Pro Asp Asp Lys Gln Arg Lys Gln Leu Ser Arg Glu Leu Asn
            90   95   100

ttg gaa cct ctt cag gtc aaa ttc tgg ttc caa aac aaa cgt acc caa
390
Leu Glu Pro Leu Gln Val Lys Phe Trp Phe Gln Asn Lys Arg Thr Gln
        105   110   115

atg aag aat cat cac gag cgg cat gag aac tca cat ctt cgg gcg gag
438
Met Lys Asn His His Glu Arg His Glu Asn Ser His Leu Arg Ala Glu
        120   125   130

aac gaa aag ctt cga aac gac aac cta aga tat cga gag gct ctt gca
486
Asn Glu Lys Leu Arg Asn Asp Asn Leu Arg Tyr Arg Glu Ala Leu Ala
135   140   145   150

aat gct tcg tgt cct aat tgt ggt ggt cca aca gct atc gga gaa atg
534

148

Asn Ala Ser Cys Pro Asn Cys Gly Gly Pro Thr Ala Ile Gly Glu Met
              155   160   165

tca ttc gac gaa cac caa ctc cgt ctc gaa aat gct cga tta agg gaa
582
Ser Phe Asp Glu His Gln Leu Arg Leu Glu Asn Ala Arg Leu Arg Glu
              170   175   180

gag atc gac cgt ata tcc gca atc gca gct aaa tac gta ggc aag cca
630
Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala Lys Tyr Val Gly Lys Pro
              185   190   195

gtc tca aac tat cca ctt atg tct cct cct cct ctt cct cca cgt cca
678
Val Ser Asn Tyr Pro Leu Met Ser Pro Pro Pro Leu Pro Pro Arg Pro
        200   205   210

cta gaa ctc gcc atg gga aat att gga gga gaa gct tat gga aac aat
726
Leu Glu Leu Ala Met Gly Asn Ile Gly Gly Glu Ala Tyr Gly Asn Asn
215   220   225   230

cca aac gat ctc ctt aag tcc atc act gca cca aca gaa tct gac aaa
774
Pro Asn Asp Leu Leu Lys Ser Ile Thr Ala Pro Thr Glu Ser Asp Lys
              235   240   245

cct gtc atc atc gac tta tcc gtg gct gca atg gaa gag ctc atg agg
822
Pro Val Ile Ile Asp Leu Ser Val Ala Ala Met Glu Glu Leu Met Arg
              250   255   260

atg gtt caa gta gac gag cct ctg tgg aag agt ttg gct tta gac gaa
870
Met Val Gln Val Asp Glu Pro Leu Trp Lys Ser Leu Ala Leu Asp Glu
              265   270   275

gaa gaa tat gca agg acc ttt cct aga ggg atc gga cct aga ccg gct
918
Glu Glu Tyr Ala Arg Thr Phe Pro Arg Gly Ile Gly Pro Arg Pro Ala
        280   285   290

gga tat aga tca gaa gct tcg cga gaa agc gcg gtt gtg atc atg aat
966
Gly Tyr Arg Ser Glu Ala Ser Arg Glu Ser Ala Val Val Ile Met Asn
295   300   305   310

cat gtt aac atc gtt gag att ctc atg gat gtg aat caa tgg tcg acg
1014
His Val Asn Ile Val Glu Ile Leu Met Asp Val Asn Gln Trp Ser Thr
              315   320   325

att ttc gcg ggg atg gtt tct aga gca atg aca tta gcg gtt tta tcg
1062
Ile Phe Ala Gly Met Val Ser Arg Ala Met Thr Leu Ala Val Leu Ser
              330   335   340

aca gga gtt gca gga aac tat aat gga gct ctt caa gtg atg agc gca
1110
Thr Gly Val Ala Gly Asn Tyr Asn Gly Ala Leu Gln Val Met Ser Ala

149

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           345                    350                    355

gag ttt caa gtt cca tct cca tta gtc cca aca cgt gaa acc tat ttc
1158
Glu Phe Gln Val Pro Ser Pro Leu Val Pro Thr Arg Glu Thr Tyr Phe
    360                    365                    370

gca cgt tac tgt aaa caa caa gga gat ggt tcg tgg gcg gtt gtc gat
1206
Ala Arg Tyr Cys Lys Gln Gln Gly Asp Gly Ser Trp Ala Val Val Asp
375                    380                    385                    390

att tcg ttg gat agt ctc caa cca aat ccc ccg gct aga tgc agg cgg
1254
Ile Ser Leu Asp Ser Leu Gln Pro Asn Pro Pro Ala Arg Cys Arg Arg
               395                    400                    405

cga gct tca gga tgt ttg att caa gaa ttg cca aat gga tat tct aag
1302
Arg Ala Ser Gly Cys Leu Ile Gln Glu Leu Pro Asn Gly Tyr Ser Lys
           410                    415                    420

gtg act tgg gtg gag cat gtg gaa gtt gat gac aga gga gtt cat aac
1350
Val Thr Trp Val Glu His Val Glu Val Asp Asp Arg Gly Val His Asn
           425                    430                    435

tta tac aaa cac atg gtt agt act ggt cat gcc ttc ggt gct aaa cgc
1398
Leu Tyr Lys His Met Val Ser Thr Gly His Ala Phe Gly Ala Lys Arg
       440                    445                    450

tgg gta gcc att ctt gac cgc caa tgc gag cgg tta gct agt gtc atg
1446
Trp Val Ala Ile Leu Asp Arg Gln Cys Glu Arg Leu Ala Ser Val Met
455                    460                    465                    470

gct aca aac att tcc tct gga gaa gtt ggc gtg ata acc aac caa gaa
1494
Ala Thr Asn Ile Ser Ser Gly Glu Val Gly Val Ile Thr Asn Gln Glu
               475                    480                    485

ggg agg agg agt atg ctg aaa ttg gca gag cgg atg gtt ata agc ttt
1542
Gly Arg Arg Ser Met Leu Lys Leu Ala Glu Arg Met Val Ile Ser Phe
           490                    495                    500

tgt gca gga gtg agt gct tca acc gct cac acg tgg act aca ttg tcc
1590
Cys Ala Gly Val Ser Ala Ser Thr Ala His Thr Trp Thr Thr Leu Ser
           505                    510                    515

ggt aca gga gct gaa gat gtt aga gtg atg act agg aag agt gtg gat
1638
Gly Thr Gly Ala Glu Asp Val Arg Val Met Thr Arg Lys Ser Val Asp
       520                    525                    530

gat cca gga agg tct cct ggt att gtt ctt agt gca gcc act tct ttt
1686
Asp Pro Gly Arg Ser Pro Gly Ile Val Leu Ser Ala Ala Thr Ser Phe
535                    540                    545                    550
```

```
tgg atc cct gtt cct cca aag cga gtc ttt gac ttc ctc aga gac gag
1734
Trp Ile Pro Val Pro Pro Lys Arg Val Phe Asp Phe Leu Arg Asp Glu
                  555             560             565

aat tca aga aat gag tgg gat att ctg tct aat gga gga gtt gtg caa
1782
Asn Ser Arg Asn Glu Trp Asp Ile Leu Ser Asn Gly Gly Val Val Gln
                  570             575             580

gaa atg gca cat att gct aac ggg agg gat acc gga aac tgt gtt tct
1830
Glu Met Ala His Ile Ala Asn Gly Arg Asp Thr Gly Asn Cys Val Ser
              585             590             595

ctt ctt cgg gta aat agt gca aac tct agc cag agc aat atg ctg atc
1878
Leu Leu Arg Val Asn Ser Ala Asn Ser Ser Gln Ser Asn Met Leu Ile
        600             605             610

cta caa gag agc tgc att gat cct aca gct tcc ttt gtg atc tat gct
1926
Leu Gln Glu Ser Cys Ile Asp Pro Thr Ala Ser Phe Val Ile Tyr Ala
615             620             625             630

cca gtc gat att gta gct atg aac ata gtg ctt aat gga ggt gat cca
1974
Pro Val Asp Ile Val Ala Met Asn Ile Val Leu Asn Gly Gly Asp Pro
                  635             640             645

gac tat gtg gct ctg ctt cca tca ggt ttt gct att ctt cct gat ggt
2022
Asp Tyr Val Ala Leu Leu Pro Ser Gly Phe Ala Ile Leu Pro Asp Gly
              650             655             660

aat gcc aat agt gga gcc cct gga gga gat gga ggg tcg ctc ttg act
2070
Asn Ala Asn Ser Gly Ala Pro Gly Gly Asp Gly Gly Ser Leu Leu Thr
              665             670             675

gtt gct ttt cag att ctg gtt gac tca gtt cct acg gct aag ctg tct
2118
Val Ala Phe Gln Ile Leu Val Asp Ser Val Pro Thr Ala Lys Leu Ser
        680             685             690

ctt ggc tct gtt gca act gtc aat aat cta ata gct tgc act gtt gag
2166
Leu Gly Ser Val Ala Thr Val Asn Asn Leu Ile Ala Cys Thr Val Glu
695             700             705             710

aga atc aaa gct tca atg tct tgt gag act gct tga aaaccatcca ttagc
2217
Arg Ile Lys Ala Ser Met Ser Cys Glu Thr Ala
                  715             720
```

<210> 88 <211> 721 <212> PRT <213> Arabidopsis thaliana <400>
88

Met Phe Glu Pro Asn Met Leu Leu Ala Ala Met Asn Asn Ala Asp Ser

1   5   10   15

Asn Asn His Asn Tyr Asn His Glu Asp Asn Asn Asn Glu Gly Phe Leu
            20   25   30

Arg Asp Asp Glu Phe Asp Ser Pro Asn Thr Lys Ser Gly Ser Glu Asn
            35   40   45

Gln Glu Gly Gly Ser Gly Asn Asp Gln Asp Pro Leu His Pro Asn Lys
            50   55   60

Lys Lys Arg Tyr His Arg His Thr Gln Leu Gln Ile Gln Glu Met Glu
65   70   75   80

Ala Phe Phe Lys Glu Cys Pro His Pro Asp Asp Lys Gln Arg Lys Gln
            85   90   95

Leu Ser Arg Glu Leu Asn Leu Glu Pro Leu Gln Val Lys Phe Trp Phe
            100   105   110

Gln Asn Lys Arg Thr Gln Met Lys Asn His His Glu Arg His Glu Asn
            115   120   125

Ser His Leu Arg Ala Glu Asn Glu Lys Leu Arg Asn Asp Asn Leu Arg
    130   135   140

Tyr Arg Glu Ala Leu Ala Asn Ala Ser Cys Pro Asn Cys Gly Gly Pro
145   150   155   160

Thr Ala Ile Gly Glu Met Ser Phe Asp Glu His Gln Leu Arg Leu Glu
            165   170   175

Asn Ala Arg Leu Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala
            180   185   190

Lys Tyr Val Gly Lys Pro Val Ser Asn Tyr Pro Leu Met Ser Pro Pro
            195   200   205

Pro Leu Pro Pro Arg Pro Leu Glu Leu Ala Met Gly Asn Ile Gly Gly
            210   215   220

Glu Ala Tyr Gly Asn Asn Pro Asn Asp Leu Leu Lys Ser Ile Thr Ala
225   230   235   240

Pro Thr Glu Ser Asp Lys Pro Val Ile Ile Asp Leu Ser Val Ala Ala
            245   250   255

152

```
Met Glu Glu Leu Met Arg Met Val Gln Val Asp Glu Pro Leu Trp Lys
        260             265             270

Ser Leu Ala Leu Asp Glu Glu Glu Tyr Ala Arg Thr Phe Pro Arg Gly
        275             280             285

Ile Gly Pro Arg Pro Ala Gly Tyr Arg Ser Glu Ala Ser Arg Glu Ser
    290             295             300

Ala Val Val Ile Met Asn His Val Asn Ile Val Glu Ile Leu Met Asp
305             310             315             320

Val Asn Gln Trp Ser Thr Ile Phe Ala Gly Met Val Ser Arg Ala Met
            325             330             335

Thr Leu Ala Val Leu Ser Thr Gly Val Ala Gly Asn Tyr Asn Gly Ala
        340             345             350

Leu Gln Val Met Ser Ala Glu Phe Gln Val Pro Ser Pro Leu Val Pro
        355             360             365

Thr Arg Glu Thr Tyr Phe Ala Arg Tyr Cys Lys Gln Gln Gly Asp Gly
    370             375             380

Ser Trp Ala Val Val Asp Ile Ser Leu Asp Ser Leu Gln Pro Asn Pro
385             390             395             400

Pro Ala Arg Cys Arg Arg Arg Ala Ser Gly Cys Leu Ile Gln Glu Leu
            405             410             415

Pro Asn Gly Tyr Ser Lys Val Thr Trp Val Glu His Val Glu Val Asp
            420             425             430

Asp Arg Gly Val His Asn Leu Tyr Lys His Met Val Ser Thr Gly His
        435             440             445

Ala Phe Gly Ala Lys Arg Trp Val Ala Ile Leu Asp Arg Gln Cys Glu
    450             455             460

Arg Leu Ala Ser Val Met Ala Thr Asn Ile Ser Ser Gly Glu Val Gly
465             470             475             480

Val Ile Thr Asn Gln Glu Gly Arg Arg Ser Met Leu Lys Leu Ala Glu
            485             490             495
```

```
Arg Met Val Ile Ser Phe Cys Ala Gly Val Ser Ala Ser Thr Ala His
        500             505             510


Thr Trp Thr Thr Leu Ser Gly Thr Gly Ala Glu Asp Val Arg Val Met
        515             520             525


Thr Arg Lys Ser Val Asp Asp Pro Gly Arg Ser Pro Gly Ile Val Leu
        530             535             540


Ser Ala Ala Thr Ser Phe Trp Ile Pro Val Pro Pro Lys Arg Val Phe
545             550             555             560


Asp Phe Leu Arg Asp Glu Asn Ser Arg Asn Glu Trp Asp Ile Leu Ser
            565             570             575


Asn Gly Gly Val Val Gln Glu Met Ala His Ile Ala Asn Gly Arg Asp
            580             585             590


Thr Gly Asn Cys Val Ser Leu Leu Arg Val Asn Ser Ala Asn Ser Ser
        595             600             605


Gln Ser Asn Met Leu Ile Leu Gln Glu Ser Cys Ile Asp Pro Thr Ala
        610             615             620


Ser Phe Val Ile Tyr Ala Pro Val Asp Ile Val Ala Met Asn Ile Val
625             630             635             640


Leu Asn Gly Gly Asp Pro Asp Tyr Val Ala Leu Leu Pro Ser Gly Phe
            645             650             655


Ala Ile Leu Pro Asp Gly Asn Ala Asn Ser Gly Ala Pro Gly Gly Asp
            660             665             670


Gly Gly Ser Leu Leu Thr Val Ala Phe Gln Ile Leu Val Asp Ser Val
        675             680             685


Pro Thr Ala Lys Leu Ser Leu Gly Ser Val Ala Thr Val Asn Asn Leu
        690             695             700


Ile Ala Cys Thr Val Glu Arg Ile Lys Ala Ser Met Ser Cys Glu Thr
705             710             715             720


Ala
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<210> 89 <211> 957 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(957) <223> G396

<400> 89
atg ggg gaa aga gat gat ggg ttg ggt ttg agt cta agc ttg gga aat
48
Met Gly Glu Arg Asp Asp Gly Leu Gly Leu Ser Leu Ser Leu Gly Asn
1   5   10   15

agt caa caa aaa gaa cca tct ctg agg ttg aat ctt atg ccg ttg aca
96
Ser Gln Gln Lys Glu Pro Ser Leu Arg Leu Asn Leu Met Pro Leu Thr
            20   25   30

act tct tct tct tct tct tcg ttt caa cac atg cac aat cag aat aac
144
Thr Ser Ser Ser Ser Ser Ser Phe Gln His Met His Asn Gln Asn Asn
        35   40   45

aat agc cat ccc cag aag att cat aac atc tct tgg act cat ctg ttt
192
Asn Ser His Pro Gln Lys Ile His Asn Ile Ser Trp Thr His Leu Phe
    50   55   60

caa tct tct ggg att aaa cgt aca act gca gag aga aac tcc gac gcc
240
Gln Ser Ser Gly Ile Lys Arg Thr Thr Ala Glu Arg Asn Ser Asp Ala
65   70   75   80

ggg tca ttt cta aga ggt ttc aac gtg aac aga gct cag tct tcg gtg
288
Gly Ser Phe Leu Arg Gly Phe Asn Val Asn Arg Ala Gln Ser Ser Val
                85   90   95

gcg gta gtg gac ttg gaa gaa gaa gcc gcc gtc gtc tcg tct cca aac
336
Ala Val Val Asp Leu Glu Glu Glu Ala Ala Val Val Ser Ser Pro Asn
            100   105   110

agc gcc gtt tcg agt ctg agt gga aat aaa agg gat ctt gcg gtg gcg
384
Ser Ala Val Ser Ser Leu Ser Gly Asn Lys Arg Asp Leu Ala Val Ala
        115   120   125

aga gga gga gat gaa aac gag gcg gag aga gct tct tgc tca cgc gga
432
Arg Gly Gly Asp Glu Asn Glu Ala Glu Arg Ala Ser Cys Ser Arg Gly
    130   135   140

ggg gga agc ggt ggt agc gac gat gaa gac ggc gga aac ggc gac gga
480
Gly Gly Ser Gly Gly Ser Asp Asp Glu Asp Gly Gly Asn Gly Asp Gly
145   150   155   160

tca agg aag aaa cta cgg tta tcg aag gat caa gct ctt gtt ctc gag
528
Ser Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ala Leu Val Leu Glu
                165   170   175

gag act ttt aaa gaa cat agc act ctt aat ccg aag caa aag ctg gct
576

```
Glu Thr Phe Lys Glu His Ser Thr Leu Asn Pro Lys Gln Lys Leu Ala
            180                 185                 190

cta gca aaa cag ttg aat cta agg gca aga caa gtt gaa gtg tgg ttt
624
Leu Ala Lys Gln Leu Asn Leu Arg Ala Arg Gln Val Glu Val Trp Phe
            195                 200                 205

cag aac cgt agg gca agg acg aag ctg aaa caa acg gag gtt gat tgt
672
Gln Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys
        210                 215                 220

gag tat tta aag aga tgt tgc gat aat ctg acc gag gag aat cga cgg
720
Glu Tyr Leu Lys Arg Cys Cys Asp Asn Leu Thr Glu Glu Asn Arg Arg
225                 230                 235                 240

ctg cag aaa gaa gtg tcg gag ctg agg gcg ttg aag ttg tct cca cat
768
Leu Gln Lys Glu Val Ser Glu Leu Arg Ala Leu Lys Leu Ser Pro His
                245                 250                 255

ctc tac atg cac atg act cct cct act act ctc acc atg tgc cct tct
816
Leu Tyr Met His Met Thr Pro Pro Thr Thr Leu Thr Met Cys Pro Ser
            260                 265                 270

tgc gaa cgt gtc tcc tcc tct gcc gcc act gtg acc gct gct cct tcc
864
Cys Glu Arg Val Ser Ser Ser Ala Ala Thr Val Thr Ala Ala Pro Ser
            275                 280                 285

act act act act cct acg gtg gtg ggg cgg cca agt cca cag cga tta
912
Thr Thr Thr Thr Pro Thr Val Val Gly Arg Pro Ser Pro Gln Arg Leu
        290                 295                 300

act cct tgg act gct att tct ctc cag caa aaa tca ggt cgc tag
957
Thr Pro Trp Thr Ala Ile Ser Leu Gln Gln Lys Ser Gly Arg
305                 310                 315


<210>  90 <211>  318 <212>  PRT <213>  Arabidopsis thaliana  <400>
90

Met Gly Glu Arg Asp Asp Gly Leu Gly Leu Ser Leu Ser Leu Gly Asn
1               5                   10                  15


Ser Gln Gln Lys Glu Pro Ser Leu Arg Leu Asn Leu Met Pro Leu Thr
            20                  25                  30


Thr Ser Ser Ser Ser Ser Ser Phe Gln His Met His Asn Gln Asn Asn
            35                  40                  45


Asn Ser His Pro Gln Lys Ile His Asn Ile Ser Trp Thr His Leu Phe
        50                  55                  60
```

156

Gln Ser Ser Gly Ile Lys Arg Thr Thr Ala Glu Arg Asn Ser Asp Ala
65   70   75   80

Gly Ser Phe Leu Arg Gly Phe Asn Val Asn Arg Ala Gln Ser Ser Val
            85   90   95

Ala Val Val Asp Leu Glu Glu Glu Ala Ala Val Val Ser Ser Pro Asn
            100   105   110

Ser Ala Val Ser Ser Leu Ser Gly Asn Lys Arg Asp Leu Ala Val Ala
            115   120   125

Arg Gly Gly Asp Glu Asn Glu Ala Glu Arg Ala Ser Cys Ser Arg Gly
    130   135   140

Gly Gly Ser Gly Gly Ser Asp Asp Glu Asp Gly Gly Asn Gly Asp Gly
145   150   155   160

Ser Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ala Leu Val Leu Glu
            165   170   175

Glu Thr Phe Lys Glu His Ser Thr Leu Asn Pro Lys Gln Lys Leu Ala
            180   185   190

Leu Ala Lys Gln Leu Asn Leu Arg Ala Arg Gln Val Glu Val Trp Phe
    195   200   205

Gln Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys
    210   215   220

Glu Tyr Leu Lys Arg Cys Cys Asp Asn Leu Thr Glu Glu Asn Arg Arg
225   230   235   240

Leu Gln Lys Glu Val Ser Glu Leu Arg Ala Leu Lys Leu Ser Pro His
            245   250   255

Leu Tyr Met His Met Thr Pro Pro Thr Thr Leu Thr Met Cys Pro Ser
            260   265   270

Cys Glu Arg Val Ser Ser Ser Ala Ala Thr Val Thr Ala Ala Pro Ser
    275   280   285

Thr Thr Thr Thr Pro Thr Val Val Gly Arg Pro Ser Pro Gln Arg Leu
    290   295   300

157

Thr Pro Trp Thr Ala Ile Ser Leu Gln Gln Lys Ser Gly Arg
305   310   315

<210> 91 <211> 1177 <212> DNA <213> Arabidopsis thaliana <220>   .
<221> CDS <222> (128)..(967) <223> G439

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tataaatctt cgtttctact ttttttttctt ccataatata gtcaattcgt tttcttaatt
60

agggcttctt ctctttgttt ctccaatctt tattagttta tttatttatt ttggttattg
120

tatacaa atg gca atg gct tta aac atg aat gct tac gta gac gag ttc
169
        Met Ala Met Ala Leu Asn Met Asn Ala Tyr Val Asp Glu Phe
        1   5   10

atg gaa gct ctt gaa cca ttc atg aag gta act tca tct tct tct act
217
Met Glu Ala Leu Glu Pro Phe Met Lys Val Thr Ser Ser Ser Ser Thr
15   20   25   30

tcg aat tca tca aat cca aaa cca tta act cct aat ttc atc cct aat
265
Ser Asn Ser Ser Asn Pro Lys Pro Leu Thr Pro Asn·Phe Ile Pro Asn
                35   40   45

aat gac caa gtc tta ccg gta tct aac caa acc ggt ccg att ggg cta
313
Asn Asp Gln Val Leu Pro Val Ser Asn Gln Thr Gly Pro Ile Gly Leu
            50   55   60

aac cag ctc act cca aca caa atc ctc caa att cag aca gag tta cat
361
Asn Gln Leu Thr Pro Thr Gln Ile Leu Gln Ile Gln Thr Glu Leu His
        65   70   75

ctc cgg caa aac caa tct cgt cgt cgc gct ggt agt cat ctt ctc acc
409
Leu Arg Gln Asn Gln Ser Arg Arg Arg Ala Gly Ser His Leu Leu Thr
    80   85   90

gct aaa cca acc tca atg aag aaa atc gac gta gca act aaa ccg gtt
457
Ala Lys Pro Thr Ser Met Lys Lys Ile Asp Val Ala Thr Lys Pro Val
95   100   105   110

aaa cta tac cga ggc gta aga cag agg caa tgg ggt aaa tgg gta gct
505
Lys Leu Tyr Arg Gly Val Arg Gln Arg Gln Trp Gly Lys Trp Val Ala
                115   120   125

gag att cgg cta cct aaa aac cga acc cgg tta tgg ctc ggt acg ttc
553
Glu Ile Arg Leu Pro Lys Asn Arg Thr Arg Leu Trp Leu Gly Thr Phe
            130   135   140

158

```
gaa acg gct caa gaa gct gca tta gct tac gat caa gca gct cat aag
601
Glu Thr Ala Gln Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala His Lys
        145              150               155

atc aga gga gac aac gct cgt ctc aat ttc cca gac att gtt cgt caa
649
Ile Arg Gly Asp Asn Ala Arg Leu Asn Phe Pro Asp Ile Val Arg Gln
    160              165               170

gga cac tat aaa cag ata ttg tct ccg tct atc aac gca aag atc gaa
697
Gly His Tyr Lys Gln Ile Leu Ser Pro Ser Ile Asn Ala Lys Ile Glu
175              180               185               190

tcc atc tgc aat agt tct gat ctt cca ctg cct cag atc gag aaa cag
745
Ser Ile Cys Asn Ser Ser Asp Leu Pro Leu Pro Gln Ile Glu Lys Gln
                 195              200               205

aac aaa aca gag gag gtg ctc tct ggt ttt tcc aaa ccg gag aaa gaa
793
Asn Lys Thr Glu Glu Val Leu Ser Gly Phe Ser Lys Pro Glu Lys Glu
            210              215               220

ccg gaa ttt ggg gag ata tac gga tgc gga tac tcg ggc tca tct cct
841
Pro Glu Phe Gly Glu Ile Tyr Gly Cys Gly Tyr Ser Gly Ser Ser Pro
            225              230               235

gag tcg gat ata acg ttg ttg gat ttc tca agc gac tgt gtg aaa gaa
889
Glu Ser Asp Ile Thr Leu Leu Asp Phe Ser Ser Asp Cys Val Lys Glu
    240              245               250

gat gag agt ttc ttg atg ggt ttg cac aag tat cct tct ttg gag att
937
Asp Glu Ser Phe Leu Met Gly Leu His Lys Tyr Pro Ser Leu Glu Ile
255              260               265               270

gat tgg gac gct ata gag aaa ctc ttc tga atccatttta tctttttgat
987
Asp Trp Asp Ala Ile Glu Lys Leu Phe
                 275

tcatttgtct ctaaattgta gaattttatt ttcagagctt tgtaagggaa gttcttgaat
1047

gagagttgca gaggactagt ggaacctaac tctgttttct tttgtaagta ttgtttataa
1107

tgggccgttg aatgggcctt attgatttaa acagcccaag tttttaaaaa aaaaaaaaaa
1167

aaaaaaaaaa
1177


<210> 92 <211> 279 <212> PRT <213> Arabidopsis thaliana <400>
92
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159

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Met Ala Met Ala Leu Asn Met Asn Ala Tyr Val Asp Glu Phe Met Glu
1               5                   10                  15


Ala Leu Glu Pro Phe Met Lys Val Thr Ser Ser Ser Ser Thr Ser Asn
            20              25                  30


Ser Ser Asn Pro Lys Pro Leu Thr Pro Asn Phe Ile Pro Asn Asn Asp
        35              40                  45


Gln Val Leu Pro Val Ser Asn Gln Thr Gly Pro Ile Gly Leu Asn Gln
    50              55                  60


Leu Thr Pro Thr Gln Ile Leu Gln Ile Gln Thr Glu Leu His Leu Arg
65              70                  75                  80


Gln Asn Gln Ser Arg Arg Arg Ala Gly Ser His Leu Leu Thr Ala Lys
            85                  90                  95


Pro Thr Ser Met Lys Lys Ile Asp Val Ala Thr Lys Pro Val Lys Leu
            100             105                 110


Tyr Arg Gly Val Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile
        115                 120                 125


Arg Leu Pro Lys Asn Arg Thr Arg Leu Trp Leu Gly Thr Phe Glu Thr
    130                 135                 140


Ala Gln Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala His Lys Ile Arg
145                 150                 155                 160


Gly Asp Asn Ala Arg Leu Asn Phe Pro Asp Ile Val Arg Gln Gly His
                165                 170                 175


Tyr Lys Gln Ile Leu Ser Pro Ser Ile Asn Ala Lys Ile Glu Ser Ile
            180                 185                 190


Cys Asn Ser Ser Asp Leu Pro Leu Pro Gln Ile Glu Lys Gln Asn Lys
        195                 200                 205


Thr Glu Glu Val Leu Ser Gly Phe Ser Lys Pro Glu Lys Glu Pro Glu
    210                 215                 220


Phe Gly Glu Ile Tyr Gly Cys Gly Tyr Ser Gly Ser Ser Pro Glu Ser
225                 230                 235                 240


Asp Ile Thr Leu Leu Asp Phe Ser Ser Asp Cys Val Lys Glu Asp Glu
```

160

```
                    245                   250                   255


Ser Phe Leu Met Gly Leu His Lys Tyr Pro Ser Leu Glu Ile Asp Trp
            260                   265                   270


Asp Ala Ile Glu Lys Leu Phe
            275



<210> 93 <211> 992 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (41)..(760) <223> G464

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55
                                         Met Arg Gly Val Ser
                                         1               5

gaa ttg gag gtg ggg aag agt aat ctt ccg gcg gag agt gag ctg gaa
103
Glu Leu Glu Val Gly Lys Ser Asn Leu Pro Ala Glu Ser Glu Leu Glu
                10                  15                  20

ttg gga tta ggg ctc agc ctc ggt ggt ggc gcg tgg aaa gag cgt ggg
151
Leu Gly Leu Gly Leu Ser Leu Gly Gly Gly Ala Trp Lys Glu Arg Gly
            25                  30                  35

agg att ctt act gct aag gat ttt cct tcc gtt ggg tct aaa cgc tct
199
Arg Ile Leu Thr Ala Lys Asp Phe Pro Ser Val Gly Ser Lys Arg Ser
            40                  45                  50

gct gaa tct tcc tct cac caa gga gct tct cct cct cgt tca agt caa
247
Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro Pro Arg Ser Ser Gln
    55                  60                  65

gtg gta gga tgg cca cca att ggg tta cac agg atg aac agt ttg gtt
295
Val Val Gly Trp Pro Pro Ile Gly Leu His Arg Met Asn Ser Leu Val
70                  75                  80                  85

aat aac caa gct atg aag gca gca aga gcg gaa gaa gga gac ggg gag
343
Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu Glu Gly Asp Gly Glu
                90                  95                  100

aag aaa gtt gtg aag aat gat gag ctc aaa gat gtg tca atg aag gtg
391
Lys Lys Val Val Lys Asn Asp Glu Leu Lys Asp Val Ser Met Lys Val
                105                 110                 115

aat ccg aaa gtt cag ggc tta ggg ttt gtt aag gtg aat atg gat gga
439
Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys Val Asn Met Asp Gly
            120                 125                 130
```

```
gtt ggt ata ggc aga aaa gtg gat atg aga gct cat tcg tct tac gaa
487
Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala His Ser Ser Tyr Glu
    135             140             145

aac ttg gct cag acg ctt gag gaa atg ttc ttt gga atg aca ggt act
535
Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe Gly Met Thr Gly Thr
150             155             160             165

act tgt cga gaa aag gtt aaa cct tta agg ctt tta gat gga tca tca
583
Thr Cys Arg Glu Lys Val Lys Pro Leu Arg Leu Leu Asp Gly Ser Ser
            170             175             180

gac ttt gta ctc act tat gaa gat aag gaa ggg gat tgg atg ctt gtt
631
Asp Phe Val Leu Thr Tyr Glu Asp Lys Glu Gly Asp Trp Met Leu Val
            185             190             195

gga gat gtt cca tgg aga atg ttt atc aac tcg gtg aaa agg ctt cgg
679
Gly Asp Val Pro Trp Arg Met Phe Ile Asn Ser Val Lys Arg Leu Arg
        200             205     -       210

atc atg gga acc tca gaa gct agt gga cta gct cca aga cgt caa gag
727
Ile Met Gly Thr Ser Glu Ala Ser Gly Leu Ala Pro Arg Arg Gln Glu
    215             220             225

cag aag gat aga caa aga aac aac cct gtt tag cttcccttcc aaagctggca
780
Gln Lys Asp Arg Gln Arg Asn Asn Pro Val
230             235

ttgtttatgt attgtttgag gtttgcaatt tactcgatac tttttgaaga aagtattttg
840

gagaatatgg ataaaagcat gcagaagctt agatatgatt tgaatccggt tttcggatat
900

ggttttgctt aggtcattca attcgtagtt ttccagtttg tttcttcttt ggctgtgtac
960

caattatcta tgttctgtga gagaaagctc tt
992


<210>  94 <211>  239 <212>  PRT <213>  Arabidopsis thaliana  <400>
94

Met Arg Gly Val Ser Glu Leu Glu Val Gly Lys Ser Asn Leu Pro Ala
1               5               10              15

Glu Ser Glu Leu Glu Leu Gly Leu Gly Leu Ser Leu Gly Gly Gly Ala
            20              25              30

Trp Lys Glu Arg Gly Arg Ile Leu Thr Ala Lys Asp Phe Pro Ser Val
        35              40              45
```

```
Gly Ser Lys Arg Ser Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro
    50              55              60
```

```
Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Leu His Arg
65              70              75              80
```

```
Met Asn Ser Leu Val Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu
            85              90              95
```

```
Glu Gly Asp Gly Glu Lys Lys Val Val Lys Asn Asp Glu Leu Lys Asp
            100             105             110
```

```
Val Ser Met Lys Val Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys
        115             120             125
```

```
Val Asn Met Asp Gly Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala
    130             135             140
```

```
His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe
145             150             155             160
```

```
Gly Met Thr Gly Thr Thr Cys Arg Glu Lys Val Lys Pro Leu Arg Leu
            165             170             175
```

```
Leu Asp Gly Ser Ser Asp Phe Val Leu Thr Tyr Glu Asp Lys Glu Gly
            180             185             190
```

```
Asp Trp Met Leu Val Gly Asp Val Pro Trp Arg Met Phe Ile Asn Ser
        195             200             205
```

```
Val Lys Arg Leu Arg Ile Met Gly Thr Ser Glu Ala Ser Gly Leu Ala
    210             215             220
```

```
Pro Arg Arg Gln Glu Gln Lys Asp Arg Gln Arg Asn Asn Pro Val
225             230             235
```

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<210> 95 <211> 1218 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1218) <223> G477
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<400> 95
atg gat tct tgg agc tac ggg aga agc gtt ttc atg tca aat gaa act
48
Met Asp Ser Trp Ser Tyr Gly Arg Ser Val Phe Met Ser Asn Glu Thr
1           5               10              15
```

```
ctt tta cct tgt gat act ttt gct aag aat aga aga ttt gaa cag aga
96
```

```
Leu Leu Pro Cys Asp Thr Phe Ala Lys Asn Arg Arg Phe Glu Gln Arg
        20                  25                  30

ctc tct aat aat gat gat gtg ttg att tct gac atg gct ggt aac tcc
144
Leu Ser Asn Asn Asp Asp Val Leu Ile Ser Asp Met Ala Gly Asn Ser
        35                  40                  45

aat gga ttc agt gct gtt tct att act aaa gtt gtt cct gaa gag gaa
192
Asn Gly Phe Ser Ala Val Ser Ile Thr Lys Val Val Pro Glu Glu Glu
        50                  55                  60

gat gag gag aac ata tct tct tct tca aag ttc tct agt cag gaa ttg
240
Asp Glu Glu Asn Ile Ser Ser Ser Ser Lys Phe Ser Ser Gln Glu Leu
65                  70                  75                  80

aat agg ata gat ttc aaa ctt agg agc ttt ttg gat tta gga aat gat
288
Asn Arg Ile Asp Phe Lys Leu Arg Ser Phe Leu Asp Leu Gly Asn Asp
                85                  90                  95

gat gat gat aca tcc tct aga ggt ttt gct ctg cca tct aaa aag tct
336
Asp Asp Asp Thr Ser Ser Arg Gly Phe Ala Leu Pro Ser Lys Lys Ser
            100                 105               .   110

cga gct tca aac ttg tgc tct cag aat ccc ttg tgt caa gtt tat ggg
384
Arg Ala Ser Asn Leu Cys Ser Gln Asn Pro Leu Cys Gln Val Tyr Gly
            115                 120                 125

tgt agt aag gat ctg agc tct tcg aaa gat tac cac aaa agg cat aga
432
Cys Ser Lys Asp Leu Ser Ser Ser Lys Asp Tyr His Lys Arg His Arg
        130                 135                 140

gtt tgc gag gct cat tcg aaa act tct gtg gtc ata gtt aat ggt ctt
480
Val Cys Glu Ala His Ser Lys Thr Ser Val Val Ile Val Asn Gly Leu
145                 150                 155                 160

gaa cag agg ttt tgt caa cag tgc agc agg ttt cat ttc ctc tca gag
528
Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Phe Leu Ser Glu
                165                 170                 175

ttt gat gat ggc aaa aga agt tgc aga agg cga tta gcc ggt cac aat
576
Phe Asp Asp Gly Lys Arg Ser Cys Arg Arg Arg Leu Ala Gly His Asn
            180                 185                 190

gaa cga aga agg aaa cct gca ttc tat ttc cta ccg ggt aag cgc cat
624
Glu Arg Arg Arg Lys Pro Ala Phe Tyr Phe Leu Pro Gly Lys Arg His
            195                 200                 205

aag ctt ctt cgc acc tct caa gat gta gta ggc aac aag ttt ctg gag
672
Lys Leu Leu Arg Thr Ser Gln Asp Val Val Gly Asn Lys Phe Leu Glu
```

164

                210   215   220

aat tca tca ttg gta ttg cca gag tca ttt cct ggt agt ctc tta tac
720
Asn Ser Ser Leu Val Leu Pro Glu Ser Phe Pro Gly Ser Leu Leu Tyr
225   230   235   240

aga gta ata gat gaa gac gac cac cgt aca agt aga ctc gtg agt ttc
768
Arg Val Ile Asp Glu Asp Asp His Arg Thr Ser Arg Leu Val Ser Phe
              245   250   255

aaa gat gaa cct act tgt tcc atg ttt cct act aat gag caa aac agc
816
Lys Asp Glu Pro Thr Cys Ser Met Phe Pro Thr Asn Glu Gln Asn Ser
              260   265   270

agc aga act tat gaa tct aaa cca gca att tat tcc acg gaa gta tcc
864
Ser Arg Thr Tyr Glu Ser Lys Pro Ala Ile Tyr Ser Thr Glu Val Ser
          275   280   285

tcc att tgg gac tta cat gag acg gcg gca tca cgc tct act cgt gct
912
Ser Ile Trp Asp Leu His Glu Thr Ala Ala Ser Arg Ser Thr Arg Ala
      290   295   300

ctc tct ctt ctg tca gct cag tcc caa caa cac ttg tct aag ttt cca
960
Leu Ser Leu Leu Ser Ala Gln Ser Gln Gln His Leu Ser Lys Phe Pro
305   310   315   320

aac aca acg ttc tca atc acc caa ccc aac caa aat ctc aat cac tca
1008
Asn Thr Thr Phe Ser Ile Thr Gln Pro Asn Gln Asn Leu Asn His Ser
              325   330   335

tca tca act gac tat cat cag atg gaa caa ccg ttg tgg atc gat cct
1056
Ser Ser Thr Asp Tyr His Gln Met Glu Gln Pro Leu Trp Ile Asp Pro
              340   345   350

ggc aag acc aat tct gct ggt tct agt tct tgt aaa gga aaa gga aca
1104
Gly Lys Thr Asn Ser Ala Gly Ser Ser Ser Cys Lys Gly Lys Gly Thr
              355   360   365

tcc acg gtt gat cta ctg caa ctg tca tca cat ctt caa aga atc gag
1152
Ser Thr Val Asp Leu Leu Gln Leu Ser Ser His Leu Gln Arg Ile Glu
          370   375   380

caa cag agg aat tac act ggt gat gtg aag cag gaa tat aat gag ctt
1200
Gln Gln Arg Asn Tyr Thr Gly Asp Val Lys Gln Glu Tyr Asn Glu Leu
385   390   395   400

tat ttc cct ggc tcc taa
1218
Tyr Phe Pro Gly Ser
              405

165

<210> 96 <211> 405 <212> PRT <213> Arabidopsis thaliana <400>
96

Met Asp Ser Trp Ser Tyr Gly Arg Ser Val Phe Met Ser Asn Glu Thr
1   5   10   15

Leu Leu Pro Cys Asp Thr Phe Ala Lys Asn Arg Arg Phe Glu Gln Arg
            20   25   30

Leu Ser Asn Asn Asp Asp Val Leu Ile Ser Asp Met Ala Gly Asn Ser
        35   40   45

Asn Gly Phe Ser Ala Val Ser Ile Thr Lys Val Val Pro Glu Glu Glu
        50   55   60

Asp Glu Glu Asn Ile Ser Ser Ser Ser Lys Phe Ser Ser Gln Glu Leu
65   70   75   80

Asn Arg Ile Asp Phe Lys Leu Arg Ser Phe Leu Asp Leu Gly Asn Asp
                85   90   95

Asp Asp Asp Thr Ser Ser Arg Gly Phe Ala Leu Pro Ser Lys Lys Ser
            100   105   110

Arg Ala Ser Asn Leu Cys Ser Gln Asn Pro Leu Cys Gln Val Tyr Gly
            115   120   125

Cys Ser Lys Asp Leu Ser Ser Ser Lys Asp Tyr His Lys Arg His Arg
        130   135   140

Val Cys Glu Ala His Ser Lys Thr Ser Val Val Ile Val Asn Gly Leu
145   150   155   160

Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Phe Leu Ser Glu
                165   170   175

Phe Asp Asp Gly Lys Arg Ser Cys Arg Arg Arg Leu Ala Gly His Asn
            180   185   190

Glu Arg Arg Arg Lys Pro Ala Phe Tyr Phe Leu Pro Gly Lys Arg His
        195   200   205

Lys Leu Leu Arg Thr Ser Gln Asp Val Val Gly Asn Lys Phe Leu Glu
        210   215   220

```
Asn Ser Ser Leu Val Leu Pro Glu Ser Phe Pro Gly Ser Leu Leu Tyr
225                 230             235                 240


Arg Val Ile Asp Glu Asp Asp His Arg Thr Ser Arg Leu Val Ser Phe
                245             250                 255


Lys Asp Glu Pro Thr Cys Ser Met Phe Pro Thr Asn Glu Gln Asn Ser
                260             265                 270


Ser Arg Thr Tyr Glu Ser Lys Pro Ala Ile Tyr Ser Thr Glu Val Ser
            275             280             285


Ser Ile Trp Asp Leu His Glu Thr Ala Ala Ser Arg Ser Thr Arg Ala
    290             295             300


Leu Ser Leu Leu Ser Ala Gln Ser Gln Gln His Leu Ser Lys Phe Pro
305             310             315                 320


Asn Thr Thr Phe Ser Ile Thr Gln Pro Asn Gln Asn Leu Asn His Ser
            325             330             335


Ser Ser Thr Asp Tyr His Gln Met Glu Gln Pro Leu Trp Ile Asp Pro
            340             345             350


Gly Lys Thr Asn Ser Ala Gly Ser Ser Ser Cys Lys Gly Lys Gly Thr
        355             360             365


Ser Thr Val Asp Leu Leu Gln Leu Ser Ser His Leu Gln Arg Ile Glu
    370             375             380


Gln Gln Arg Asn Tyr Thr Gly Asp Val Lys Gln Glu Tyr Asn Glu Leu
385             390             395                 400


Tyr Phe Pro Gly Ser
                405
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<221> CDS <222> (1)..(588) <223> G490

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48
Met Arg Arg Pro Lys Ser Ser His Val Arg Met Glu Pro Val Ala Pro
1           5               10              15


cgt tca cat aac acg atg cca atg ctt gat caa ttt cga tct aat cat
96
Arg Ser His Asn Thr Met Pro Met Leu Asp Gln Phe Arg Ser Asn His
                20              25              30
```

cct gaa aca agc aag atc gag ggg gtc tct tcg ttg gac aca gct ctg
144
Pro Glu Thr Ser Lys Ile Glu Gly Val Ser Ser Leu Asp Thr Ala Leu
        35   40   45

aag gtg ttt tgg aat aat caa agg gag cag cta gga aac ttt gca ggc
192
Lys Val Phe Trp Asn Asn Gln Arg Glu Gln Leu Gly Asn Phe Ala Gly
    50   55   60

caa act cat ttg ccg cta tct agg gtc aga aag att ttg aaa tct gat
240
Gln Thr His Leu Pro Leu Ser Arg Val Arg Lys Ile Leu Lys Ser Asp
65   70   75   80

cct gaa gtc aag aag ata agc tgt gat gtt cct gct ttg ttt tcg aaa
288
Pro Glu Val Lys Lys Ile Ser Cys Asp Val Pro Ala Leu Phe Ser Lys
            85   90   95

gcc tgt gaa tac ttc att cta gag gta aca tta cga gct tgg atg cat
336
Ala Cys Glu Tyr Phe Ile Leu Glu Val Thr Leu Arg Ala Trp Met His
            100   105   110

act caa tca tgc act cgt gag acc atc cgg cgt tgt gat atc ttc cag
384
Thr Gln Ser Cys Thr Arg Glu Thr Ile Arg Arg Cys Asp Ile Phe Gln
        115   120   125

gcc gta aag aac tca gga act tat gat ttc ctg att gat cgt gtc cct
432
Ala Val Lys Asn Ser Gly Thr Tyr Asp Phe Leu Ile Asp Arg Val Pro
    130   135   140

ttt gga ccg cac tgt gtc acc cat cag ggt gtg caa cct cct gct gaa
480
Phe Gly Pro His Cys Val Thr His Gln Gly Val Gln Pro Pro Ala Glu
145   150   155   160

atg att ttg ccg gat atg aat gtt cca atc gat atg gac cag att gag
528
Met Ile Leu Pro Asp Met Asn Val Pro Ile Asp Met Asp Gln Ile Glu
            165   170   175

gag gag aat atg atg gaa gag cgc tct gtc ggg ttt gac ctc aac tgt
576
Glu Glu Asn Met Met Glu Glu Arg Ser Val Gly Phe Asp Leu Asn Cys
            180   185   190

gat ctc cag tga
588
Asp Leu Gln
        195

<210> 98 <211> 195 <212> PRT <213> Arabidopsis thaliana <400>
98

Met Arg Arg Pro Lys Ser Ser His Val Arg Met Glu Pro Val Ala Pro

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1                    5                        10                       15
```

```
Arg Ser His Asn Thr Met Pro Met Leu Asp Gln Phe Arg Ser Asn His
        20              25                  30
```

```
Pro Glu Thr Ser Lys Ile Glu Gly Val Ser Ser Leu Asp Thr Ala Leu
        35              40                  45
```

```
Lys Val Phe Trp Asn Asn Gln Arg Glu Gln Leu Gly Asn Phe Ala Gly
    50              55                  60
```

```
Gln Thr His Leu Pro Leu Ser Arg Val Arg Lys Ile Leu Lys Ser Asp
65              70                  75                  80
```

```
Pro Glu Val Lys Lys Ile Ser Cys Asp Val Pro Ala Leu Phe Ser Lys
                85                  90                  95
```

```
Ala Cys Glu Tyr Phe Ile Leu Glu Val Thr Leu Arg Ala Trp Met His
            100             105                 110
```

```
Thr Gln Ser Cys Thr Arg Glu Thr Ile Arg Arg Cys Asp Ile Phe Gln
        115             120                 125
```

```
Ala Val Lys Asn Ser Gly Thr Tyr Asp Phe Leu Ile Asp Arg Val Pro
    130             135                 140
```

```
Phe Gly Pro His Cys Val Thr His Gln Gly Val Gln Pro Pro Ala Glu
145             150                 155                 160
```

```
Met Ile Leu Pro Asp Met Asn Val Pro Ile Asp Met Asp Gln Ile Glu
                165                 170                 175
```

```
Glu Glu Asn Met Met Glu Glu Arg Ser Val Gly Phe Asp Leu Asn Cys
            180                 185                 190
```

```
Asp Leu Gln
        195
```

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gcaaccttca aactaaaact cgagagacaa gaaatcctca gaatctttaa ctta atg
57
                                                            Met
                                                            1
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```
gcg ctc gag gct ctt aca tca cca aga tta gct tct ccg att cct cct
105
Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro Pro
          5                   10                  15


ttg ttc gaa gat tct tca gtc ttc cat gga gtc gag cac tgg aca aag
153
Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr Lys
         20                  25                  30


ggt aag cga tct aag aga tca aga tcc gat ttc cac cac caa aac ctc
201
Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn Leu
     35                  40                  45


act gag gaa gag tat cta gct ttt tgc ctc atg ctt ctc gct cgc gac
249
Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg Asp
50                  55                  60                  65


aac cgt cag cct cct cct cct ccg gcg gtg gag aag ttg agc tac aag
297
Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr Lys
             70                  75                  80


tgt agc gtc tgc gac aag acg ttc tct tct tac caa gct ctc ggt ggt
345
Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly Gly
             85                  90                  95


cac aag gca agc cac cgt aag aac tta tca cag act ctc tcc ggc gga
393
His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly Gly
         100                 105                 110


gga gat gat cat tca acc tcg tcg gcg aca acc aca tcc gcc gtg act
441
Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val Thr
     115                 120                 125


act gga agt ggg aaa tca cac gtt tgc acc atc tgt aac aag tct ttt
489
Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser Phe
130                 135                 140                 145


cct tcc ggt caa gct ctc ggc gga cac aag cgg tgc cac tac gaa gga
537
Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly
             150                 155                 160


aac aac aac atc aac act agt agc gtg tcc aac tcc gaa ggt gcg ggg
585
Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala Gly
             165                 170                 175


tcc act agc cac gtt agc agt agc cac cgt ggg ttt gac ctc aac atc
633
Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn Ile
         180                 185                 190
```

170

cct ccg atc cct gaa ttc tcg atg gtc aac gga gac gac gaa gtc atg
681
Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val Met
    195   200   205

agc cct atg ccg gcg aag aag cct cgg ttt gac ttt ccg gtc aaa ctt
729
Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys Leu
210   215   220   225

caa ctt taa ggaaatttac ttagacgata agatttcgtt tgtatactgt
778
Gln Leu

tgagagttgt gtaggaattt gttgactgta cataccaaat tggactttga ctgattccaa
838

ttcttcttgt tctttcattt taaaaattat taaaccgatt ctttaccaca aa
890

<210> 100 <211> 227 <212> PRT <213> Arabidopsis thaliana <400>
100

Met Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro
1   5   10   15

Pro Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr
            20   25   30

Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn
            35   40   45

Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg
    50   55   60

Asp Asn Arg Gln Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr
65   70   75   80

Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly
            85   90   95

Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly
        100   105   110

Gly Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val
        115   120   125

Thr Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser
        130   135   140

171

```
Phe Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu
145             150             155             160


Gly Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala
            165             170             175


Gly Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn
        180             185             190


Ile Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val
    195             200             205


Met Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys
    210             215             220


Leu Gln Leu
225
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<210> 101 <211> 842 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (192)..(698) <223> G557

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cagagatctg acggcggtag cagagtaatc tattccttcc caaaatgtct cgcaattaga
60

ttctttccaa gttcttctgt aaatcccaag tcccgctctt ttcctctttta tccttttcac
120

cagcttcgct actaagacaa caaatctttc cctctctctc tcgcctgatc gatcttcaaa
180

gagtaagaaa a atg cag gaa caa gcg act agc tct tta gct gca agc tct
230
            Met Gln Glu Gln Ala Thr Ser Ser Leu Ala Ala Ser Ser
            1               5                   10

tta cca tca agc agc gag agg tca tca agc tct gct cca cat ttg gag
278
Leu Pro Ser Ser Ser Glu Arg Ser Ser Ser Ser Ala Pro His Leu Glu
    15              20                  25

atc aaa gaa gga att gaa agc gat gag gag ata cgg cga gtg ccg gag
326
Ile Lys Glu Gly Ile Glu Ser Asp Glu Glu Ile Arg Arg Val Pro Glu
30              35                  40                  45

ttt gga gga gaa gct gtc gga aaa gaa act tcc ggt aga gaa tct gga
374
Phe Gly Gly Glu Ala Val Gly Lys Glu Thr Ser Gly Arg Glu Ser Gly
            50                  55                  60

tcg gcg acc ggt cag gag cgg aca cag gcg act gtc gga gaa agt caa
422
Ser Ala Thr Gly Gln Glu Arg Thr Gln Ala Thr Val Gly Glu Ser Gln
            65                  70                  75
```

```
agg aag cga ggg agg aca ccg gcg gag aaa gag aac aag cgg ctg aag
470
Arg Lys Arg Gly Arg Thr Pro Ala Glu Lys Glu Asn Lys Arg Leu Lys
        80                      85                  90

agg ttg ttg agg aac aga gtt tca gct cag caa gca aga gag agg aaa
518
Arg Leu Leu Arg Asn Arg Val Ser Ala Gln Gln Ala Arg Glu Arg Lys
    95                      100                 105

aag gct tac ttg agc gag ttg gaa aac aga gtg aaa gac ttg gag aac
566
Lys Ala Tyr Leu Ser Glu Leu Glu Asn Arg Val Lys Asp Leu Glu Asn
110                 115                 120                     125

aaa aac tct gaa ctt gaa gag cga ctc tct act ctt cag aac gag aac
614
Lys Asn Ser Glu Leu Glu Glu Arg Leu Ser Thr Leu Gln Asn Glu Asn
                130                 135                 140

cag atg ctt aga cat att ctg aag aac aca aca gga aac aag aga gga
662
Gln Met Leu Arg His Ile Leu Lys Asn Thr Thr Gly Asn Lys Arg Gly
            145                 150                 155

ggt ggt ggt ggt tct aat gct gat gca agc ctt tga tctccttctt
708
Gly Gly Gly Gly Ser Asn Ala Asp Ala Ser Leu
            160                 165

cttcttgtgt tatatttttg tggataaaat ttacagagaa ttgtatcaat aattatcatg
768

ttaaaattat atgggatgtg agagctaata ttgcaattgt agaccaagtt ctcttaaaaa
828

aaaaaaaaaa aaaa
842


<210> 102 <211> 168 <212> PRT <213> Arabidopsis thaliana <400>
102

Met Gln Glu Gln Ala Thr Ser Ser Leu Ala Ala Ser Ser Leu Pro Ser
1               5                   10                  15


Ser Ser Glu Arg Ser Ser Ser Ser Ala Pro His Leu Glu Ile Lys Glu
            20                  25                  30


Gly Ile Glu Ser Asp Glu Glu Ile Arg Arg Val Pro Glu Phe Gly Gly
        35                  40                  45


Glu Ala Val Gly Lys Glu Thr Ser Gly Arg Glu Ser Gly Ser Ala Thr
    50                  55                  60


Gly Gln Glu Arg Thr Gln Ala Thr Val Gly Glu Ser Gln Arg Lys Arg
```

```
65                    70                 75                    80
```

Gly Arg Thr Pro Ala Glu Lys Glu Asn Lys Arg Leu Lys Arg Leu Leu
                85   90   95

Arg Asn Arg Val Ser Ala Gln Gln Ala Arg Glu Arg Lys Lys Ala Tyr
                100   105   110

Leu Ser Glu Leu Glu Asn Arg Val Lys Asp Leu Glu Asn Lys Asn Ser
            115   120   125

Glu Leu Glu Glu Arg Leu Ser Thr Leu Gln Asn Glu Asn Gln Met Leu
        130   135   140

Arg His Ile Leu Lys Asn Thr Thr Gly Asn Lys Arg Gly Gly Gly Gly
145   150   155   160

Gly Ser Asn Ala Asp Ala Ser Leu   --
                165

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<221> CDS <222> (141)..(995) <223> G568

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60

tctgcgtgta ggatactact agacaattga caaccaaaga ctaaagctgt gttgttggtt
120

cacttctgtt ctcttttcca atg ttg tca tca gct aag cat cag aga aac cat
173
                Met Leu Ser Ser Ala Lys His Gln Arg Asn His
                1   5   10

aga ctc tct gct aca aac aag aac cag act ctc acc aaa gtt tct tcc
221
Arg Leu Ser Ala Thr Asn Lys Asn Gln Thr Leu Thr Lys Val Ser Ser
            15   20   25

att tca tcc tca tca cca tcg tct tct tct tca tca tca tca acc tca
269
Ile Ser Ser Ser Ser Pro Ser Ser Ser Ser Ser Ser Ser Thr Ser
        30   35   40

tca tca tct cct tta cct tct caa gac tct caa gcc cag aag aga tct
317
Ser Ser Ser Pro Leu Pro Ser Gln Asp Ser Gln Ala Gln Lys Arg Ser
        45   50   55

ctt gtc acc atg gaa gaa gtt tgg aat gac atc aac ctt gct tcc atc
365
Leu Val Thr Met Glu Glu Val Trp Asn Asp Ile Asn Leu Ala Ser Ile
60   65   70   75

174

```
cac cac cta aac cga cac agc cct cat cca caa cac aac cac gag cca
413
His His Leu Asn Arg His Ser Pro His Pro Gln His Asn His Glu Pro
                 80            85                90

agg ttc agg ggc caa aac cac cac aac caa aac cct aac tca atc ttc
461
Arg Phe Arg Gly Gln Asn His His Asn Gln Asn Pro Asn Ser Ile Phe
             95              100             105

caa gat ttt ctc aaa gga tct ttg aac cag gaa cca gca ccc aca agc
509
Gln Asp Phe Leu Lys Gly Ser Leu Asn Gln Glu Pro Ala Pro Thr Ser
         110             115             120

cag acc acg ggt tct gcg cct aat ggc gat tcc acc acg gtc act gtt
557
Gln Thr Thr Gly Ser Ala Pro Asn Gly Asp Ser Thr Thr Val Thr Val
     125             130             135

ctt tac agc tct cct ttt cca cct cct gca act gtt ctg agc ttg aat
605
Leu Tyr Ser Ser Pro Phe Pro Pro Pro Ala Thr Val Leu Ser Leu Asn
140             145             150                 155

tcc ggc gct ggc ttc gag ttt ctc gat aac caa gat cct ctt gtt acc
653
Ser Gly Ala Gly Phe Glu Phe Leu Asp Asn Gln Asp Pro Leu Val Thr
             160             165             170

tca aac tct aat ctt cat acc cac cat cac ctc tca aac gct cat gcc
701
Ser Asn Ser Asn Leu His Thr His His His Leu Ser Asn Ala His Ala
         175             180             185

ttc aac acc tct ttc gag gct ctg gtt cca tcc agt tct ttt ggt aag
749
Phe Asn Thr Ser Phe Glu Ala Leu Val Pro Ser Ser Ser Phe Gly Lys
         190             195             200

aaa aga ggc caa gat tcc aat gaa ggt tca ggg aat aga aga cat aag
797
Lys Arg Gly Gln Asp Ser Asn Glu Gly Ser Gly Asn Arg Arg His Lys
     205             210             215

cgt atg atc aag aac aga gaa tct gca gct cgt tcc cgc gct agg aaa
845
Arg Met Ile Lys Asn Arg Glu Ser Ala Ala Arg Ser Arg Ala Arg Lys
220             225             230                 235

cag gct tat aca aac gag tta gaa ctt gaa gtt gct cac ttg cag gca
893
Gln Ala Tyr Thr Asn Glu Leu Glu Leu Glu Val Ala His Leu Gln Ala
             240             245             250

gaa aat gca aga ctc aag aga caa caa gat caa aaa atg gct gca gca
941
Glu Asn Ala Arg Leu Lys Arg Gln Gln Asp Gln Lys Met Ala Ala Ala
             255             260             265
```

att cag caa ccc aaa aag aac aca ctt caa cgg tct tcc aca gct cca
989
Ile Gln Gln Pro Lys Lys Asn Thr Leu Gln Arg Ser Ser Thr Ala Pro
            270   275   280

ttt tga gaaatctaca agtccttgtt tctcttttgg ggattgagat tgtctcatga
1045
Phe

agaagtgaaa aaatggcaaa agtttgtacc cttttttatt agctataagt ataactaagc
1105

ctaaaattgt agaactaaga tattgtaggg gaaaaaagaa gatgtaaaac aaaagacccg
1165

gaaagagaaa aggatctttc aatttcctaa ggcacaggaa cacctgtcct gggtcctctc
1225

ttaatgttct gtcgttttcc tatgcaaacc ctttttcac ttctgtacta acttatactt
1285

gtattcttg
1294

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104

Met Leu Ser Ser Ala Lys His Gln Arg Asn His Arg Leu Ser Ala Thr
1   5   10   15

Asn Lys Asn Gln Thr Leu Thr Lys Val Ser Ser Ile Ser Ser Ser Ser
            20   25   30

Pro Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Ser Pro Leu
        35   40   45

Pro Ser Gln Asp Ser Gln Ala Gln Lys Arg Ser Leu Val Thr Met Glu
    50   55   60

Glu Val Trp Asn Asp Ile Asn Leu Ala Ser Ile His His Leu Asn Arg
65   70   75   80

His Ser Pro His Pro Gln His Asn His Glu Pro Arg Phe Arg Gly Gln
                85   90   95

Asn His His Asn Gln Asn Pro Asn Ser Ile Phe Gln Asp Phe Leu Lys
                100   105   110

Gly Ser Leu Asn Gln Glu Pro Ala Pro Thr Ser Gln Thr Thr Gly Ser
            115   120   125

```
Ala Pro Asn Gly Asp Ser Thr Thr Val Thr Val Leu Tyr Ser Ser Pro
    130              135          140


Phe Pro Pro Pro Ala Thr Val Leu Ser Leu Asn Ser Gly Ala Gly Phe
145              150          155                      160


Glu Phe Leu Asp Asn Gln Asp Pro Leu Val Thr Ser Asn Ser Asn Leu
                165              170              175


His Thr His His His Leu Ser Asn Ala His Ala Phe Asn Thr Ser Phe
            180              185              190


Glu Ala Leu Val Pro Ser Ser Ser Phe Gly Lys Lys Arg Gly Gln Asp
        195              200              205


Ser Asn Glu Gly Ser Gly Asn Arg Arg His Lys Arg Met Ile Lys Asn
    210              215              220


Arg Glu Ser Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Asn
225              230              235                      240


Glu Leu Glu Leu Glu Val Ala His Leu Gln Ala Glu Asn Ala Arg Leu
            245              250              255


Lys Arg Gln Gln Asp Gln Lys Met Ala Ala Ala Ile Gln Gln Pro Lys
            260              265              270


Lys Asn Thr Leu Gln Arg Ser Ser Thr Ala Pro Phe
        275              280
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ccaaaaaaca aagcattcta tgctattctg ttctgttctc ca atg ttg tca tca
54
                                               Met Leu Ser Ser
                                                 1


gca aag cat aat aag atc aac aac cat agt gcc ttt tca att tcc tct
102
Ala Lys His Asn Lys Ile Asn Asn His Ser Ala Phe Ser Ile Ser Ser
5                10               15                      20


tca tca tca tca tta tca aca tca tcc tcc cta ggc cat aac aaa tct
150
Ser Ser Ser Ser Leu Ser Thr Ser Ser Ser Leu Gly His Asn Lys Ser
                25               30                      35


caa gtc acc atg gaa gaa gta tgg aaa gaa atc aac ctt ggt tca ctt
198
```

```
Gln Val Thr Met Glu Glu Val Trp Lys Glu Ile Asn Leu Gly Ser Leu
            40                  45                  50

cac tac cat cgg caa cta aac att ggt cat gaa cca atg tta aag aac
246
His Tyr His Arg Gln Leu Asn Ile Gly His Glu Pro Met Leu Lys Asn
            55                  60                  65

caa aac cct aat aac tcc atc ttt caa gat ttc ctc aac atg cct ctg
294
Gln Asn Pro Asn Asn Ser Ile Phe Gln Asp Phe Leu Asn Met Pro Leu
        70                  75                  80

aat caa cca cca cca cca cca cca cct tcc tct tcc acc att gtc
342
Asn Gln Pro Pro Pro Pro Pro Pro Pro Ser Ser Ser Thr Ile Val
85                  90                  95                  100

act gct ctc tat ggc tct ctg cct ctt ccg cct cct gcc act gtc ctc
390
Thr Ala Leu Tyr Gly Ser Leu Pro Leu Pro Pro Pro Ala Thr Val Leu
                105                 110                 115

agc tta aac tcc ggt gtt gga ttc gag ttt ctt gat acc aca gaa aat
438
Ser Leu Asn Ser Gly Val Gly Phe Glu Phe Leu Asp Thr Thr Glu Asn
                120                 125                 130

ctt ctt gct tct aac cct cgc tcc ttt gag gaa tct gca aag ttt ggt
486
Leu Leu Ala Ser Asn Pro Arg Ser Phe Glu Glu Ser Ala Lys Phe Gly
            135                 140                 145

tgt ctt ggt aag aaa aga ggc caa gat tct gat gat act aga gga gac
534
Cys Leu Gly Lys Lys Arg Gly Gln Asp Ser Asp Asp Thr Arg Gly Asp
        150                 155                 160

aga agg tat aag cgt atg atc aag aac aga gaa tct gct gct cgt tca
582
Arg Arg Tyr Lys Arg Met Ile Lys Asn Arg Glu Ser Ala Ala Arg Ser
165                 170                 175                 180

agg gct agg aag cag gca tat aca aac gaa ctt gag ctt gaa att gct
630
Arg Ala Arg Lys Gln Ala Tyr Thr Asn Glu Leu Glu Leu Glu Ile Ala
                185                 190                 195

cac ttg cag aca gag aat gca aga ctc aag ata caa caa gag cag ctg
678
His Leu Gln Thr Glu Asn Ala Arg Leu Lys Ile Gln Gln Glu Gln Leu
                200                 205                 210

aaa ata gcc gaa gca act caa aac caa gta aag aaa aca cta caa cgg
726
Lys Ile Ala Glu Ala Thr Gln Asn Gln Val Lys Lys Thr Leu Gln Arg
                215                 220                 225

tct tcc aca gct cca ttt tga gaaaaatcta ctatttcttt ttggggggagt
777
Ser Ser Thr Ala Pro Phe
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230

ttcaagtgtt tcttatgaag atgagaaaaa cagaaaaagt ttgtacattt tagctaagtt
837

aaatttgtgg tggtaagtaa tgtaaaagaa aagtgtgtgt agaagaaaag tgtctagaaa
897

aagaaagcaa ctaactttct tcttcttctc tggtttccta tcaactcttt tgacttttgt
957

actttttttc ttctctactt aacctctatt attgtaatgc caagtcaagt ccttatctag
1017

ctagtacatg agtttctgtt ttcactggtt aagccat
1054

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106

Met Leu Ser Ser Ala Lys His Asn Lys Ile Asn Asn His Ser Ala Phe
1   5   10   15

Ser Ile Ser Ser Ser Ser Ser Ser Leu Ser Thr Ser Ser Ser Leu Gly
            20   25   30

His Asn Lys Ser Gln Val Thr Met Glu Glu Val Trp Lys Glu Ile Asn
        35   40   45

Leu Gly Ser Leu His Tyr His Arg Gln Leu Asn Ile Gly His Glu Pro
    50   55   60

Met Leu Lys Asn Gln Asn Pro Asn Asn Ser Ile Phe Gln Asp Phe Leu
65   70   75   80

Asn Met Pro Leu Asn Gln Pro Pro Pro Pro Pro Pro Pro Ser Ser
            85   90   95

Ser Thr Ile Val Thr Ala Leu Tyr Gly Ser Leu Pro Leu Pro Pro Pro
            100   105   110

Ala Thr Val Leu Ser Leu Asn Ser Gly Val Gly Phe Glu Phe Leu Asp
            115   120   125

Thr Thr Glu Asn Leu Leu Ala Ser Asn Pro Arg Ser Phe Glu Glu Ser
    130   135   140

Ala Lys Phe Gly Cys Leu Gly Lys Lys Arg Gly Gln Asp Ser Asp Asp
145   150   155   160

179

```
Thr Arg Gly Asp Arg Arg Tyr Lys Arg Met Ile Lys Asn Arg Glu Ser
              165             170             175   .


Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Asn Glu Leu Glu
              180             185             190


Leu Glu Ile Ala His Leu Gln Thr Glu Asn Ala Arg Leu Lys Ile Gln
          195             200             205


Gln Glu Gln Leu Lys Ile Ala Glu Ala Thr Gln Asn Gln Val Lys Lys
    210             215             220


Thr Leu Gln Arg Ser Ser Thr Ala Pro Phe
225             230
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60

aatgttttag ctttaactgc tttttttttg ttgttggtgt a atg ata tca cag aga
116
                                     Met Ile Ser Gln Arg
                                      1               5

gaa gaa aga gaa gag aag aag cag aga gtg atg gga gat aag aaa ttg
164
Glu Glu Arg Glu Glu Lys Lys Gln Arg Val Met Gly Asp Lys Lys Leu
              10             15             20

att tca tct tct tct tct tcc tcg gtt tac gat act cgt atc aat cat
212
Ile Ser Ser Ser Ser Ser Ser Ser Val Tyr Asp Thr Arg Ile Asn His
          25             30             35

cat ctt cat cat cct ccg tct tct tcc gac gaa atc tct cag ttt ctc
260
His Leu His His Pro Pro Ser Ser Ser Asp Glu Ile Ser Gln Phe Leu
          40             45             50

cgg cat att ttc gac cgt tct tct cct tta cct tct tac tac tcc ccg
308
Arg His Ile Phe Asp Arg Ser Ser Pro Leu Pro Ser Tyr Tyr Ser Pro
      55             60             65

gcg acg act aca acg acg gcg tct ttg att ggt gtg cac ggg agc ggt
356
Ala Thr Thr Thr Thr Thr Ala Ser Leu Ile Gly Val His Gly Ser Gly
70             75             80             85

gac cca cat gca gat aac tcg aga agt ctc gtt tct cat cat cca ccg
404
Asp Pro His Ala Asp Asn Ser Arg Ser Leu Val Ser His His Pro Pro
              90             95             100
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tca gat tct gtg ctt atg tcg aaa cgt gtc gga gat ttc tct gag gtt
452
Ser Asp Ser Val Leu Met Ser Lys Arg Val Gly Asp Phe Ser Glu Val
            105                     110                 115

tta atc ggc gga gga tca ggc tca gcc gcc gcg tgt ttt ggt ttc tcc
500
Leu Ile Gly Gly Gly Ser Gly Ser Ala Ala Ala Cys Phe Gly Phe Ser
        120                 125                 130

ggt ggt ggt aat aat aac aac gtt caa gga aat agc tct ggg act cga
548
Gly Gly Gly Asn Asn Asn Asn Val Gln Gly Asn Ser Ser Gly Thr Arg
        135                 140                 145

gta tcg tct tct tcc gtt gga gct agt ggc aac gag aca gat gag tat
596
Val Ser Ser Ser Ser Val Gly Ala Ser Gly Asn Glu Thr Asp Glu Tyr
150                 155                 160                 165

gac tgt gaa agc gag gaa gga gga gaa gct gta gtt gat gaa gct ccc
644
Asp Cys Glu Ser Glu Glu Gly Gly Glu Ala Val Val Asp Glu Ala Pro
                170                 175                 180

tct tcc aag tca ggt cct tct tct cgt agt tca tct aaa aga tgc aga
692
Ser Ser Lys Ser Gly Pro Ser Ser Arg Ser Ser Ser Lys Arg Cys Arg
            185                 190                 195

gct gct gaa gtt cat aat ctc tct gag aag agg agg aga agt aga att
740
Ala Ala Glu Val His Asn Leu Ser Glu Lys Arg Arg Arg Ser Arg Ile
            200                 205                 210

aat gaa aaa atg aaa gct tta caa agt ctc atc cct aat tca aat aag
788
Asn Glu Lys Met Lys Ala Leu Gln Ser Leu Ile Pro Asn Ser Asn Lys
    215                 220                 225

acg gat aag gct tca atg ctt gat gaa gcc att gag tat ctg aaa cag
836
Thr Asp Lys Ala Ser Met Leu Asp Glu Ala Ile Glu Tyr Leu Lys Gln
230                 235                 240                 245

ctt cag ctc caa gtt cag atg ttg act atg aga aat gga ata aac ttg
884
Leu Gln Leu Gln Val Gln Met Leu Thr Met Arg Asn Gly Ile Asn Leu
                250                 255                 260

cat cct ttg tgt tta cct gga act aca tta cac cca ttg caa ctc tct
932
His Pro Leu Cys Leu Pro Gly Thr Thr Leu His Pro Leu Gln Leu Ser
            265                 270                 275

cag att cga ccc cct gaa gca acc aat gat cct ctg ctt aat cat acc
980
Gln Ile Arg Pro Pro Glu Ala Thr Asn Asp Pro Leu Leu Asn His Thr
            280                 285                 290
```

aat cag ttt gct tcg act tct aat gca ccg gaa atg atc aat act gtg
1028
Asn Gln Phe Ala Ser Thr Ser Asn Ala Pro Glu Met Ile Asn Thr Val
    295   300   305

gct tct tca tac gct ttg gaa cct tct att cgc agt cac ttt gga cct
1076
Ala Ser Ser Tyr Ala Leu Glu Pro Ser Ile Arg Ser His Phe Gly Pro
310   315   320   325

ttc cct ctc ctt act tca ccc gtg gag atg agt cgg gaa ggt ggg tta
1124
Phe Pro Leu Leu Thr Ser Pro Val Glu Met Ser Arg Glu Gly Gly Leu
                330   335   340

act cat cca agg ttg aac att ggt cat tcc aac gca aac ata acc ggg
1172
Thr His Pro Arg Leu Asn Ile Gly His Ser Asn Ala Asn Ile Thr Gly
                345   350   355

gaa caa gct ctg ttt gat gga caa cct gac cta aaa gat cga att act
1220
Glu Gln Ala Leu Phe Asp Gly Gln Pro Asp Leu Lys Asp Arg Ile Thr
            360   365   370

tga acagtgtccc aacttcggga tctctatgtg ttcttgtttc ttagaacgca
1273

agccataaag ctgtctgac
1292

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108

Met Ile Ser Gln Arg Glu Glu Arg Glu Glu Lys Lys Gln Arg Val Met
1   5   10   15

Gly Asp Lys Lys Leu Ile Ser Ser Ser Ser Ser Ser Val Tyr Asp
            20   25   30

Thr Arg Ile Asn His His Leu His His Pro Pro Ser Ser Ser Asp Glu
        35   40   45

Ile Ser Gln Phe Leu Arg His Ile Phe Asp Arg Ser Ser Pro Leu Pro
    50   55   60

Ser Tyr Tyr Ser Pro Ala Thr Thr Thr Thr Thr Ala Ser Leu Ile Gly
65   70   75   80

Val His Gly Ser Gly Asp Pro His Ala Asp Asn Ser Arg Ser Leu Val
                85   90   95

Ser His His Pro Pro Ser Asp Ser Val Leu Met Ser Lys Arg Val Gly
            100   105   110

182

```
Asp Phe Ser Glu Val Leu Ile Gly Gly Gly Ser Gly Ser Ala Ala Ala
        115                 120                 125

Cys Phe Gly Phe Ser Gly Gly Gly Asn Asn Asn Asn Val Gln Gly Asn
    130             135                 140

Ser Ser Gly Thr Arg Val Ser Ser Ser Ser Val Gly Ala Ser Gly Asn
145                 150                 155                 160

Glu Thr Asp Glu Tyr Asp Cys Glu Ser Glu Glu Gly Gly Glu Ala Val
                165                 170                 175

Val Asp Glu Ala Pro Ser Ser Lys Ser Gly Pro Ser Ser Arg Ser Ser
            180             185                 190

Ser Lys Arg Cys Arg Ala Ala Glu Val His Asn Leu Ser Glu Lys Arg
        195                 200                 205

Arg Arg Ser Arg Ile Asn Glu Lys Met Lys Ala Leu Gln Ser Leu Ile
    210                 215                 220

Pro Asn Ser Asn Lys Thr Asp Lys Ala Ser Met Leu Asp Glu Ala Ile
225                 230                 235                 240

Glu Tyr Leu Lys Gln Leu Gln Leu Gln Val Gln Met Leu Thr Met Arg
            245                 250                 255

Asn Gly Ile Asn Leu His Pro Leu Cys Leu Pro Gly Thr Thr Leu His
            260                 265                 270

Pro Leu Gln Leu Ser Gln Ile Arg Pro Pro Glu Ala Thr Asn Asp Pro
        275                 280                 285

Leu Leu Asn His Thr Asn Gln Phe Ala Ser Thr Ser Asn Ala Pro Glu
    290                 295                 300

Met Ile Asn Thr Val Ala Ser Ser Tyr Ala Leu Glu Pro Ser Ile Arg
305                 310                 315                 320

Ser His Phe Gly Pro Phe Pro Leu Leu Thr Ser Pro Val Glu Met Ser
            325                 330                 335

Arg Glu Gly Gly Leu Thr His Pro Arg Leu Asn Ile Gly His Ser Asn
            340                 345                 350
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183

Ala Asn Ile Thr Gly Glu Gln Ala Leu Phe Asp Gly Gln Pro Asp Leu
      355   360   365

Lys Asp Arg Ile Thr
      370

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57
                                                  Met Asp Leu Ser
                                                   1

gta ctt gat agg ctt aag tgg ctg caa cag caa caa atg gtt tca cct
105
Val Leu Asp Arg Leu Lys Trp Leu Gln Gln Gln Gln Met Val Ser Pro
5   10   15   20

gag ttt ctt cag ata ctt ggc tca gat ggg aga gaa gag ctc aaa aga
153
Glu Phe Leu Gln Ile Leu Gly Ser Asp Gly Arg Glu Glu Leu Lys Arg
                 25   30   35

gtt gag agt tac ttg gga aac aac aat gat gag ctg cag agt ttc aga
201
Val Glu Ser Tyr Leu Gly Asn Asn Asn Asp Glu Leu Gln Ser Phe Arg
              40   45   50

cat ttt ccc gaa ttc gga ccg gat tat gat act act gat ggc tgc att
249
His Phe Pro Glu Phe Gly Pro Asp Tyr Asp Thr Thr Asp Gly Cys Ile
          55   60   65

tct agg aca agt agc ttc cat atg gag cca gtg aag aat aat gga cac
297
Ser Arg Thr Ser Ser Phe His Met Glu Pro Val Lys Asn Asn Gly His
      70   75   80

agc aga gcc att acc ttg cag aac aag aga aaa cca gag ggt aag aca
345
Ser Arg Ala Ile Thr Leu Gln Asn Lys Arg Lys Pro Glu Gly Lys Thr
85   90   95   100

gaa aag aga gag aag aag aag atc aaa gca gag gat gaa aca gag cca
393
Glu Lys Arg Glu Lys Lys Lys Ile Lys Ala Glu Asp Glu Thr Glu Pro
                 105   110   115

agc atg aaa ggg aaa tca aac atg agt aac aca gag aca tct tca gaa
441
Ser Met Lys Gly Lys Ser Asn Met Ser Asn Thr Glu Thr Ser Ser Glu
              120   125   130

att cag aaa cca gat tac att cat gtt agg gct aga cga ggt gaa gcc
489
Ile Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg Arg Gly Glu Ala

184

```
                 135                    140                    145

acc gac aga cat agc tta gca gag agg gca aga aga gaa aag ata agc
537
Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser
    150                    155                    160


aag aag atg aaa tgt cta caa gat att gtt cct gga tgc aac aaa gtt
585
Lys Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val
165                    170                    175                    180


act gga aaa gct ggt atg ctt gat gag atc atc aac tat gtc caa tct
633
Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser
                   185                    190                    195


ctg caa caa caa gtc gag ttc ttg tcg atg aaa ctc tct gtc ata aat
681
Leu Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu Ser Val Ile Asn
               200                    205                    210


cca gaa ctt gag tgt cat atc gat gat tta tcc gca aaa cag ttt cag
729
Pro Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala Lys Gln Phe Gln
           215                    220                    225


gct tac ttc aca ggt cct cca gaa ggt gac tcg aag cag tca atc atg
777
Ala Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys Gln Ser Ile Met
    230                    235                    240


gcg gat ttt cgg tct ttt cca tta cat cag caa gga tct tta gat tac
825
Ala Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly Ser Leu Asp Tyr
245                    250                    255                    260


tca gtc ata aac tca gac cac acc aca tct ctc ggc gct aaa gat cat
873
Ser Val Ile Asn Ser Asp His Thr Thr Ser Leu Gly Ala Lys Asp His
               265                    270                    275


aca tca tca agc tgg gaa act cac tca cag tgt ctt tac aac agc ttg
921
Thr Ser Ser Ser Trp Glu Thr His Ser Gln Cys Leu Tyr Asn Ser Leu
               280                    285                    290


aga acc gat tct gtt tcc aat ttc ttc agc ctc aag taa aaaaattagg
970
Arg Thr Asp Ser Val Ser Asn Phe Phe Ser Leu Lys
        295                    300


gatagcctca ttaaaaaaat cgcggttttt tgttgttgtc ttatccattt atctatctta
1030


tctgaaattt gaaccagaaa gacagaggaa accaatccaa agatctttct caatctatta
1090


tcttcataca aatatagtga tttacatata ttccagggga tatgtatatg tgtagaagaa
1150
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agagaaaaaa ctcttgtggt catagcaatt cctttttttg tacattgtag aatcaaactc
1210

ttgtggtcgt aacaattatt tccttcacaa attacaacta cacttgtatt aatggagatg
1270

ccttttggcc ctgggatcaa ca
1292

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110

Met Asp Leu Ser Val Leu Asp Arg Leu Lys Trp Leu Gln Gln Gln Gln
1   5   10   15

Met Val Ser Pro Glu Phe Leu Gln Ile Leu Gly Ser Asp Gly Arg Glu
            20   25   30

Glu Leu Lys Arg Val Glu Ser Tyr Leu Gly Asn Asn Asn Asp Glu Leu
        35   40   45

Gln Ser Phe Arg His Phe Pro Glu Phe Gly Pro Asp Tyr Asp Thr Thr
    50   55   60

Asp Gly Cys Ile Ser Arg Thr Ser Ser Phe His Met Glu Pro Val Lys
65   70   75   80

Asn Asn Gly His Ser Arg Ala Ile Thr Leu Gln Asn Lys Arg Lys Pro
                85   90   95

Glu Gly Lys Thr Glu Lys Arg Glu Lys Lys Lys Ile Lys Ala Glu Asp
                100   105   110

Glu Thr Glu Pro Ser Met Lys Gly Lys Ser Asn Met Ser Asn Thr Glu
            115   120   125

Thr Ser Ser Glu Ile Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg
    130   135   140

Arg Gly Glu Ala Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg
145   150   155   160

Glu Lys Ile Ser Lys Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly
                165   170   175

Cys Asn Lys Val Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn
                180   185   190

186

Tyr Val Gln Ser Leu Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu
    195   200   205

Ser Val Ile Asn Pro Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala
    210   215   220

Lys Gln Phe Gln Ala Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys
225   230   235   240

Gln Ser Ile Met Ala Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly
          245   250   255

Ser Leu Asp Tyr Ser Val Ile Asn Ser Asp His Thr Thr Ser Leu Gly
      260   265   270

Ala Lys Asp His Thr Ser Ser Ser Trp Glu Thr His Ser Gln Cys Leu
      275   280   285

Tyr Asn Ser Leu Arg Thr Asp Ser Val Ser Asn Phe Phe Ser Leu Lys
    290   295   300

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60

ttcacttcca tcaaaactct ctctctatat ctctctctct atatatctct ctctatatct
120

ctctctctct tcactctctc tttctttcaa a atg gaa aaa ctc atg gtt ccg
172
                                        Met Glu Lys Leu Met Val Pro
                                        1   5

aca tgg aga ccc gac ccg gtt tac cgt cca ccg gaa aca cca ctc gaa
220
Thr Trp Arg Pro Asp Pro Val Tyr Arg Pro Pro Glu Thr Pro Leu Glu
        10   15   20

ccg atg gag ttt tta gct cgt tca tgg agc gtc tct gct ctc gaa gtc
268
Pro Met Glu Phe Leu Ala Arg Ser Trp Ser Val Ser Ala Leu Glu Val
        25   30   35

tcc aag gct cta aca cca ccc aac cct cag att ctc ctc tcc aaa acc
316
Ser Lys Ala Leu Thr Pro Pro Asn Pro Gln Ile Leu Leu Ser Lys Thr
40   45   50   55

gaa gaa gaa gaa gaa gaa gaa ccc atc tcc tct gtc gta gac ggc gac
364
Glu Glu Glu Glu Glu Glu Glu Pro Ile Ser Ser Val Val Asp Gly Asp

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                     60                     65                     70

ggc gac acg gaa gac acc gga ctt gtc acc gga aac cca ttc tcc ttc
412
Gly Asp Thr Glu Asp Thr Gly Leu Val Thr Gly Asn Pro Phe Ser Phe
            75                  80                  85

gct tgt tca gaa act tct caa atg gtc atg gat cgt atc ttg tct cac
460
Ala Cys Ser Glu Thr Ser Gln Met Val Met Asp Arg Ile Leu Ser His
            90                  95                 100

tct caa gaa gta tca cca aga aca tct ggt cgg cta tct cac agt agt
508
Ser Gln Glu Val Ser Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser
        105                 110                 115

ggt cca ctt aat ggt tct ttg acc gac agt cct cct gtg tct cct ccc
556
Gly Pro Leu Asn Gly Ser Leu Thr Asp Ser Pro Pro Val Ser Pro Pro
120                 125                 130                 135

gaa tcc gac gac att aag caa ttt tgc aga gcg aac aaa aat tca ttg
604
Glu Ser Asp Asp Ile Lys Gln Phe Cys Arg Ala Asn Lys Asn Ser Leu
                140                 145                 150

aac agt gta aat tct cag ttc cgt tca acg gcg gca act ccg gga cct
652
Asn Ser Val Asn Ser Gln Phe Arg Ser Thr Ala Ala Thr Pro Gly Pro
            155                 160                 165

ata acc gct aca gct aca cag tcc aag acg gtg gga cgg tgg ctt aag
700
Ile Thr Ala Thr Ala Thr Gln Ser Lys Thr Val Gly Arg Trp Leu Lys
        170                 175                 180

gac cgg aga gag aaa aag aaa gag gag act cgg gct cat aac gct cag
748
Asp Arg Arg Glu Lys Lys Lys Glu Glu Thr Arg Ala His Asn Ala Gln
    185                 190                 195

att cac gct gct gtc tct gtc gcc ggc gtt gct gca gct gtt gct gct
796
Ile His Ala Ala Val Ser Val Ala Gly Val Ala Ala Ala Val Ala Ala
200                 205                 210                 215

att gca gca gcc acc gct gcg tct tct agc tgt ggt aag gat gag cag
844
Ile Ala Ala Ala Thr Ala Ala Ser Ser Ser Cys Gly Lys Asp Glu Gln
            220                 225                 230

atg gct aaa act gac atg gcc gtt gct tct gct gcg acc ctt gtg gct
892
Met Ala Lys Thr Asp Met Ala Val Ala Ser Ala Ala Thr Leu Val Ala
            235                 240                 245

gct cag tgt gtg gaa gct gct gaa gtt atg gga gct gag aga gag tat
940
Ala Gln Cys Val Glu Ala Ala Glu Val Met Gly Ala Glu Arg Glu Tyr
        250                 255                 260
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ttg gct tct gtt gtt agc tcc gcc gtc aat gtt cgt tct gcc gga gat
988
Leu Ala Ser Val Val Ser Ser Ala Val Asn Val Arg Ser Ala Gly Asp
    265   270   275

att atg act ctc acc gcc gga gca gct aca gct tta aga gga gtg caa
1036
Ile Met Thr Leu Thr Ala Gly Ala Ala Thr Ala Leu Arg Gly Val Gln
280   285   290   295

aca ttg aag gca agg gca atg aag gaa gtg tgg aac ata gca tca gtg
1084
Thr Leu Lys Ala Arg Ala Met Lys Glu Val Trp Asn Ile Ala Ser Val
                300   305   310

ata cca atg gat aaa gga ctc act tct aca gga gga agc agc aat aat
1132
Ile Pro Met Asp Lys Gly Leu Thr Ser Thr Gly Gly Ser Ser Asn Asn
                315   320   325

gtt aat ggt agc aat gga agc tca agc agt agt cac agt ggt gaa ctt
1180
Val Asn Gly Ser Asn Gly Ser Ser Ser Ser Ser His Ser Gly Glu Leu
            330   335   340

gta caa cag gag aat ttc ttg gga act tgt agt aga gaa tgg ctc gct
1228
Val Gln Gln Glu Asn Phe Leu Gly Thr Cys Ser Arg Glu Trp Leu Ala
    345   350   355

aga ggt tgt gaa ctc ctc aaa cgc act cgc aaa ggt gat ctc cac tgg
1276
Arg Gly Cys Glu Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu His Trp
360   365   370   375

aag ata gta tct gtt tac atc aac aaa atg aat cag gtt atg ttg aag
1324
Lys Ile Val Ser Val Tyr Ile Asn Lys Met Asn Gln Val Met Leu Lys
            380   385   390

atg aag agc agg cat gtt gga gga acc ttc acc aag aag aaa aag aac
1372
Met Lys Ser Arg His Val Gly Gly Thr Phe Thr Lys Lys Lys Lys Asn
            395   400   405

att gtg ctt gat gtg atc aag aat gtc ccg gcc tgg cct gga cga cat
1420
Ile Val Leu Asp Val Ile Lys Asn Val Pro Ala Trp Pro Gly Arg His
            410   415   420

ttg cta gag gga gga gat gat cta aga tac ttc ggt ttg aag acg gtt
1468
Leu Leu Glu Gly Gly Asp Asp Leu Arg Tyr Phe Gly Leu Lys Thr Val
    425   430   435

atg cga ggt gat gtt gaa ttc gag gtc aag agc caa agg gaa tat gaa
1516
Met Arg Gly Asp Val Glu Phe Glu Val Lys Ser Gln Arg Glu Tyr Glu
440   445   450   455

189

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atg tgg aca caa ggt gtc tca agg ctt ctt gtt ctt gct gct gag agg
1564
Met Trp Thr Gln Gly Val Ser Arg Leu Leu Val Leu Ala Ala Glu Arg
                460             465                 470

aag ttt agg atg tga ataaacgttc aatggctgct tggtttaagt gtgagttttt
1619
Lys Phe Arg Met
             475


ttttaactta tgtggtcaaa tttcattagt aggggttctt ttaaggtaat ggtttttttgg
1679

gttgggtata ggataaaatg gacctaccag tcaaggtgag gaagcatttg ggtaaacaaa
1739

acttagtggg ggtgatctgt aatatctatg ttcttagttt ttttttggtt gttggtggtc
1799

tttttgtata aaaaaacaaa gttgaagtaa tagatatata gtatgtttta attttaaa
1857
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112

Met Glu Lys Leu Met Val Pro Thr Trp Arg Pro Asp Pro Val Tyr Arg
1               5               10                  15


Pro Pro Glu Thr Pro Leu Glu Pro Met Glu Phe Leu Ala Arg Ser Trp
            20              25                  30


Ser Val Ser Ala Leu Glu Val Ser Lys Ala Leu Thr Pro Pro Asn Pro
        35              40                  45


Gln Ile Leu Leu Ser Lys Thr Glu Glu Glu Glu Glu Glu Pro Ile
    50              55                  60


Ser Ser Val Val Asp Gly Asp Gly Asp Thr Glu Asp Thr Gly Leu Val
65              70              75                  80


Thr Gly Asn Pro Phe Ser Phe Ala Cys Ser Glu Thr Ser Gln Met Val
                85              90                  95


Met Asp Arg Ile Leu Ser His Ser Gln Glu Val Ser Pro Arg Thr Ser
            100             105                 110


Gly Arg Leu Ser His Ser Ser Gly Pro Leu Asn Gly Ser Leu Thr Asp
        115             120                 125


Ser Pro Pro Val Ser Pro Pro Glu Ser Asp Asp Ile Lys Gln Phe Cys
    130             135                 140
```

190

Arg Ala Asn Lys Asn Ser Leu Asn Ser Val Asn Ser Gln Phe Arg Ser
145   150   155   160

Thr Ala Ala Thr Pro Gly Pro Ile Thr Ala Thr Ala Thr Gln Ser Lys
                165   170   175

Thr Val Gly Arg Trp Leu Lys Asp Arg Arg Glu Lys Lys Lys Glu Glu
                180   185   190

Thr Arg Ala His Asn Ala Gln Ile His Ala Ala Val Ser Val Ala Gly
        195   200   205

Val Ala Ala Ala Val Ala Ala Ile Ala Ala Ala Thr Ala Ala Ser Ser
210   215   220

Ser Cys Gly Lys Asp Glu Gln Met Ala Lys Thr Asp Met Ala Val Ala
225   230   235   240

Ser Ala Ala Thr Leu Val Ala Ala Gln Cys Val Glu Ala Ala Glu Val
                245   250   255

Met Gly Ala Glu Arg Glu Tyr Leu Ala Ser Val Val Ser Ser Ala Val
        260   265   270

Asn Val Arg Ser Ala Gly Asp Ile Met Thr Leu Thr Ala Gly Ala Ala
        275   280   285

Thr Ala Leu Arg Gly Val Gln Thr Leu Lys Ala Arg Ala Met Lys Glu
    290   295   300

Val Trp Asn Ile Ala Ser Val Ile Pro Met Asp Lys Gly Leu Thr Ser
305   310   315   320

Thr Gly Gly Ser Ser Asn Asn Val Asn Gly Ser Asn Gly Ser Ser Ser
                325   330   335

Ser Ser His Ser Gly Glu Leu Val Gln Gln Glu Asn Phe Leu Gly Thr
        340   345   350

Cys Ser Arg Glu Trp Leu Ala Arg Gly Cys Glu Leu Leu Lys Arg Thr
        355   360   365

Arg Lys Gly Asp Leu His Trp Lys Ile Val Ser Val Tyr Ile Asn Lys
    370   375   380

191

```
Met Asn Gln Val Met Leu Lys Met Lys Ser Arg His Val Gly Gly Thr
385             390             395             400
```

```
Phe Thr Lys Lys Lys Lys Asn Ile Val Leu Asp Val Ile Lys Asn Val
                405             410             415
```

```
Pro Ala Trp Pro Gly Arg His Leu Leu Glu Gly Gly Asp Asp Leu Arg
            420             425             430
```

```
Tyr Phe Gly Leu Lys Thr Val Met Arg Gly Asp Val Glu Phe Glu Val
        435             440             445
```

```
Lys Ser Gln Arg Glu Tyr Glu Met Trp Thr Gln Gly Val Ser Arg Leu
    450             455             460
```

```
Leu Val Leu Ala Ala Glu Arg Lys Phe Arg Met
465             470             475
```

```
<400> 113
atg gag atc atg cgt cca ggg gtc tca gaa aac act ttg aaa gga aaa
48
Met Glu Ile Met Arg Pro Gly Val Ser Glu Asn Thr Leu Lys Gly Lys
1               5               10              15
```

```
ata aga atc aca acg cgg tgc atg tgg ctt gac aaa gga aga ctt tta
96
Ile Arg Ile Thr Thr Arg Cys Met Trp Leu Asp Lys Gly Arg Leu Leu
            20              25              30
```

```
gat gca ctt cac aaa gca gct cat gct gct cta tca agt tgt cct gtg
144
Asp Ala Leu His Lys Ala Ala His Ala Ala Leu Ser Ser Cys Pro Val
        35              40              45
```

```
aca tgt ccc ttg tct cac atg gaa aga aca gtc tcc gaa gtc ctg agg
192
Thr Cys Pro Leu Ser His Met Glu Arg Thr Val Ser Glu Val Leu Arg
    50              55              60
```

```
aag att gta agg aag tac agt ggt aaa agg cct gaa gtc atc gct ata
240
Lys Ile Val Arg Lys Tyr Ser Gly Lys Arg Pro Glu Val Ile Ala Ile
65              70              75              80
```

```
gcc act gag aat cca atg gct gtc cga gct gat gag gtc agt gcg aga
288
Ala Thr Glu Asn Pro Met Ala Val Arg Ala Asp Glu Val Ser Ala Arg
                85              90              95
```

```
ctg tct ggt gat cca agt gtt ggt tct gga gtt gca gct tta agg aaa
336
Leu Ser Gly Asp Pro Ser Val Gly Ser Gly Val Ala Ala Leu Arg Lys
```

192

```
                100                    105                    110

gtt gtt gaa gga aat gac aaa aga agt cgg gcg aag aaa gca cct tca
384
Val Val Glu Gly Asn Asp Lys Arg Ser Arg Ala Lys Lys Ala Pro Ser
        115                    120                    125

caa gaa gct tcc ccc aaa gaa gta gat cgc act ttg gaa gat gat atc
432
Gln Glu Ala Ser Pro Lys Glu Val Asp Arg Thr Leu Glu Asp Asp Ile
    130                    135                    140

att gat agt gca aga cta ctg gct gaa gaa gaa act gcg gca tca aca
480
Ile Asp Ser Ala Arg Leu Leu Ala Glu Glu Glu Thr Ala Ala Ser Thr
145                    150                    155                    160

tac acg gaa gaa gtt gat acg ccc gtt ggg agt tct tca gaa gag tca
528
Tyr Thr Glu Glu Val Asp Thr Pro Val Gly Ser Ser Ser Glu Glu Ser
                165                    170                    175

gac gat ttt tgg aaa tca ttc atc aat cca tca tcg tca cct tca ccg
576
Asp Asp Phe Trp Lys Ser Phe Ile Asn Pro Ser Ser Ser Pro Ser Pro
                180                    185                    190

agt gaa aca gaa aat atg aat aag gta gct gat acg gag cct aaa gca
624
Ser Glu Thr Glu Asn Met Asn Lys Val Ala Asp Thr Glu Pro Lys Ala
        195                    200                    205

gag ggt aag gaa aac agc aga gac gac gat gaa tta gct gat gct tca
672
Glu Gly Lys Glu Asn Ser Arg Asp Asp Asp Glu Leu Ala Asp Ala Ser
    210                    215                    220

gat tct gaa acc aag tca tca cca aaa cgt gtg agg aag aac aaa tgg
720
Asp Ser Glu Thr Lys Ser Ser Pro Lys Arg Val Arg Lys Asn Lys Trp
225                    230                    235                    240

aaa ccg gag gag ata aag aag gta atc aga atg cga gga gag ctg cac
768
Lys Pro Glu Glu Ile Lys Lys Val Ile Arg Met Arg Gly Glu Leu His
                245                    250                    255

agt aga ttt caa gtg gtg aaa ggt aga atg gca ttg tgg gaa gag atc
816
Ser Arg Phe Gln Val Val Lys Gly Arg Met Ala Leu Trp Glu Glu Ile
        260                    265                    270

tct tca aat cta tca gct gaa gga atc aat cga agc ccg gga caa tgc
864
Ser Ser Asn Leu Ser Ala Glu Gly Ile Asn Arg Ser Pro Gly Gln Cys
        275                    280                    285

aaa tct ctc tgg gca tca ctt att cag aaa tac gag gag agc aag gct
912
Lys Ser Leu Trp Ala Ser Leu Ile Gln Lys Tyr Glu Glu Ser Lys Ala
        290                    295                    300
```

193

gat gag aga agc aag acg agt tgg cca cat ttt gag gat atg aac aac
960
Asp Glu Arg Ser Lys Thr Ser Trp Pro His Phe Glu Asp Met Asn Asn
305   310   315   320

att ttg tca gag cta ggc aca cct gcg tct taa
993
Ile Leu Ser Glu Leu Gly Thr Pro Ala Ser
                 325   330

<210> 114 <211> 330 <212> PRT <213> Arabidopsis thaliana <400>
114

Met Glu Ile Met Arg Pro Gly Val Ser Glu Asn Thr Leu Lys Gly Lys
1   5   10   15

Ile Arg Ile Thr Thr Arg Cys Met Trp Leu Asp Lys Gly Arg Leu Leu
          20   25   30

Asp Ala Leu His Lys Ala Ala His Ala Ala Leu Ser Ser Cys Pro Val
          35   40   45

Thr Cys Pro Leu Ser His Met Glu Arg Thr Val Ser Glu Val Leu Arg
       50   55   60

Lys Ile Val Arg Lys Tyr Ser Gly Lys Arg Pro Glu Val Ile Ala Ile
65   70   75   80

Ala Thr Glu Asn Pro Met Ala Val Arg Ala Asp Glu Val Ser Ala Arg
                85   90   95

Leu Ser Gly Asp Pro Ser Val Gly Ser Gly Val Ala Ala Leu Arg Lys
             100   105   110

Val Val Glu Gly Asn Asp Lys Arg Ser Arg Ala Lys Lys Ala Pro Ser
          115   120   125

Gln Glu Ala Ser Pro Lys Glu Val Asp Arg Thr Leu Glu Asp Asp Ile
          130   135   140

Ile Asp Ser Ala Arg Leu Leu Ala Glu Glu Glu Thr Ala Ala Ser Thr
145   150   155   160

Tyr Thr Glu Glu Val Asp Thr Pro Val Gly Ser Ser Ser Glu Glu Ser
             165   170   175

Asp Asp Phe Trp Lys Ser Phe Ile Asn Pro Ser Ser Ser Pro Ser Pro
             180   185   190

194

```
Ser Glu Thr Glu Asn Met Asn Lys Val Ala Asp Thr Glu Pro Lys Ala
        195                 200                 205


Glu Gly Lys Glu Asn Ser Arg Asp Asp Asp Glu Leu Ala Asp Ala Ser
    210                 215                 220


Asp Ser Glu Thr Lys Ser Ser Pro Lys Arg Val Arg Lys Asn Lys Trp
225                 230                 235                 240


Lys Pro Glu Glu Ile Lys Lys Val Ile Arg Met Arg Gly Glu Leu His
                245                 250                 255


Ser Arg Phe Gln Val Val Lys Gly Arg Met Ala Leu Trp Glu Glu Ile
            260                 265                 270


Ser Ser Asn Leu Ser Ala Glu Gly Ile Asn Arg Ser Pro Gly Gln Cys
        275                 280                 285


Lys Ser Leu Trp Ala Ser Leu Ile Gln Lys Tyr Glu Glu Ser Lys Ala
    290                 295                 300


Asp Glu Arg Ser Lys Thr Ser Trp Pro His Phe Glu Asp Met Asn Asn
305                 310                 315                 320


Ile Leu Ser Glu Leu Gly Thr Pro Ala Ser
                325                 330
```

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60

ttcggctgaa tataaatctg aaaaa atg gat caa gat cag cat cct cag tac
112
                       Met Asp Gln Asp Gln His Pro Gln Tyr
                       1                 5

ggt ata ccg gag ctc cgg cag ctc atg aaa ggc gga gga agg acg act
160
Gly Ile Pro Glu Leu Arg Gln Leu Met Lys Gly Gly Gly Arg Thr Thr
10                 15                 20                 25

act aca aca ccg tct act tct tct cat ttt ccc tct gat ttc ttc ggt
208
Thr Thr Thr Pro Ser Thr Ser Ser His Phe Pro Ser Asp Phe Phe Gly
                30                 35                 40
```

ttt aac ctt gct ccg gtg cag cca ccg cca cac cgt ctt cat cag ttc
256
Phe Asn Leu Ala Pro Val Gln Pro Pro Pro His Arg Leu His Gln Phe
              45   50   His   55

act act gat caa gat atg ggt ttc ttg cca cgt ggc ata cat gga ttg
304
Thr Thr Asp Gln Asp Met Gly Phe Leu Pro Arg Gly Ile His Gly Leu
              60   65   70

ggt gga ggt tct tca acg gct gga aat aac agt aac tta aac gcg agt
352
Gly Gly Gly Ser Ser Thr Ala Gly Asn Asn Ser Asn Leu Asn Ala Ser
      75   80   85

act agt ggt gga gga gtt ggg ttt agt ggg ttt ctt gac ggt ggt ggt
400
Thr Ser Gly Gly Gly Val Gly Phe Ser Gly Phe Leu Asp Gly Gly Gly
90   95   100   105

ttc ggc agc gga gta gga gga gac ggt gga gga act gga agg tgg ccg
448
Phe Gly Ser Gly Val Gly Gly Asp Gly Gly Gly Thr Gly Arg Trp Pro
              110   115   120

aga caa gaa acc cta act ctg ttg gaa att aga tct cgt ctt gat cat
496
Arg Gln Glu Thr Leu Thr Leu Leu Glu Ile Arg Ser Arg Leu Asp His
              125   130   135

aaa ttc aaa gaa gct aat cat aaa gga cct ctt tgg gat gaa gtt tct
544
Lys Phe Lys Glu Ala Asn His Lys Gly Pro Leu Trp Asp Glu Val Ser
              140   145   150

agg att atg tcc gag gaa cat gga tac caa agg agt ggg aag aaa tgc
592
Arg Ile Met Ser Glu Glu His Gly Tyr Gln Arg Ser Gly Lys Lys Cys
      155   160   165

aga gag aag ttt gag aat ctg tac aaa tac tat agt aag act aaa gaa
640
Arg Glu Lys Phe Glu Asn Leu Tyr Lys Tyr Tyr Ser Lys Thr Lys Glu
170   175   180   185

ggc gaa gcc gga aga caa gac gga aaa cat cac aga ttt ttc cgc cag
688
Gly Glu Ala Gly Arg Gln Asp Gly Lys His His Arg Phe Phe Arg Gln
              190   195   200

ctc caa gcg cta tac ggg gat tct aat aac ttg gtt tct tgt ccc aat
736
Leu Gln Ala Leu Tyr Gly Asp Ser Asn Asn Leu Val Ser Cys Pro Asn
              205   210   215

cat aac acg cag ttc atg agc agt gct ctt cat ggt ttc cat act caa
784
His Asn Thr Gln Phe Met Ser Ser Ala Leu His Gly Phe His Thr Gln
              220   225   230

196

```
aac cct atg aac gtt gct aca aca acg tcc aac atc cat aac gtt gat
832
Asn Pro Met Asn Val Ala Thr Thr Thr Ser Asn Ile His Asn Val Asp
    235             240             245

agt gtt cat ggt ttt cat caa agc ctt agt ctt tct aac aac tac aac
880
Ser Val His Gly Phe His Gln Ser Leu Ser Leu Ser Asn Asn Tyr Asn
250             255             260             265

tcc tcc gag ctt gag ctg atg act tcc tct tcg gaa ggg aat gat tct
928
Ser Ser Glu Leu Glu Leu Met Thr Ser Ser Ser Glu Gly Asn Asp Ser
            270             275             280

agt agt aga agg aaa aag agg agt tgg aaa gcg aag ata aag gag ttc
976
Ser Ser Arg Arg Lys Lys Arg Ser Trp Lys Ala Lys Ile Lys Glu Phe
        285             290             295

att gat acg aac atg aaa agg ttg ata gag agg caa gat gtt tgg ctt
1024
Ile Asp Thr Asn Met Lys Arg Leu Ile Glu Arg Gln Asp Val Trp Leu
        300             305             310

gag aag ttg aca aag gtt att gaa gac aaa gag gaa caa cgg atg atg
1072
Glu Lys Leu Thr Lys Val Ile Glu Asp Lys Glu Glu Gln Arg Met Met
    315             320             325

aaa gaa gag gaa tgg agg aag att gaa gct gca agg att gat aaa gag
1120
Lys Glu Glu Glu Trp Arg Lys Ile Glu Ala Ala Arg Ile Asp Lys Glu
330             335             340             345

cat ttg ttt tgg gct aaa gag agg gcg agg atg gaa gct agg gat gtt
1168
His Leu Phe Trp Ala Lys Glu Arg Ala Arg Met Glu Ala Arg Asp Val
            350             355             360

gcg gtg att gag gca ttg caa tac ttg aca gga aag cca ttg ata aag
1216
Ala Val Ile Glu Ala Leu Gln Tyr Leu Thr Gly Lys Pro Leu Ile Lys
            365             370             375

ccg ctg tgt tca tcc ccg gaa gag agg aca aat ggt aat aat gag atc
1264
Pro Leu Cys Ser Ser Pro Glu Glu Arg Thr Asn Gly Asn Asn Glu Ile
            380             385             390

cga aac aat agt gag aca cag aat gag aat gga agc gat caa acg atg
1312
Arg Asn Asn Ser Glu Thr Gln Asn Glu Asn Gly Ser Asp Gln Thr Met
        395             400             405

act aac aat gtt tgt gtt aaa gga agt agt agc tgc tgg ggt gag caa
1360
Thr Asn Asn Val Cys Val Lys Gly Ser Ser Ser Cys Trp Gly Glu Gln
410             415             420             425
```

197

gag att tta aag ctt atg gag ata aga acg agc atg gac tcg acc ttt
1408
Glu Ile Leu Lys Leu Met Glu Ile Arg Thr Ser Met Asp Ser Thr Phe
            430   435   440

caa gag ata tta gga ggg tgc tcg gat gag ttt cta tgg gag gaa atc
1456
Gln Glu Ile Leu Gly Gly Cys Ser Asp Glu Phe Leu Trp Glu Glu Ile
            445   450   455

gca gcg aag ttg att cag tta ggg ttt gat cag aga agt gcc tta tta
1504
Ala Ala Lys Leu Ile Gln Leu Gly Phe Asp Gln Arg Ser Ala Leu Leu
            460   465   470

tgc aag gaa aag tgg gaa tgg ata agc aat gga atg agg aaa gaa aag
1552
Cys Lys Glu Lys Trp Glu Trp Ile Ser Asn Gly Met Arg Lys Glu Lys
        475   480   485

aag caa atc aac aag aaa aga aag gat aat tcg tcc agc tgc ggc gtg
1600
Lys Gln Ile Asn Lys Lys Arg Lys Asp Asn Ser Ser Ser Cys Gly Val
490   495   -- 500   505

tac tac ccg aga aac gaa gaa aat cca atc tac aat aat cga gaa agt
1648
Tyr Tyr Pro Arg Asn Glu Glu Asn Pro Ile Tyr Asn Asn Arg Glu Ser
            510   515   520

gga tat aat gat aat gat ccg cat caa atc aac gaa caa ggc aat gta
1696
Gly Tyr Asn Asp Asn Asp Pro His Gln Ile Asn Glu Gln Gly Asn Val
            525   530   535

ggt tct tca aca tca aac gca aac gca aac gca aac gta acc act gga
1744
Gly Ser Ser Thr Ser Asn Ala Asn Ala Asn Ala Asn Val Thr Thr Gly
            540   545   550

aat ccg agc ggt gca atg gct gct agt aca aac tgc ttc ccg ttc ttc
1792
Asn Pro Ser Gly Ala Met Ala Ala Ser Thr Asn Cys Phe Pro Phe Phe
        555   560   565

atg gga gat gga gat cag aat ttg tgg gag agt tat ggt ttg agg ctc
1840
Met Gly Asp Gly Asp Gln Asn Leu Trp Glu Ser Tyr Gly Leu Arg Leu
570   575   580   585

agt aaa gaa gag aat cag taa gtaatttctc ttaatgaaga agaagaaggt
1891
Ser Lys Glu Glu Asn Gln
            590

aatcatgtgg ttaactaatt cttttgagtt agctatatat gagataaacc ttgacttagc
1951

tattatatgt cacatgctgc ttagaattaa gaaatatttg ttggggctta acgaattata
2011

tatcagcata tataagatga gagtctaaga attatatcaa attaggcttt aaccaacgta
2071

cgattatata ttatgttttc atgtatttat tctgtaagac tttttaatat caatctttct
2131

ctaaa
2136

<210> 116 <211> 591 <212> PRT <213> Arabidopsis thaliana <400>
116

Met Asp Gln Asp Gln His Pro Gln Tyr Gly Ile Pro Glu Leu Arg Gln
1   5   10   15

Leu Met Lys Gly Gly Gly Arg Thr Thr Thr Thr Thr Pro Ser Thr Ser
            20   25   30

Ser His Phe Pro Ser Asp Phe Phe Gly Phe Asn Leu Ala Pro Val Gln
        35   40   45

Pro Pro Pro His Arg Leu His Gln Phe Thr Thr Asp Gln Asp Met Gly
    50   55   60

Phe Leu Pro Arg Gly Ile His Gly Leu Gly Gly Gly Ser Ser Thr Ala
65   70   75   80

Gly Asn Asn Ser Asn Leu Asn Ala Ser Thr Ser Gly Gly Gly Val Gly
                85   90   95

Phe Ser Gly Phe Leu Asp Gly Gly Gly Phe Gly Ser Gly Val Gly Gly
            100   105   110

Asp Gly Gly Gly Thr Gly Arg Trp Pro Arg Gln Glu Thr Leu Thr Leu
        115   120   125

Leu Glu Ile Arg Ser Arg Leu Asp His Lys Phe Lys Glu Ala Asn His
    130   135   140

Lys Gly Pro Leu Trp Asp Glu Val Ser Arg Ile Met Ser Glu Glu His
145   150   155   160

Gly Tyr Gln Arg Ser Gly Lys Lys Cys Arg Glu Lys Phe Glu Asn Leu
                165   170   175

Tyr Lys Tyr Tyr Ser Lys Thr Lys Glu Gly Glu Ala Gly Arg Gln Asp
            180   185   190

```
Gly Lys His His Arg Phe Phe Arg Gln Leu Gln Ala Leu Tyr Gly Asp
        195                 200             205

Ser Asn Asn Leu Val Ser Cys Pro Asn His Asn Thr Gln Phe Met Ser
    210             215             220

Ser Ala Leu His Gly Phe His Thr Gln Asn Pro Met Asn Val Ala Thr
225             230             235                 240

Thr Thr Ser Asn Ile His Asn Val Asp Ser Val His Gly Phe His Gln
            245             250             255

Ser Leu Ser Leu Ser Asn Asn Tyr Asn Ser Ser Glu Leu Glu Leu Met
        260             265             270

Thr Ser Ser Ser Glu Gly Asn Asp Ser Ser Ser Arg Arg Lys Lys Arg
        275             280             285

Ser Trp Lys Ala Lys Ile Lys Glu Phe Ile Asp Thr Asn Met Lys Arg
    290             295             300

Leu Ile Glu Arg Gln Asp Val Trp Leu Glu Lys Leu Thr Lys Val Ile
305             310             315                 320

Glu Asp Lys Glu Glu Gln Arg Met Met Lys Glu Glu Glu Trp Arg Lys
            325             330             335

Ile Glu Ala Ala Arg Ile Asp Lys Glu His Leu Phe Trp Ala Lys Glu
            340             345             350

Arg Ala Arg Met Glu Ala Arg Asp Val Ala Val Ile Glu Ala Leu Gln
        355             360             365

Tyr Leu Thr Gly Lys Pro Leu Ile Lys Pro Leu Cys Ser Ser Pro Glu
    370             375             380

Glu Arg Thr Asn Gly Asn Asn Glu Ile Arg Asn Asn Ser Glu Thr Gln
385             390             395                 400

Asn Glu Asn Gly Ser Asp Gln Thr Met Thr Asn Asn Val Cys Val Lys
            405             410             415

Gly Ser Ser Ser Cys Trp Gly Glu Gln Glu Ile Leu Lys Leu Met Glu
        420             425             430

Ile Arg Thr Ser Met Asp Ser Thr Phe Gln Glu Ile Leu Gly Gly Cys
```

200

```
        435                    440                    445
```

```
Ser Asp Glu Phe Leu Trp Glu Glu Ile Ala Ala Lys Leu Ile Gln Leu
    450                455                460
```

```
Gly Phe Asp Gln Arg Ser Ala Leu Leu Cys Lys Glu Lys Trp Glu Trp
465                470                475                480
```

```
Ile Ser Asn Gly Met Arg Lys Glu Lys Lys Gln Ile Asn Lys Lys Arg
                485                490                495
```

```
Lys Asp Asn Ser Ser Ser Cys Gly Val Tyr Tyr Pro Arg Asn Glu Glu
            500                505                510
```

```
Asn Pro Ile Tyr Asn Asn Arg Glu Ser Gly Tyr Asn Asp Asn Asp Pro
        515                520                525
```

```
His Gln Ile Asn Glu Gln Gly Asn Val Gly Ser Ser Thr Ser Asn Ala
    530                535                540
```

```
Asn Ala Asn Ala Asn Val Thr Thr Gly Asn Pro Ser Gly Ala Met Ala
545                550                555                560
```

```
Ala Ser Thr Asn Cys Phe Pro Phe Phe Met Gly Asp Gly Asp Gln Asn
                ·565                570                575
```

```
Leu Trp Glu Ser Tyr Gly Leu Arg Leu Ser Lys Glu Glu Asn Gln
            580                585                590
```

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ttcacttgag aacaacccc tttgaactcg atcaagaaag ctaagtttga agaatcaaga
60
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```
atg gtg cgg aca ccg tgt tgc aaa gcc gaa cta ggg tta aag aaa gga
108
Met Val Arg Thr Pro Cys Cys Lys Ala Glu Leu Gly Leu Lys Lys Gly
1               5                   10                  15
```

```
gct tgg act ccc gag gaa gat cag aag ctt ctc tct tac ctt aac cgc
156
Ala Trp Thr Pro Glu Glu Asp Gln Lys Leu Leu Ser Tyr Leu Asn Arg
            20                25                30
```

```
cac ggt gaa ggt gga tgg cga act ctc ccc gaa aaa gct gga ctc aag
204
His Gly Glu Gly Gly Trp Arg Thr Leu Pro Glu Lys Ala Gly Leu Lys
        35                40                45
```

```
aga tgc ggc aaa agc tgc aga ctg aga tgg gcc aat tat ctt aga cct
252
Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ala Asn Tyr Leu Arg Pro
    50              55              60

gac atc aaa aga gga gag ttc act gaa gac gaa gaa cgt tca atc atc
300
Asp Ile Lys Arg Gly Glu Phe Thr Glu Asp Glu Glu Arg Ser Ile Ile
65              70              75              80

tct ctt cac gcc ctt cac ggc aac aaa tgg tct gct ata gct cgt gga
348
Ser Leu His Ala Leu His Gly Asn Lys Trp Ser Ala Ile Ala Arg Gly
            85              90              95

cta cca gga aga acc gat aac gag atc aag aac tac tgg aac act cat
396
Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
            100             105             110

atc aaa aaa cgt ttg atc aag aaa ggt att gat cca gtt aca cac aag
444
Ile Lys Lys Arg Leu Ile Lys Lys Gly Ile Asp Pro Val Thr His Lys
        115             120             125

ggc ata acc tcc ggt acc gac aaa tca gaa aac ctc ccg gag aaa caa
492
Gly Ile Thr Ser Gly Thr Asp Lys Ser Glu Asn Leu Pro Glu Lys Gln
    130             135             140

aat gtt aat ctg aca act agt gac cat gat ctt gat aat gac aag gcg
540
Asn Val Asn Leu Thr Thr Ser Asp His Asp Leu Asp Asn Asp Lys Ala
145             150             155             160

aag aag aac aac aag aat ttt gga tta tca tcg gct agt ttc ttg aac
588
Lys Lys Asn Asn Lys Asn Phe Gly Leu Ser Ser Ala Ser Phe Leu Asn
                165             170             175

aaa gta gct aat agg ttc gga aag aga atc aat cag agt gtt ctg tct
636
Lys Val Ala Asn Arg Phe Gly Lys Arg Ile Asn Gln Ser Val Leu Ser
            180             185             190

gag att atc gga agt gga ggc cca ctt gct tct act agt cac act act
684
Glu Ile Ile Gly Ser Gly Gly Pro Leu Ala Ser Thr Ser His Thr Thr
        195             200             205

aat act aca act aca agt gtt tcc gtt gac tct gaa tca gtt aag tca
732
Asn Thr Thr Thr Thr Ser Val Ser Val Asp Ser Glu Ser Val Lys Ser
    210             215             220

acg agt tct tcc ttc gca cca acc tcg aat ctt ctc tgc cat ggg acc
780
Thr Ser Ser Ser Phe Ala Pro Thr Ser Asn Leu Leu Cys His Gly Thr
225             230             235             240
```

202

gtt gca aca aca cca gtt tca tcg aac ttt gac gtt gat ggt aac gtt
828
Val Ala Thr Thr Pro Val Ser Ser Asn Phe Asp Val Asp Gly Asn Val
              245   250   255

aat ctg acg tgt tct tcg tcc acg ttc tct gat tcc tcc gtt aac aat
876
Asn Leu Thr Cys Ser Ser Ser Thr Phe Ser Asp Ser Ser Val Asn Asn
              260   265   270

cct cta atg tac tgc gat aat ttc gtt ggt aat aac aac gtt gat gat
924
Pro Leu Met Tyr Cys Asp Asn Phe Val Gly Asn Asn Asn Val Asp Asp
          275   280   285

gag gat act atc ggg ttc tcc aca ttt ctg aat gat gaa gat ttc atg
972
Glu Asp Thr Ile Gly Phe Ser Thr Phe Leu Asn Asp Glu Asp Phe Met
    290   295   300

atg ttg gag gag tct tgt gtt gaa aac act gcg ttc atg aaa gaa ctt
1020
Met Leu Glu Glu Ser Cys Val Glu Asn Thr Ala Phe Met Lys Glu Leu
305   310   315   320

acg agg ttt ctt cac gag gat gaa aac gac gtc gtt gat gtg acg ccg
1068
Thr Arg Phe Leu His Glu Asp Glu Asn Asp Val Val Asp Val Thr Pro
              325   330   335

gtc tat gaa cgt caa gac ttg ttt gac gaa att gat aac tat ttt gga
1116
Val Tyr Glu Arg Gln Asp Leu Phe Asp Glu Ile Asp Asn Tyr Phe Gly
          340   345   350

tga gtgaaactca taatcgatga atcccacgtg accatgtcaa tatgatgtct
1169

atggatatgt taccttgatg atgttgatgg taataataat aaataataga tggtgatgat
1229

gaccatgcat gaatcatgaa tgtagttcgt gttgtcacat atgcttgtgt ttttgtgttt
1289

ttttttttg gtctgaagtg tgttgtttcg ttgtaaatgg attataaatg gtgatgtaat
1349

aattataatg ttaaaaaaaa aaaaaaaaa aaaaa
1384

<210> 118 <211> 352 <212> PRT <213> Arabidopsis thaliana <400>
118

Met Val Arg Thr Pro Cys Cys Lys Ala Glu Leu Gly Leu Lys Lys Gly
1   5   10   15

Ala Trp Thr Pro Glu Glu Asp Gln Lys Leu Leu Ser Tyr Leu Asn Arg
          20   25   30

```
His Gly Glu Gly Gly Trp Arg Thr Leu Pro Glu Lys Ala Gly Leu Lys
        35                  40                  45


Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ala Asn Tyr Leu Arg Pro
    50                  55                  60


Asp Ile Lys Arg Gly Glu Phe Thr Glu Asp Glu Glu Arg Ser Ile Ile
65                  70                  75                  80


Ser Leu His Ala Leu His Gly Asn Lys Trp Ser Ala Ile Ala Arg Gly
            85                  90                  95


Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
            100                 105                 110


Ile Lys Lys Arg Leu Ile Lys Lys Gly Ile Asp Pro Val Thr His Lys
        115                 120                 125


Gly Ile Thr Ser Gly Thr Asp Lys Ser Glu Asn Leu Pro Glu Lys Gln
    130                 135                 140


Asn Val Asn Leu Thr Thr Ser Asp His Asp Leu Asp Asn Asp Lys Ala
145                 150                 155                 160


Lys Lys Asn Asn Lys Asn Phe Gly Leu Ser Ser Ala Ser Phe Leu Asn
            165                 170                 175


Lys Val Ala Asn Arg Phe Gly Lys Arg Ile Asn Gln Ser Val Leu Ser
            180                 185                 190


Glu Ile Ile Gly Ser Gly Gly Pro Leu Ala Ser Thr Ser His Thr Thr
        195                 200                 205


Asn Thr Thr Thr Thr Ser Val Ser Val Asp Ser Glu Ser Val Lys Ser
    210                 215                 220


Thr Ser Ser Ser Phe Ala Pro Thr Ser Asn Leu Leu Cys His Gly Thr
225                 230                 235                 240


Val Ala Thr Thr Pro Val Ser Ser Asn Phe Asp Val Asp Gly Asn Val
            245                 250                 255


Asn Leu Thr Cys Ser Ser Ser Thr Phe Ser Asp Ser Ser Val Asn Asn
            260                 265                 270
```

204

```
Pro Leu Met Tyr Cys Asp Asn Phe Val Gly Asn Asn Asn Val Asp Asp
        275             280             285
```

```
Glu Asp Thr Ile Gly Phe Ser Thr Phe Leu Asn Asp Glu Asp Phe Met
    290             295             300
```

```
Met Leu Glu Glu Ser Cys Val Glu Asn Thr Ala Phe Met Lys Glu Leu
305             310             315             320
```

```
Thr Arg Phe Leu His Glu Asp Glu Asn Asp Val Val Asp Val Thr Pro
            325             330             335
```

```
Val Tyr Glu Arg Gln Asp Leu Phe Asp Glu Ile Asp Asn Tyr Phe Gly
        340             345             350
```

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<221> CDS <222> (338)..(2275) <223> G680
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ttttgcttcc gatttgatta tttccgggaa cgatgacttc tccggggagt tcccggtgag
120

atgataagtc agattgcata cttgtctcct ccatggctac tctcaagggt tttggctgcg
180

gtggattcgt ttggtttctc tagaatctaa agaggttatc acaacggctt tgcaatttga
240

aaactttcat gtttggggag atcaaagatg gtttcttttt tatactttac ttgttagaga
300

ggatttgaag cagcgaatag ctgcaaccgg tcctgtt atg gat act aat aca tct
355
                                        Met Asp Thr Asn Thr Ser
                                        1                   5

gga gaa gaa tta tta gct aag gca aga aag cca tat aca ata aca aag
403
Gly Glu Glu Leu Leu Ala Lys Ala Arg Lys Pro Tyr Thr Ile Thr Lys
            10              15              20

cag cga gag cga tgg act gag gat gag cat gag agg ttt cta gaa gcc
451
Gln Arg Glu Arg Trp Thr Glu Asp Glu His Glu Arg Phe Leu Glu Ala
        25              30              35

ttg agg ctt tat gga aga gct tgg caa cga att gaa gaa cat att ggg
499
Leu Arg Leu Tyr Gly Arg Ala Trp Gln Arg Ile Glu Glu His Ile Gly
    40              45              50

aca aag act gct gtt cag atc aga agt cat gca caa aag ttc ttc aca
547
```

```
Thr Lys Thr Ala Val Gln Ile Arg Ser His Ala Gln Lys Phe Phe Thr
55              60              65                      70
    .

aag ttg gag aaa gag gct gaa gtt aaa ggc atc cct gtt tgc caa gct
595
Lys Leu Glu Lys Glu Ala Glu Val Lys Gly Ile Pro Val Cys Gln Ala
                75              80                      85

ttg gac ata gaa att ccg cct cct cgt cct aaa cga aaa ccc aat act
643
Leu Asp Ile Glu Ile Pro Pro Pro Arg Pro Lys Arg Lys Pro Asn Thr
            90              95              100

cct tat cct cga aaa cct ggg aac aac ggt aca tct tcc tct caa gta
691
Pro Tyr Pro Arg Lys Pro Gly Asn Asn Gly Thr Ser Ser Ser Gln Val
            105             110             115

tca tca gca aaa gat gca aaa ctt gtt tca tcg gcc tct tct tca cag
739
Ser Ser Ala Lys Asp Ala Lys Leu Val Ser Ser Ala Ser Ser Ser Gln
    120             125 .             130

ttg aat cag gcg ttc ttg gat ttg gaa aaa atg ccg ttc tct gag aaa
787
Leu Asn Gln Ala Phe Leu Asp Leu Glu Lys Met Pro Phe Ser Glu Lys
135             140             145  .             150

aca tca act gga aaa gaa aat caa gat gag aat tgc tcg ggt gtt tct
835
Thr Ser Thr Gly Lys Glu Asn Gln Asp Glu Asn Cys Ser Gly Val Ser
                155             160             165

act gtg aac aag tat ccc tta cca acg aaa cag gta agt ggc gac att
883
Thr Val Asn Lys Tyr Pro Leu Pro Thr Lys Gln Val Ser Gly Asp Ile
            170             175             180

gaa aca agt aag acc tca act gtg gac aac gcg gtt caa gat gtt ccc
931
Glu Thr Ser Lys Thr Ser Thr Val Asp Asn Ala Val Gln Asp Val Pro
            185             190             195

aag aag aac aaa gac aaa gat ggt aac gat ggt act act gtg cac agc
979
Lys Lys Asn Lys Asp Lys Asp Gly Asn Asp Gly Thr Thr Val His Ser
    200             205             210

atg caa aac tac cct tgg cat ttc cac gca gat att gtg aac ggg aat
1027
Met Gln Asn Tyr Pro Trp His Phe His Ala Asp Ile Val Asn Gly Asn
215             220             225             230

ata gca aaa tgc cct caa aat cat ccc tca ggt atg gta tct caa gac
1075
Ile Ala Lys Cys Pro Gln Asn His Pro Ser Gly Met Val Ser Gln Asp
            235             240             245.

ttc atg ttt cat cct atg aga gaa gaa act cac ggg cac gca aat ctt
1123
Phe Met Phe His Pro Met Arg Glu Glu Thr His Gly His Ala Asn Leu
```

206

```
                250                      255                      260

caa gct aca aca gca tct gct act act aca gct tct cat caa gcg ttt
1171
Gln Ala Thr Thr Ala Ser Ala Thr Thr Thr Ala Ser His Gln Ala Phe
        265                      270                      275

cca gct tgt cat tca cag gat gat tac cgt tcg ttt ctc cag ata tca
1219
Pro Ala Cys His Ser Gln Asp Asp Tyr Arg Ser Phe Leu Gln Ile Ser
    280                      285                      290

tct act ttc tcc aat ctt att atg tca act ctc cta cag aat cct gca
1267
Ser Thr Phe Ser Asn Leu Ile Met Ser Thr Leu Leu Gln Asn Pro Ala
295                      300                      305                  310

gct cat gct gca gct aca ttc gct gct tcg gtc tgg cct tat gcg agt
1315
Ala His Ala Ala Ala Thr Phe Ala Ala Ser Val Trp Pro Tyr Ala Ser
                315              320                      325

gtc ggg aat tct ggt gat tca tca acc cca atg agc tct tct cct cca
1363
Val Gly Asn Ser Gly Asp Ser Ser Thr Pro Met Ser Ser Ser Pro Pro
            330                      335                      340

agt ata act gcc att gcc gct gct aca gta gct gct gca act gct tgg
1411
Ser Ile Thr Ala Ile Ala Ala Ala Thr Val Ala Ala Ala Thr Ala Trp
        345                      350                      355

tgg gct tct cat gga ctt ctt cct gta tgc gct cca gct cca ata aca
1459
Trp Ala Ser His Gly Leu Leu Pro Val Cys Ala Pro Ala Pro Ile Thr
    360                      365                      370

tgt gtt cca ttc tca act gtt gca gtt cca act cca gca atg act gaa
1507
Cys Val Pro Phe Ser Thr Val Ala Val Pro Thr Pro Ala Met Thr Glu
375                      380                      385                  390

atg gat acc gtt gaa aat act caa ccg ttt gag aaa caa aac aca gct
1555
Met Asp Thr Val Glu Asn Thr Gln Pro Phe Glu Lys Gln Asn Thr Ala
                395                      400                      405

ctg caa gat caa acc ttg gct tcg aaa tct cca gct tca tca tct gat
1603
Leu Gln Asp Gln Thr Leu Ala Ser Lys Ser Pro Ala Ser Ser Ser Asp
            410                      415                      420

gat tca gat gag act gga gta acc aag cta aat gcc gac tca aaa acc
1651
Asp Ser Asp Glu Thr Gly Val Thr Lys Leu Asn Ala Asp Ser Lys Thr
            425                      430                      435

aat gat gat aaa att gag gag gtt gtt gtt act gcc gct gtg cat gac
1699
Asn Asp Asp Lys Ile Glu Glu Val Val Val Thr Ala Ala Val His Asp
        440                      445                      450
```

207

tca aac act gcc cag aag aaa aat ctt gtg gac cgc tca tcg tgt ggc
1747
Ser Asn Thr Ala Gln Lys Lys Asn Leu Val Asp Arg Ser Ser Cys Gly
455   460   465   470

tca aat aca cct tca ggg agt gac gca gaa act gat gca tta gat aaa
1795
Ser Asn Thr Pro Ser Gly Ser Asp Ala Glu Thr Asp Ala Leu Asp Lys
                475   480   485

atg gag aaa gat aaa gag gat gtg aag gag aca gat gag aat cag cca
1843
Met Glu Lys Asp Lys Glu Asp Val Lys Glu Thr Asp Glu Asn Gln Pro
            490   495   500

gat gtt att gag tta aat aac cgt aag att aaa atg aga gac aac aac
1891
Asp Val Ile Glu Leu Asn Asn Arg Lys Ile Lys Met Arg Asp Asn Asn
            505   510   515

agc aac aac aat gca act act gat tcg tgg aag gaa gtc tcc gaa gag
1939
Ser Asn Asn Asn Ala Thr Thr Asp Ser Trp Lys Glu Val Ser Glu Glu
        520   525   530

ggt cgt ata gcg ttt cag gct ctc ttt gca aga gaa aga ttg cct caa
1987
Gly Arg Ile Ala Phe Gln Ala Leu Phe Ala Arg Glu Arg Leu Pro Gln
535   540   545   550

agc ttt tcg cct cct caa gtg gca gag aat gtg aat aga aaa caa agt
2035
Ser Phe Ser Pro Pro Gln Val Ala Glu Asn Val Asn Arg Lys Gln Ser
                555   560   565

gac acg tca atg cca ttg gct cct aat ttc aaa agc cag gat tct tgt
2083
Asp Thr Ser Met Pro Leu Ala Pro Asn Phe Lys Ser Gln Asp Ser Cys
                570   575   580

gct gca gac caa gaa gga gta gta atg atc ggt gtt gga aca tgc aag
2131
Ala Ala Asp Gln Glu Gly Val Val Met Ile Gly Val Gly Thr Cys Lys
            585   590   595

agt ctt aaa acg aga cag aca gga ttt aag cca tac aag aga tgt tca
2179
Ser Leu Lys Thr Arg Gln Thr Gly Phe Lys Pro Tyr Lys Arg Cys Ser
    600   605   610

atg gaa gtg aaa gag agc caa gtt ggg aac ata aac aat caa agt gat
2227
Met Glu Val Lys Glu Ser Gln Val Gly Asn Ile Asn Asn Gln Ser Asp
615   620   625   630

gaa aaa gtc tgc aaa agg ctt cga ttg gaa gga gaa gct tct aca tga
2275
Glu Lys Val Cys Lys Arg Leu Arg Leu Glu Gly Glu Ala Ser Thr
            635   640   645

208

cagacttgga ggtaaaaaaa aaacatccac attttttatca atatctttaa atctagtgtt
2335

agtagtttgc ttctccaatc tttatgaaag agactttttaa ttttccttcc gaacatttct
2395

ttggtcatgt caggttctgt accatattac cccatgtctt gtctcttgtc tctgtttgtg
2455

tatgctactt gtggtctata tgtcatctgc tactactgtt aattaaccat taagcaatgg
2515

atttgtcttt a
2526

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Met Asp Thr Asn Thr Ser Gly Glu Glu Leu Leu Ala Lys Ala Arg Lys
1   5   10   15

Pro Tyr Thr Ile Thr Lys Gln Arg Glu Arg Trp Thr Glu Asp Glu His
            20   25   30

Glu Arg Phe Leu Glu Ala Leu Arg Leu Tyr Gly Arg Ala Trp Gln Arg
        35   40   45

Ile Glu Glu His Ile Gly Thr Lys Thr Ala Val Gln Ile Arg Ser His
    50   55   60

Ala Gln Lys Phe Phe Thr Lys Leu Glu Lys Glu Ala Glu Val Lys Gly
65   70   75   80

Ile Pro Val Cys Gln Ala Leu Asp Ile Glu Ile Pro Pro Pro Arg Pro
                85   90   95

Lys Arg Lys Pro Asn Thr Pro Tyr Pro Arg Lys Pro Gly Asn Asn Gly
            100   105   110

Thr Ser Ser Ser Gln Val Ser Ser Ala Lys Asp Ala Lys Leu Val Ser
        115   120   125

Ser Ala Ser Ser Ser Gln Leu Asn Gln Ala Phe Leu Asp Leu Glu Lys
    130   135   140

Met Pro Phe Ser Glu Lys Thr Ser Thr Gly Lys Glu Asn Gln Asp Glu
145   150   155   160

Asn Cys Ser Gly Val Ser Thr Val Asn Lys Tyr Pro Leu Pro Thr Lys
                165   170   175

209

```
Gln Val Ser Gly Asp Ile Glu Thr Ser Lys Thr Ser Thr Val Asp Asn
            180                 185             190

Ala Val Gln Asp Val Pro Lys Lys Asn Lys Asp Lys Asp Gly Asn Asp
            195                 200             205

Gly Thr Thr Val His Ser Met Gln Asn Tyr Pro Trp His Phe His Ala
    210                 215                 220

Asp Ile Val Asn Gly Asn Ile Ala Lys Cys Pro Gln Asn His Pro Ser
225                 230             235                 240

Gly Met Val Ser Gln Asp Phe Met Phe His Pro Met Arg Glu Glu Thr
                245             250             255

His Gly His Ala Asn Leu Gln Ala Thr Thr Ala Ser Ala Thr Thr Thr
            260             265 -             270

Ala Ser His Gln Ala Phe Pro Ala Cys His Ser Gln Asp Asp Tyr Arg
        275             280             285

Ser Phe Leu Gln Ile Ser Ser Thr Phe Ser Asn Leu Ile Met Ser Thr
    290             295                 300

Leu Leu Gln Asn Pro Ala Ala His Ala Ala Ala Thr Phe Ala Ala Ser
305             310             315                 320

Val Trp Pro Tyr Ala Ser Val Gly Asn Ser Gly Asp Ser Ser Thr Pro
            325             330             335

Met Ser Ser Ser Pro Pro Ser Ile Thr Ala Ile Ala Ala Ala Thr Val
            340             345             350

Ala Ala Ala Thr Ala Trp Trp Ala Ser His Gly Leu Leu Pro Val Cys
        355             360             365

Ala Pro Ala Pro Ile Thr Cys Val Pro Phe Ser Thr Val Ala Val Pro
    370             375·            380

Thr Pro Ala Met Thr Glu Met Asp Thr Val Glu Asn Thr Gln Pro Phe
385             390             395                 400

Glu Lys Gln Asn Thr Ala Leu Gln Asp Gln Thr Leu Ala Ser Lys Ser
            405             410             415
```

210

```
Pro Ala Ser Ser Ser Asp Asp Ser Asp Glu Thr Gly Val Thr Lys Leu
        420             425             430

Asn Ala Asp Ser Lys Thr Asn Asp Asp Lys Ile Glu Glu Val Val Val
        435             440             445

Thr Ala Ala Val His Asp Ser Asn Thr Ala Gln Lys Lys Asn Leu Val
    450             455             460

Asp Arg Ser Ser Cys Gly Ser Asn Thr Pro Ser Gly Ser Asp Ala Glu
465             470             475             480

Thr Asp Ala Leu Asp Lys Met Glu Lys Asp Lys Glu Asp Val Lys Glu
            485             490             495

Thr Asp Glu Asn Gln Pro Asp Val Ile Glu Leu Asn Asn Arg Lys Ile
        500             505             510

Lys Met Arg Asp Asn Asn Ser Asn Asn Asn Ala Thr Thr Asp Ser Trp
        515             520             525

Lys Glu Val Ser Glu Glu Gly Arg Ile Ala Phe Gln Ala Leu Phe Ala
    530             535             540

Arg Glu Arg Leu Pro Gln Ser Phe Ser Pro Pro Gln Val Ala Glu Asn
545             550             555             560

Val Asn Arg Lys Gln Ser Asp Thr Ser Met Pro Leu Ala Pro Asn Phe
            565             570             575

Lys Ser Gln Asp Ser Cys Ala Ala Asp Gln Glu Gly Val Val Met Ile
            580             585             590

Gly Val Gly Thr Cys Lys Ser Leu Lys Thr Arg Gln Thr Gly Phe Lys
        595             600             605

Pro Tyr Lys Arg Cys Ser Met Glu Val Lys Glu Ser Gln Val Gly Asn
    610             615             620

Ile Asn Asn Gln Ser Asp Glu Lys Val Cys Lys Arg Leu Arg Leu Glu
625             630             635             640

Gly Glu Ala Ser Thr
            645
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211

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<221> CDS <222> (271)..(2079) <223> G716

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atacggacat aaccgtccgt tgtgtcctgt ttataaagtt ttgctttttt tattttctcc
120

attgatgggt cttttctttc ttctctctct cgtgtttctt tcatggggtt aagactagtg
180

tttaccgcgt gaaggttttt ttttctttct attttctttc atttcctctc cttctacttc
240

ttcttctcca gttctcatct gggttcttca atg gcg agt gtt gaa ggt gat gat
294
                                    Met Ala Ser Val Glu Gly Asp Asp
                                    1   5

gat ttc gga agt tct tcg tca agg tct tat caa gat caa cta tac aca
342
Asp Phe Gly Ser Ser Ser Ser Arg Ser Tyr Gln Asp Gln Leu Tyr Thr
    10   15   20

gag cta tgg aaa gtt tgt gca ggt cca tta gtg gaa gtt cct cgt gct
390
Glu Leu Trp Lys Val Cys Ala Gly Pro Leu Val Glu Val Pro Arg Ala
25   30   35   40

caa gag aga gtt ttc tac ttc cct cag ggt cac atg gaa caa ctt gtg
438
Gln Glu Arg Val Phe Tyr Phe Pro Gln Gly His Met Glu Gln Leu Val
                45   50   55

gcg tca act aat caa gga atc aat tca gaa gaa ata cct gtt ttt gat
486
Ala Ser Thr Asn Gln Gly Ile Asn Ser Glu Glu Ile Pro Val Phe Asp
                60   65   70

ctt cct cca aag ata ctt tgt cga gtt ctt gat gtc act tta aag gcg
534
Leu Pro Pro Lys Ile Leu Cys Arg Val Leu Asp Val Thr Leu Lys Ala
            75   80   85

gag cat gaa aca gat gag gtt tac gct cag atc aca tta caa cca gag
582
Glu His Glu Thr Asp Glu Val Tyr Ala Gln Ile Thr Leu Gln Pro Glu
        90   95   100

gaa gat caa agt gaa cca aca agt ctt gat cca cct att gtt gga cca
630
Glu Asp Gln Ser Glu Pro Thr Ser Leu Asp Pro Pro Ile Val Gly Pro
105   110   115   120

act aag caa gag ttt cat tcg ttt gtt aag att tta acg gct tca gat
678
Thr Lys Gln Glu Phe His Ser Phe Val Lys Ile Leu Thr Ala Ser Asp
                125   130   135

212

```
aca agc act cat ggt gga ttc tct gtt ctt cgt aaa cac gcc act gaa
726
Thr Ser Thr His Gly Gly Phe Ser Val Leu Arg Lys His Ala Thr Glu
            140               145             150

tgc ttg cct tct ttg gat atg aca caa gct act cct act caa gaa ctt
774
Cys Leu Pro Ser Leu Asp Met Thr Gln Ala Thr Pro Thr Gln Glu Leu
        155               160             165

gtg act aga gat ctt cat ggc ttt gaa tgg agg ttt aag cat ata ttc
822
Val Thr Arg Asp Leu His Gly Phe Glu Trp Arg Phe Lys His Ile Phe
    170               175             180

aga gga caa cca cgg agg cat ttg ctt act acg ggt tgg agt aca ttt
870
Arg Gly Gln Pro Arg Arg His Leu Leu Thr Thr Gly Trp Ser Thr Phe
185               190               195                 200

gta tcc tcg aaa aga ctt gta gct gga gat gct ttt gtg ttc ttg agg
918
Val Ser Ser Lys Arg Leu Val Ala Gly Asp Ala Phe Val Phe Leu Arg
            205               210               215

ggt gag aat ggg gat tta cgg gtt gga gtg aga cga tta gct cgg cat
966
Gly Glu Asn Gly Asp Leu Arg Val Gly Val Arg Arg Leu Ala Arg His
            220               225               230

caa agc aca atg cct act tcg gtt att tca agt cag agc atg cat ttg
1014
Gln Ser Thr Met Pro Thr Ser Val Ile Ser Ser Gln Ser Met His Leu
            235               240               245

gga gtt ctt gct aca gct tct cat gct gtg cgt aca aca aca atc ttt
1062
Gly Val Leu Ala Thr Ala Ser His Ala Val Arg Thr Thr Thr Ile Phe
    250               255               260

gtt gtc ttt tac aag cct agg ata agc caa ttc ata gtt ggg gtg aac
1110
Val Val Phe Tyr Lys Pro Arg Ile Ser Gln Phe Ile Val Gly Val Asn
265               270               275                 280

aag tat atg gaa gct ata aag cat gga ttt tct ctc ggt acc cga ttc
1158
Lys Tyr Met Glu Ala Ile Lys His Gly Phe Ser Leu Gly Thr Arg Phe
            285               290               295

aga atg agg ttt gaa gga gaa gag tct cct gag aga ata ttt act ggt
1206
Arg Met Arg Phe Glu Gly Glu Glu Ser Pro Glu Arg Ile Phe Thr Gly
            300               305             310

acg att gtg gga agt gga gat cta tct tca caa tgg cca gct tct aaa
1254
Thr Ile Val Gly Ser Gly Asp Leu Ser Ser Gln Trp Pro Ala Ser Lys
        315               320             325
```

tgg agg tca ttg cag gta caa tgg gat gag cca aca aca gtt cag aga
1302
Trp Arg Ser Leu Gln Val Gln Trp Asp Glu Pro Thr Thr Val Gln Arg
    330   335   340

cca gat aaa gtc tca cca tgg gag ata gag cct ttc ttg gca act tcc
1350
Pro Asp Lys Val Ser Pro Trp Glu Ile Glu Pro Phe Leu Ala Thr Ser
345   350   355   360

cca att tca act cct gct caa caa cca caa tcg aaa tgc aag cgg tca
1398
Pro Ile Ser Thr Pro Ala Gln Gln Pro Gln Ser Lys Cys Lys Arg Ser
                365   370   375

aga ccc atc gag cca tca gtt aaa aca cca gcc cca cct agt ttc ttg
1446
Arg Pro Ile Glu Pro Ser Val Lys Thr Pro Ala Pro Pro Ser Phe Leu
            380   385   390

tac agc ctc cct cag agc caa gat tcc att aat gca tcc ctt aaa ctg
1494
Tyr Ser Leu Pro Gln Ser Gln Asp Ser Ile Asn Ala Ser Leu Lys Leu
        395   400   405

ttt caa gat cca tca ctt gag aga att tca ggt gga tac tcc tca aac
1542
Phe Gln Asp Pro Ser Leu Glu Arg Ile Ser Gly Gly Tyr Ser Ser Asn
    410   415   420

aac agc ttc aaa ccc gag act cct cct cct cca acg aat tgt agc tat
1590
Asn Ser Phe Lys Pro Glu Thr Pro Pro Pro Thr Asn Cys Ser Tyr
425   430   435   440

agg ttg ttt gga ttt gat ctc aca agc aat tct cct gct cca atc cct
1638
Arg Leu Phe Gly Phe Asp Leu Thr Ser Asn Ser Pro Ala Pro Ile Pro
            445   450   455

caa gac aag caa ccg atg gat act tgt gga gct gcc aag tgt caa gaa
1686
Gln Asp Lys Gln Pro Met Asp Thr Cys Gly Ala Ala Lys Cys Gln Glu
            460   465   470

ccc atc act cca acc tca atg agt gag cag aag aag caa caa aca tca
1734
Pro Ile Thr Pro Thr Ser Met Ser Glu Gln Lys Lys Gln Gln Thr Ser
        475   480   485

aga agt cga act aaa gtg caa atg caa ggc att gcg gtt ggt cgt gcg
1782
Arg Ser Arg Thr Lys Val Gln Met Gln Gly Ile Ala Val Gly Arg Ala
    490   495   500

gtt gat tta aca ctg ttg aaa tct tac gat gaa ctg att gat gag ctt
1830
Val Asp Leu Thr Leu Leu Lys Ser Tyr Asp Glu Leu Ile Asp Glu Leu
505   510   515   520

214

```
gag gag atg ttt gag att caa gga cag ctt ctt gcc cga gac aaa tgg
1878
Glu Glu Met Phe Glu Ile Gln Gly Gln Leu Leu Ala Arg Asp Lys Trp
                525             530             535

atc gtt gtc ttc act gat gat gaa gga gat atg atg ctt gct ggt gat
1926
Ile Val Val Phe Thr Asp Asp Glu Gly Asp Met Met Leu Ala Gly Asp
            540             545             550

gat ccg tgg aat gag ttt tgc aag atg gca aag aag ata ttt ata tat
1974
Asp Pro Trp Asn Glu Phe Cys Lys Met Ala Lys Lys Ile Phe Ile Tyr
        555             560             565

tcg agc gat gag gtt aag aaa atg aca acg aaa ctg aag att tct tcg
2022
Ser Ser Asp Glu Val Lys Lys Met Thr Thr Lys Leu Lys Ile Ser Ser
    570             575             580

tcg tta gag aat gag gaa tat ggt aat gaa tca ttc gaa aat cgt agt
2070
Ser Leu Glu Asn Glu Glu Tyr Gly Asn Glu Ser Phe Glu Asn Arg Ser
585             590             595             600

agg ggg tga gagttttagc tgttaattaa ggttaattcg gcgacgtcgt
2119
Arg Gly

tttagtgcgt aagtgtctaa agactttttt tttagtctgt gtatataaag tcttgtcctc
2179

tttttcatgt caatttttca agttggcgat ttaatatttc ggttttggga cagtggttga
2239

tggggcggtt ttacatttt tatgtgtatg tacttgttcc aaaaccattc aattttcaaa
2299
```

```
<210> 122 <211> 602 <212> PRT <213> Arabidopsis thaliana <400>
122

Met Ala Ser Val Glu Gly Asp Asp Asp Phe Gly Ser Ser Ser Ser Arg
1               5               10              15

Ser Tyr Gln Asp Gln Leu Tyr Thr Glu Leu Trp Lys Val Cys Ala Gly
            20              25              30

Pro Leu Val Glu Val Pro Arg Ala Gln Glu Arg Val Phe Tyr Phe Pro
            35              40              45

Gln Gly His Met Glu Gln Leu Val Ala Ser Thr Asn Gln Gly Ile Asn
    50              55              60

Ser Glu Glu Ile Pro Val Phe Asp Leu Pro Pro Lys Ile Leu Cys Arg
65              70              75              80
```

Val Leu Asp Val Thr Leu Lys Ala Glu His Glu Thr Asp Glu Val Tyr
          85   90   95

Ala Gln Ile Thr Leu Gln Pro Glu Glu Asp Gln Ser Glu Pro Thr Ser
            100   105   110

Leu Asp Pro Pro Ile Val Gly Pro Thr Lys Gln Glu Phe His Ser Phe
        115   120   125

Val Lys Ile Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe Ser
    130   135   140

Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Ser Leu Asp Met Thr
145   150   155   160

Gln Ala Thr Pro Thr Gln Glu Leu Val Thr Arg Asp Leu His Gly Phe
            165   170   175

Glu Trp Arg Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His Leu
            180   185   190

Leu Thr Thr Gly Trp Ser Thr Phe Val Ser Ser Lys Arg Leu Val Ala
        195   200   205

Gly Asp Ala Phe Val Phe Leu Arg Gly Glu Asn Gly Asp Leu Arg Val
    210   215   220

Gly Val Arg Arg Leu Ala Arg His Gln Ser Thr Met Pro Thr Ser Val
225   230   235   240

Ile Ser Ser Gln Ser Met His Leu Gly Val Leu Ala Thr Ala Ser His
            245   250   255

Ala Val Arg Thr Thr Thr Ile Phe Val Val Phe Tyr Lys Pro Arg Ile
        260   265   270

Ser Gln Phe Ile Val Gly Val Asn Lys Tyr Met Glu Ala Ile Lys His
        275   280   285

Gly Phe Ser Leu Gly Thr Arg Phe Arg Met Arg Phe Glu Gly Glu Glu
    290   295   300

Ser Pro Glu Arg Ile Phe Thr Gly Thr Ile Val Gly Ser Gly Asp Leu
305   310   315   320

216

Ser Ser Gln Trp Pro Ala Ser Lys Trp Arg Ser Leu Gln Val Gln Trp
            325   330   335

Asp Glu Pro Thr Thr Val Gln Arg Pro Asp Lys Val Ser Pro Trp Glu
            340   345   350

Ile Glu Pro Phe Leu Ala Thr Ser Pro Ile Ser Thr Pro Ala Gln Gln
            355   360   365

Pro Gln Ser Lys Cys Lys Arg Ser Arg Pro Ile Glu Pro Ser Val Lys
    370   375   380

Thr Pro Ala Pro Pro Ser Phe Leu Tyr Ser Leu Pro Gln Ser Gln Asp
385   390   395   400

Ser Ile Asn Ala Ser Leu Lys Leu Phe Gln Asp Pro Ser Leu Glu Arg
            405   410   415

Ile Ser Gly Gly Tyr Ser Ser Asn Asn Ser Phe Lys Pro Glu Thr Pro
            420   425   430

Pro Pro Pro Thr Asn Cys Ser Tyr Arg Leu Phe Gly Phe Asp Leu Thr
            435   440   445

Ser Asn Ser Pro Ala Pro Ile Pro Gln Asp Lys Gln Pro Met Asp Thr
    450   455   460

Cys Gly Ala Ala Lys Cys Gln Glu Pro Ile Thr Pro Thr Ser Met Ser
465   470   475   480

Glu Gln Lys Lys Gln Gln Thr Ser Arg Ser Arg Thr Lys Val Gln Met
            485   490   495

Gln Gly Ile Ala Val Gly Arg Ala Val Asp Leu Thr Leu Leu Lys Ser
            500   505   510

Tyr Asp Glu Leu Ile Asp Glu Leu Glu Glu Met Phe Glu Ile Gln Gly
            515   520   525

Gln Leu Leu Ala Arg Asp Lys Trp Ile Val Val Phe Thr Asp Asp Glu
            530   535   540

Gly Asp Met Met Leu Ala Gly Asp Asp Pro Trp Asn Glu Phe Cys Lys
545   550   555   560

217

```
Met Ala Lys Lys Ile Phe Ile Tyr Ser Ser Asp Glu Val Lys Lys Met
            565                 570                 575
```

```
Thr Thr Lys Leu Lys Ile Ser Ser Ser Leu Glu Asn Glu Glu Tyr Gly
            580                 585                 590
```

```
Asn Glu Ser Phe Glu Asn Arg Ser Arg Gly
            595                 600
```

<210> 123 <211> 513 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(513) <223> G736

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<400> 123
atg gcg act caa gat tct caa ggg att aaa ctc ttt ggc aaa act att
48
Met Ala Thr Gln Asp Ser Gln Gly Ile Lys Leu Phe Gly Lys Thr Ile
1               5                   10                  15
```

```
gca ttt aac act cga aca ata aaa aat gaa gaa gag aca cac ccg ccg
96
Ala Phe Asn Thr Arg Thr Ile Lys Asn Glu Glu Glu Thr His Pro Pro
            20                  25                  30
```

```
gag caa gaa gcc aca ata gcc gtt aga tca tca toa tca tcg gat ctg
144
Glu Gln Glu Ala Thr Ile Ala Val Arg Ser Ser Ser Ser Ser Asp Leu
        35                  40                  45
```

```
acg gcc gag aag cgt ccg gat aag atc ata gca tgt cca aga tgc aag
192
Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Ala Cys Pro Arg Cys Lys
    50                  55                  60
```

```
agc atg gag aca aag ttc tgt tac ttc aac aac tac aac ggt aat cag
240
Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Gly Asn Gln
65                  70                  75                  80
```

```
cct cga cac ttt tgt aaa ggc tgc cac cgt tac tgg acc gcc ggt ggt
288
Pro Arg His Phe Cys Lys Gly Cys His Arg Tyr Trp Thr Ala Gly Gly
                85                  90                  95
```

```
gca ctc cgg aac gtt ccc gtc ggc gcc ggt cgt cgg aag tcc aaa cca
336
Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro
            100                 105                 110
```

```
cct ggt cgt gtc gtg gtt ggt atg ctt gga gat gga aat ggt gtt cgc
384
Pro Gly Arg Val Val Val Gly Met Leu Gly Asp Gly Asn Gly Val Arg
            115                 120                 125
```

```
caa gtc gag ctt ata aat ggc ttg ctc gtt gag gag tgg cag cat gcc
432
Gln Val Glu Leu Ile Asn Gly Leu Leu Val Glu Glu Trp Gln His Ala
        130                 135                 140
```

218

gca gcc gca gct cac ggt agt ttc cgg cat gat ttt ccc atg aag cgg
480
Ala Ala Ala Ala His Gly Ser Phe Arg His Asp Phe Pro Met Lys Arg
145   150   155   160

ctc cgg tgt tac tcc gac ggt caa tcg tgc tga
513
Leu Arg Cys Tyr Ser Asp Gly Gln Ser Cys
              165   170

<210> 124 <211> 170 <212> PRT <213> Arabidopsis thaliana <400>
124

Met Ala Thr Gln Asp Ser Gln Gly Ile Lys Leu Phe Gly Lys Thr Ile
1   5   10   15

Ala Phe Asn Thr Arg Thr Ile Lys Asn Glu Glu Glu Thr His Pro Pro
        20   25   30

Glu Gln Glu Ala Thr Ile Ala Val Arg Ser Ser Ser Ser Ser Asp Leu
        35   40   45

Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Ala Cys Pro Arg Cys Lys
    50   55   60

Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Gly Asn Gln
65   70   75   80

Pro Arg His Phe Cys Lys Gly Cys His Arg Tyr Trp Thr Ala Gly Gly
            85   90   95

Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro
            100   105   110

Pro Gly Arg Val Val Val Gly Met Leu Gly Asp Gly Asn Gly Val Arg
        115   120   125

Gln Val Glu Leu Ile Asn Gly Leu Leu Val Glu Glu Trp Gln His Ala
        130   135   140

Ala Ala Ala His Gly Ser Phe Arg His Asp Phe Pro Met Lys Arg
145   150   155   160

Leu Arg Cys Tyr Ser Asp Gly Gln Ser Cys
              165   170

<210> 125 <211> 1707 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (98)..(1444) <223> G748

219

<400> 125
ccacgcgtcc gcactctccc aaatctctct tctttaacaa caaaaaaaaa atcacagaga
60

catagagaga agaagacgga acagaggctc caaaaaa atg atg atg gag act aga
115
                                              Met Met Met Glu Thr Arg
                                              1   5

gat cca gct att aag ctt ttc ggt atg aaa atc cct ttt ccg tcg gtt
163
Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile Pro Phe Pro Ser Val
            10   15   20

ttt gaa tcg gca gtt acg gtg gag gat gac gaa gaa gat gac tgg agc
211
Phe Glu Ser Ala Val Thr Val Glu Asp Asp Glu Glu Asp Asp Trp Ser
        25   30   35

ggc gga gat gac aaa tca cca gag aag gta act cca gag tta tca gat
259
Gly Gly Asp Asp Lys Ser Pro Glu Lys Val Thr Pro Glu Leu Ser Asp
    40   45   50

aag aac aac aac aac tgt aac gac aac agt ttt aac aat tcg aaa ccc
307
Lys Asn Asn Asn Asn Cys Asn Asp Asn Ser Phe Asn Asn Ser Lys Pro
55   60   65   70

gaa acc ttg gac aaa gag gaa gcg aca tca act gat cag ata gag agt
355
Glu Thr Leu Asp Lys Glu Glu Ala Thr Ser Thr Asp Gln Ile Glu Ser
            75   80   85

agt gac acg cct gag gat aat cag cag acg aca cct gat ggt aaa acc
403
Ser Asp Thr Pro Glu Asp Asn Gln Gln Thr Thr Pro Asp Gly Lys Thr
        90   95   100

cta aag aaa ccg act aag att cta ccg tgt ccg aga tgc aaa agc atg
451
Leu Lys Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Lys Ser Met
        105   110   115

gag acc aag ttc tgt tat tac aac aac tac aac ata aac cag cct cgt
499
Glu Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Ile Asn Gln Pro Arg
    120   125   130

cat ttc tgc aag gct tgt cag aga tat tgg act gct gga ggg act atg
547
His Phe Cys Lys Ala Cys Gln Arg Tyr Trp Thr Ala Gly Gly Thr Met
135   140   145   150

agg aat gtt cct gtg ggg gca gga cgt cgt aag aac aaa agc tca tct
595
Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Asn Lys Ser Ser Ser
                155   160   165

tct cat tac cgt cac atc act att tcc gag gct ctt gag gct gcg agg
643

220

```
Ser His Tyr Arg His Ile Thr Ile Ser Glu Ala Leu Glu Ala Ala Arg
             170              175              180

ctt gac ccg ggc tta cag gca aac aca agg gtc ttg agt ttt ggt ctc
691
Leu Asp Pro Gly Leu Gln Ala Asn Thr Arg Val Leu Ser Phe Gly Leu
             185              190              195

gaa gct cag cag cag cac gtt gct gct ccc atg aca cct gtt atg aag
739
Glu Ala Gln Gln Gln His Val Ala Ala Pro Met Thr Pro Val Met Lys
         200              205              210

cta caa gaa gat caa aag gtc tca aac ggt gct agg aac agg ttt cac
787
Leu Gln Glu Asp Gln Lys Val Ser Asn Gly Ala Arg Asn Arg Phe His
215              220              225              230

ggg tta gcg gat caa cgg ctt gta gct cgg gta gag aat gga gat gat
835
Gly Leu Ala Asp Gln Arg Leu Val Ala Arg Val Glu Asn Gly Asp Asp
             235              240              245

tgc tca agc gga tcc tct gtg acc acc tct aac aat cac tca gtg gat
883
Cys Ser Ser Gly Ser Ser Val Thr Thr Ser Asn Asn His Ser Val Asp
         250              255              260

gaa tca aga gca caa agc ggc agt gtt gtt gaa gca caa atg aac aac
931
Glu Ser Arg Ala Gln Ser Gly Ser Val Val Glu Ala Gln Met Asn Asn
         265              270              275

aac aac aac aat aac atg aat ggt tat gct tgc atc cca ggt gtt cca
979
Asn Asn Asn Asn Asn Met Asn Gly Tyr Ala Cys Ile Pro Gly Val Pro
     280              285              290

tgg cct tac acg tgg aat cca gcg atg cct cca cca ggt ttt tac ccg
1027
Trp Pro Tyr Thr Trp Asn Pro Ala Met Pro Pro Pro Gly Phe Tyr Pro
295              300              305              310

cct cca ggg tat cca atg ccg ttt tac cct tac tgg acc atc cca atg
1075
Pro Pro Gly Tyr Pro Met Pro Phe Tyr Pro Tyr Trp Thr Ile Pro Met
             315              320              325

cta cca ccg cat caa tcc tca tcg cct ata agc caa aag tgt tca aat
1123
Leu Pro Pro His Gln Ser Ser Ser Pro Ile Ser Gln Lys Cys Ser Asn
             330              335              340

aca aac tct ccg act ctc gga aag cat ccg aga gat gaa gga tca tcg
1171
Thr Asn Ser Pro Thr Leu Gly Lys His Pro Arg Asp Glu Gly Ser Ser
         345              350              355

aaa aag gac aat gag aca gag cga aaa cag aag gcc ggg tgc gtt ctg
1219
Lys Lys Asp Asn Glu Thr Glu Arg Lys Gln Lys Ala Gly Cys Val Leu
```

221

```
        360                    365                        370

gtc ccg aaa acg ttg aga ata gat gat cct aac gaa gca gca aag agc
1267
Val Pro Lys Thr Leu Arg Ile Asp Asp Pro Asn Glu Ala Ala Lys Ser
375                    380                    385                    390

tcg ata tgg aca aca ttg gga atc aag aac gag gcg atg tgc aaa gcc
1315
Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Ala Met Cys Lys Ala
                  395                    400                    405

ggt ggt atg ttc aaa ggg ttt gat cat aag aca aag atg tat aac aac
1363  ·
Gly Gly Met Phe Lys Gly Phe Asp His Lys Thr Lys Met Tyr Asn Asn
                  410                    415                    420

gac aaa gct gag aac tcc cct gtt ctt tct gct aac cct gct gct cta
1411
Asp Lys Ala Glu Asn Ser Pro Val Leu Ser Ala Asn Pro Ala Ala Leu
          425                    430                    435

tca aga tca cac aat ttc cat gaa cag att tag agttacatat gtatatgtat
1464                                              ‒
Ser Arg Ser His Asn Phe His Glu Gln Ile
      440                    445

atatgtatga ttgattgtat gtatagatga tactggagaa tgatgagttt ttgagaatca
1524

aactcttttc ttctttctag tgattgcctt tattccttta catgttttgg ttctctgtac
1584

actatttgat ttaccttttt tactttcttt cttcatttgt caggaaatgt tggaagataa
1644

cattaatggt aaaaagttgg tgtggaccgt tgttgcgttg gcatttcaaa aaaaaaaaaa
1704

aaa
1707


<210>  126 <211>  448 <212>  PRT <213>  Arabidopsis thaliana  <400>
126

Met Met Met Glu Thr Arg Asp Pro Ala Ile Lys Leu Phe Gly Met Lys
1                  5                    10                    15


Ile Pro Phe Pro Ser Val Phe Glu Ser Ala Val Thr Val Glu Asp Asp
          20                    25                    30


Glu Glu Asp Asp Trp Ser Gly Gly Asp Asp Lys Ser Pro Glu Lys Val
          35                    40                    45


Thr Pro Glu Leu Ser Asp Lys Asn Asn Asn Asn Cys Asn Asp Asn Ser
      50                    55                    60
```

```
Phe Asn Asn Ser Lys Pro Glu Thr Leu Asp Lys Glu Glu Ala Thr Ser
65                  70              75                  80


Thr Asp Gln Ile Glu Ser Ser Asp Thr Pro Glu Asp Asn Gln Gln Thr
                85              90                  95


Thr Pro Asp Gly Lys Thr Leu Lys Lys Pro Thr Lys Ile Leu Pro Cys
            100             105             110


Pro Arg Cys Lys Ser Met Glu Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr
        115             120             125


Asn Ile Asn Gln Pro Arg His Phe Cys Lys Ala Cys Gln Arg Tyr Trp
    130             135             140


Thr Ala Gly Gly Thr Met Arg Asn Val Pro Val Gly Ala Gly Arg Arg
145             150             155             160


Lys Asn Lys Ser Ser Ser Ser His Tyr Arg His Ile Thr Ile Ser Glu
            165             170             175


Ala Leu Glu Ala Ala Arg Leu Asp Pro Gly Leu Gln Ala Asn Thr Arg
        180             185             190


Val Leu Ser Phe Gly Leu Glu Ala Gln Gln Gln His Val Ala Ala Pro
    195             200             205


Met Thr Pro Val Met Lys Leu Gln Glu Asp Gln Lys Val Ser Asn Gly
210             215             220


Ala Arg Asn Arg Phe His Gly Leu Ala Asp Gln Arg Leu Val Ala Arg
225             230             235             240


Val Glu Asn Gly Asp Asp Cys Ser Ser Gly Ser Ser Val Thr Thr Ser
            245             250             255


Asn Asn His Ser Val Asp Glu Ser Arg Ala Gln Ser Gly Ser Val Val
        260             265             270


Glu Ala Gln Met Asn Asn Asn Asn Asn Asn Asn Met Asn Gly Tyr Ala
    275             280             285


Cys Ile Pro Gly Val Pro Trp Pro Tyr Thr Trp Asn Pro Ala Met Pro
    290             295             300
```

```
Pro Pro Gly Phe Tyr Pro Pro Pro Gly Tyr Pro Met Pro Phe Tyr Pro
305             310             315             320
```

```
Tyr Trp Thr Ile Pro Met Leu Pro Pro His Gln Ser Ser Ser Pro Ile
            325             330             .   335
```

```
Ser Gln Lys Cys Ser Asn Thr Asn Ser Pro Thr Leu Gly Lys His Pro
        340             345             350
```

```
Arg Asp Glu Gly Ser Ser Lys Lys Asp Asn Glu Thr Glu Arg Lys Gln
        355             360             365
```

```
Lys Ala Gly Cys Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro
    370             375             380
```

```
Asn Glu Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn
385             390             395             400
```

```
Glu Ala Met Cys Lys Ala Gly Gly Met Phe Lys Gly Phe Asp His Lys
            405             410             415
```

```
Thr Lys Met Tyr Asn Asn Asp Lys Ala Glu Asn Ser Pro Val Leu Ser
            420             425         .   430
```

```
Ala Asn Pro Ala Ala Leu Ser Arg Ser His Asn Phe His Glu Gln Ile
        435             440             445
```

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<210>  127 <211>  766 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (110)..(712) <223>  G779
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```
<400>  127
gacatgcatg taagcattcg gttaattaat cgagtcaaag atatatatca gtaaatacat
60

atgtgtatat ttctggaaaa agaatatata tattgagaaa taagaaaag atg aaa atg
118
                                                     Met Lys Met
                                                      1

gaa aat ggt atg tat aaa aag aaa gga gtg tgc gac tct tgt gtc tcg
166
Glu Asn Gly Met Tyr Lys Lys Lys Gly Val Cys Asp Ser Cys Val Ser·
  5                  10                  15

tcc aaa agc aga tcc aac cac agc ccc aaa aga agc atg atg gag cct
214
Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met Met Glu Pro
20                  25                  30                  35

cag cct cac cat ctc ctc atg gat tgg aac aaa gct aat gat ctt ctc
262
Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu Leu
```

```
                        40                    45                    50

aca caa gaa cac gca gct ttt ctc aat gat cct cac cat ctc atg tta
310
Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met Leu
            55                    60                    65

gat cca cct ccc gaa acc cta att cac ttg gac gaa gac gaa gag tac
358
Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu Tyr
        70                    75                    80

gat gaa gac atg gat·gcg atg aag gag atg cag tac atg atc gcc gtc
406
Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala Val
        85                    90                    95

atg cag ccc gta gac atc gac cct gcc acg gtc cct aag ccg aac cgc
454
Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn Arg
100                   105                   110                   115

cgt aac gta agg ata agc gac gat cct cag acg gtg gtt gct cgt cgg
502
Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg Arg
                120                   125                   130

cgt cgg gaa agg atc agc gag aag atc cga att ctc aag agg atc gtg
550
Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Ile Val
            135                   140                   145

cct ggt ggt gcg aag atg gac aca gct tcc atg ctc gac gaa gcc ata
598
Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile
            150                   155                   160

cgt tac acc aag ttc ttg aaa cgg cag gtg agg att ctt cag cct cac
646
Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro His
        165                   170                   175

tct cag att gga gct cct atg gct aac ccc tct tac ctt tgt tat tac
694
Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys· Tyr Tyr
180                    185                   190                   195

cac aac tcc caa ccc tga tgaactacac agaagctcgc tagctagaca
742
His Asn Ser Gln Pro
                200

tttggtgtca tcctctcaac cttt
766


<210>  128 <211>  200 <212>  PRT <213>  Arabidopsis thaliana  <400>
128

Met Lys Met Glu Asn Gly Met Tyr Lys Lys Lys Gly Val Cys Asp Ser
1               5                    10                   15
```

```
Cys Val Ser Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met
          20              25              30

Met Glu Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn
          35              40              45

Asp Leu Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His
     50              55              60

Leu Met Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp
65              70              75              80

Glu Glu Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met
              85              90              95

Ile Ala Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys
          100             105             110

Pro Asn Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val
          115             120             125

Ala Arg Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys
     130             135             140

Arg Ile Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp
145             150             155             160

Glu Ala Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu
              165             170             175

Gln Pro His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu
          180             185             190

Cys Tyr Tyr His Asn Ser Gln Pro
          195             200
```

<210> 129 <211> 1913 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (259)..(1593) <223> G789

<400> 129
ggcaagaaga accttagcct ctctttcttc tttctctctc tctctctctg tggtactgtt
60

ctgtttcaac tttactccct cagtttcaga acaattccct atctagaaga gagataaaac
120

cgagaaggtt ttggagatag aatctttttgt tcttcttttg tccctccttg ctcgattttt
180

gttacgtgtg aagcaataaa aaaaaactga tatagctaaa tcttccatcc attcagaggc
240

ttctaaatct gatctgac atg gaa caa gtg ttt gct gat tgg aat ttt gaa
291
                      Met Glu Gln Val Phe Ala Asp Trp Asn Phe Glu
                       1   5   10

gat aat ttt cac atg tcc act aat aaa aga tca atc aga cca gaa gat
339
Asp Asn Phe His Met Ser Thr Asn Lys Arg Ser Ile Arg Pro Glu Asp
              15   20   25

gaa tta gtg gag cta ttg tgg aga gat ggt caa gtg gtt tta caa agc
387
Glu Leu Val Glu Leu Leu Trp Arg Asp Gly Gln Val Val Leu Gln Ser
          30   35   40

caa gct cgt aga gaa ccg tca gtc caa gtc caa acc cac aaa caa gaa
435
Gln Ala Arg Arg Glu Pro Ser Val Gln Val Gln Thr His Lys Gln Glu
      45   50   55

acc cta aga aaa ccc aac aat att ttt ctt gac aac caa gaa aca gta
483
Thr Leu Arg Lys Pro Asn Asn Ile Phe Leu Asp Asn Gln Glu Thr Val
60   65   70   75

caa aag cct aac tac gct gct cta gat gat caa gaa acc gtc tcc tgg
531
Gln Lys Pro Asn Tyr Ala Ala Leu Asp Asp Gln Glu Thr Val Ser Trp
                  80   85   90

ata caa tac cct ccg gat gac gtc atc gac cct ttc gaa tcc gag ttc
579
Ile Gln Tyr Pro Pro Asp Asp Val Ile Asp Pro Phe Glu Ser Glu Phe
                  95   100   105

tcc tct cat ttc ttc tct tcg atc gat cac ctc gga ggt cct gag aag
627
Ser Ser His Phe Phe Ser Ser Ile Asp His Leu Gly Gly Pro Glu Lys
          110   115   120

cca cga acg atc gaa gag aca gtt aag cat gag gct caa gcc atg gct
675
Pro Arg Thr Ile Glu Glu Thr Val Lys His Glu Ala Gln Ala Met Ala
      125   130   135

cct cct aag ttt aga tcc tcg gtt ata aca gtc gga ccg agt cat tgc
723
Pro Pro Lys Phe Arg Ser Ser Val Ile Thr Val Gly Pro Ser His Cys
140   145   150   155

ggc agc aac cag tca aca aat att cat cag gcc act aca ctt ccg gtt
771
Gly Ser Asn Gln Ser Thr Asn Ile His Gln Ala Thr Thr Leu Pro Val
                  160   165   170

tct atg agt gat aga agc aag aac gtc gaa gaa aga ctt gac act tcg
819
Ser Met Ser Asp Arg Ser Lys Asn Val Glu Glu Arg Leu Asp Thr Ser
        175   180   185

tca ggt ggc tcc tcc ggt tgc agc tat gga agg aac aac aaa gaa acc
867
Ser Gly Gly Ser Ser Gly Cys Ser Tyr Gly Arg Asn Asn Lys Glu Thr
        190   195   200

gtt agt gga aca agt gta acc att gac cgt aaa aga aaa cat gtt atg
915
Val Ser Gly Thr Ser Val Thr Ile Asp Arg Lys Arg Lys His Val Met
    205   210   215

gat gct gat caa gaa tct gtg tct caa tca gat ata ggt ttg acc tca
963
Asp Ala Asp Gln Glu Ser Val Ser Gln Ser Asp Ile Gly Leu Thr Ser
220   225   230   235

acc gat gat caa acc atg ggt aac aaa tcg agc caa cgg tca gga tct
1011
Thr Asp Asp Gln Thr Met Gly Asn Lys Ser Ser Gln Arg Ser Gly Ser
        240   245   250

act cga aga agc cgt gca gct gaa gtt cat aat ctc tca gaa agg agg
1059
Thr Arg Arg Ser Arg Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg
        255   260   265

agg aga gat cgg atc aat gaa aga atg aaa gct ctt caa gaa ctc ata
1107
Arg Arg Asp Arg Ile Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile
        270   275   280

cct cac tgc agc aga aca gat aaa gct tcg ata ttg gat gaa gca att
1155
Pro His Cys Ser Arg Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile
    285   290   295

gat tac tta aaa tca ctt caa atg caa ctc caa gtg atg tgg atg gga
1203
Asp Tyr Leu Lys Ser Leu Gln Met Gln Leu Gln Val Met Trp Met Gly
300   305   310   315

agt gga atg gcg gcg gcg gca gca gca gca gca agt ccg atg atg ttt
1251
Ser Gly Met Ala Ala Ala Ala Ala Ala Ala Ala Ser Pro Met Met Phe
        320   325   330

ccc ggg gta caa tca tct cca tac att aat cag atg gct atg caa agt
1299
Pro Gly Val Gln Ser Ser Pro Tyr Ile Asn Gln Met Ala Met Gln Ser
        335   340   345

cag atg caa ttg tct caa ttc ccg gtt atg aac cgg tcc gct ccg cag
1347
Gln Met Gln Leu Ser Gln Phe Pro Val Met Asn Arg Ser Ala Pro Gln
        350   355   360

228

```
aac cat ccc ggt tta gta tgt caa aac ccg gta cag ttg cag ctc caa
1395
Asn His Pro Gly Leu Val Cys Gln Asn Pro Val Gln Leu Gln Leu Gln
    365                 370                 375

gca cag aac caa atc tta tcg gag cag ctc gct agg tac atg ggc ggg   .
1443
Ala Gln Asn Gln Ile Leu Ser Glu Gln Leu Ala Arg Tyr Met Gly Gly
380                 385                 390                 395

att ccc cag atg ccg ccg gcg gga aat cag atg cag acc gtg caa caa
1491
Ile Pro Gln Met Pro Pro Ala Gly Asn Gln Met Gln Thr Val Gln Gln
                400                 405                 410

caa cca gcg gac atg ttg gga ttt gga tct ccg gcg gga ccg caa agt
1539
Gln Pro Ala Asp Met Leu Gly Phe Gly Ser Pro Ala Gly Pro Gln Ser
            415                 420                 425

caa ctg tcg gca ccg gcg acc acc gac agt ctt cat atg ggt aaa ata
1587
Gln Leu Ser Ala Pro Ala Thr Thr Asp Ser Leu His Met Gly Lys Ile
            430                 435                 440

ggc tga cttggcatat agttttcctc cgaaattatt cttcttacag ttggtgattg
1643
Gly

ttatttattt ttggtcgcct aagcaagcat aaaagctaag tcaaatgtat tatagagatc
1703

taataagtta gtctcatact tataacttat ttttaaacag ttgaattata gtatcaatca
1763

agtgttggga acctaaagat catacatgtg tcaatacttt tatatttgtt ctcaaggttc
1823

atcagaaaaa caaaataaaa aggatagact aggcctgcat ttgacattat catgggcttt
1883

tttgggtcta tgaatatgaa cattaacccc
1913


<210>  130 <211>  444 <212>  PRT <213>  Arabidopsis thaliana  <400>
130

Met Glu Gln Val Phe Ala Asp Trp Asn Phe Glu Asp Asn Phe His Met
1               5                   10                  15

Ser Thr Asn Lys Arg Ser Ile Arg Pro Glu Asp Glu Leu Val Glu Leu
            20                  25                  30

Leu Trp Arg Asp Gly Gln Val Val Leu Gln Ser Gln Ala Arg Arg Glu
        35                  40                  45
```

Pro Ser Val Gln Val Gln Thr His Lys Gln Glu Thr Leu Arg Lys Pro
    50   55   60

Asn Asn Ile Phe Leu Asp Asn Gln Glu Thr Val Gln Lys Pro Asn Tyr
65   70   75   80

Ala Ala Leu Asp Asp Gln Glu Thr Val Ser Trp Ile Gln Tyr Pro Pro
            85   90   95

Asp Asp Val Ile Asp Pro Phe Glu Ser Glu Phe Ser Ser His Phe Phe
            100   105   110

Ser Ser Ile Asp His Leu Gly Gly Pro Glu Lys Pro Arg Thr Ile Glu
            115   120   125

Glu Thr Val Lys His Glu Ala Gln Ala Met Ala Pro Pro Lys Phe Arg
        130   135   140

Ser Ser Val Ile Thr Val Gly Pro Ser His Cys Gly Ser Asn Gln Ser
145   150   155   160

Thr Asn Ile His Gln Ala Thr Thr Leu Pro Val Ser Met Ser Asp Arg
            165   170   175

Ser Lys Asn Val Glu Glu Arg Leu Asp Thr Ser Ser Gly Gly Ser Ser
            180   185   190

Gly Cys Ser Tyr Gly Arg Asn Asn Lys Glu Thr Val Ser Gly Thr Ser
        195   200   205

Val Thr Ile Asp Arg Lys Arg Lys His Val Met Asp Ala Asp Gln Glu
        210   215   220

Ser Val Ser Gln Ser Asp Ile Gly Leu Thr Ser Thr Asp Asp Gln Thr
225   230   235   240

Met Gly Asn Lys Ser Ser Gln Arg Ser Gly Ser Thr Arg Arg Ser Arg
            245   250   255

Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg Arg Arg Asp Arg Ile
        260   265   270

Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile Pro His Cys Ser Arg
        275   280   285

Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile Asp Tyr Leu Lys Ser

230

```
            290                    295                    300
```

```
Leu Gln Met Gln Leu Gln Val Met Trp Met Gly Ser Gly Met Ala Ala
305                 310                 315                 320
```

```
Ala Ala Ala Ala Ala Ala Ser Pro Met Met Phe Pro Gly Val Gln Ser
                325                 330                 335
```

```
Ser Pro Tyr Ile Asn Gln Met Ala Met Gln Ser Gln Met Gln Leu Ser
            340                 345                 350
```

```
Gln Phe Pro Val Met Asn Arg Ser Ala Pro Gln Asn His Pro Gly Leu
            355                 360                 365
```

```
Val Cys Gln Asn Pro Val Gln Leu Gln Leu Gln Ala Gln Asn Gln Ile
        370                 375                 380
```

```
Leu Ser Glu Gln Leu Ala Arg Tyr Met Gly Gly Ile Pro Gln Met Pro
385                 390                 395                 400
```

```
Pro Ala Gly Asn Gln Met Gln Thr Val Gln Gln Gln Pro Ala Asp Met
                405                 410                 415
```

```
Leu Gly Phe Gly Ser Pro Ala Gly Pro Gln Ser Gln Leu Ser Ala Pro
            420                 425                 430
```

```
Ala Thr Thr Asp Ser Leu His Met Gly Lys Ile Gly
            435                 440
```

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<210>   131 <211>   1107 <212>   DNA <213>   Arabidopsis thaliana   <220>
<221>   CDS <222>   (173)..(877) <223>   G791
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60

ctttcgatct ctctgatcgc cgccgggaac attcaatttc ccgggagttc aacaaaaaaa
120

aaactctccg tttttatttt tcccccttttt tcaccggtgg aagtttccgg ag atg gtg
178
                                                            Met Val
                                                             1

tca ccc gaa aac gct aat tgg att tgt gac ttg atc gat gct gat tac
226
Ser Pro Glu Asn Ala Asn Trp Ile Cys Asp Leu Ile Asp Ala Asp Tyr
        5                   10                  15

gga agt ttc aca atc caa ggt cct ggt ttc tct tgg cct gtt cag caa
274
```

```
           Gly Ser Phe Thr Ile Gln Gly Pro Gly Phe Ser Trp Pro Val Gln Gln
               20                  25                  30

cct att ggt gtt tct tct aac tcc agt gct gga gtt gat ggc tcg gct
322
Pro Ile Gly Val Ser Ser Asn Ser Ser Ala Gly Val Asp Gly Ser Ala
35                  40                  45                  50

gga aac tca gaa gct agc aaa gaa cct gga tcc aaa aag agg ggg aga
370
Gly Asn Ser Glu Ala Ser Lys Glu Pro Gly Ser Lys Lys Arg Gly Arg
                55                  60                  65

tgt gaa tca tcc tct gcc act agc tcg aaa gca tgt aga gag aag cag
418
Cys Glu Ser Ser Ser Ala Thr Ser Ser Lys Ala Cys Arg Glu Lys Gln
                70                  75                  80

cga cgg gac agg ttg aat gac aag ttt atg gaa ttg ggt gca att ttg
466
Arg Arg Asp Arg Leu Asn Asp Lys Phe Met Glu Leu Gly Ala Ile Leu
            85                  90                  95

gag cct gga aat cct ccc aaa aca gac aag gct gct atc ttg gtt gat
514
Glu Pro Gly Asn Pro Pro Lys Thr Asp Lys Ala Ala Ile Leu Val Asp
        100                 105                 110

gct gtc cgc atg gtg aca cag cta cgg ggc gag gcc cag aag ctg aag
562
Ala Val Arg Met Val Thr Gln Leu Arg Gly Glu Ala Gln Lys Leu Lys
115                 120                 125                 130

gac tcc aat tca agt ctt cag gac aaa atc aaa gag tta aag act gag
610
Asp Ser Asn Ser Ser Leu Gln Asp Lys Ile Lys Glu Leu Lys Thr Glu
                135                 140                 145

aaa aac gag ctg cga gat gag aaa cag agg ctg aag aca gag aaa gaa
658
Lys Asn Glu Leu Arg Asp Glu Lys Gln Arg Leu Lys Thr Glu Lys Glu
                150                 155                 160

aag ctg gag cag cag ctg aaa gcc atg aat gct cct caa cca agt ttt
706
Lys Leu Glu Gln Gln Leu Lys Ala Met Asn Ala Pro Gln Pro Ser Phe
            165                 170                 175

ttc cca gcc cca cct atg atg cct act gct ttt gct tca gcg caa ggc
754
Phe Pro Ala Pro Pro Met Met Pro Thr Ala Phe Ala Ser Ala Gln Gly
        180                 185                 190

caa gct cct gga aac aag atg gtg cca atc atc agt tac cca gga gtt
802
Gln Ala Pro Gly Asn Lys Met Val Pro Ile Ile Ser Tyr Pro Gly Val
195                 200                 205                 210

gcc atg tgg cag ttc atg cct cct gct tca gtc gat act tct cag gat
850
Ala Met Trp Gln Phe Met Pro Pro Ala Ser Val Asp Thr Ser Gln Asp
```

232

                    215   220   225

cat gtc ctt cgt cct cct gtt gct taa tcaagaaaaa tcatcaaccg
897
His Val Leu Arg Pro Pro Val Ala
                230

gtttgcttct tgcttccgct taaaagaaaa gtctccattt gttttgctct cctctctttc
957

tcggctttct tagtcttatc cttttgcttt gtcgtgttat' catcgtaact gttatctgtt
1017

gaacaatgat atgacattgt aaactccaat tgcttcgcgc aatgttatct attcacatgt
1077

aaatttaagt agagtttggc aaaaaaaaaa
1107

<210> 132 <211> 234 <212> PRT <213> Arabidopsis thaliana <400>
132

Met Val Ser Pro Glu Asn Ala Asn Trp Ile Cys Asp Leu Ile Asp Ala
1   5   10   15

Asp Tyr Gly Ser Phe Thr Ile Gln Gly Pro Gly Phe Ser Trp Pro Val
            20   25   30

Gln Gln Pro Ile Gly Val Ser Ser Asn Ser Ser Ala Gly Val Asp Gly
        35   40   45

Ser Ala Gly Asn Ser Glu Ala Ser Lys Glu Pro Gly Ser Lys Lys Arg
    50   55   60

Gly Arg Cys Glu Ser Ser Ser Ala Thr Ser Ser Lys Ala Cys Arg Glu
65   70   75   80

Lys Gln Arg Arg Asp Arg Leu Asn Asp Lys Phe Met Glu Leu Gly Ala
                85   90   95

Ile Leu Glu Pro Gly Asn Pro Pro Lys Thr Asp Lys Ala Ala Ile Leu
            100   105   110

Val Asp Ala Val Arg Met Val Thr Gln Leu Arg Gly Glu Ala Gln Lys
        115   120   125

Leu Lys Asp Ser Asn Ser Ser Leu Gln Asp Lys Ile Lys Glu Leu Lys
    130   135   140

Thr Glu Lys Asn Glu Leu Arg Asp Glu Lys Gln Arg Leu Lys Thr Glu
145   150   155   160

```
Lys Glu Lys Leu Glu Gln Gln Leu Lys Ala Met Asn Ala Pro Gln Pro
            165                 170                 175

Ser Phe Phe Pro Ala Pro Pro Met Met Pro Thr Ala Phe Ala Ser Ala
            180                 185                 190

Gln Gly Gln Ala Pro Gly Asn Lys Met Val Pro Ile Ile Ser Tyr Pro
            195                 200                 205

Gly Val Ala Met Trp Gln Phe Met Pro Pro Ala Ser Val Asp Thr Ser
        210                 215                 220

Gln Asp His Val Leu Arg Pro Pro Val Ala
225                 230
```

<210> 133 <211> 1009 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (27)..(746) <223> 6801

<400> 133

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gatagtgata acgaaatcct aattcc atg gcc gac aac gac gga gca gtg agt
53
                               Met Ala Asp Asn Asp Gly Ala Val Ser
                               1                   5

aac ggc atc ata gtc gag cag acg tca aac aaa gga cct ctt aac gcc
101
Asn Gly Ile Ile Val Glu Gln Thr Ser Asn Lys Gly Pro Leu Asn Ala
10                  15                  20                  25

gtt aag aaa cca ccg tct aaa gat cga cac agc aaa gtt gac gga aga
149
Val Lys Lys Pro Pro Ser Lys Asp Arg His Ser Lys Val Asp Gly Arg
                30                  35                  40

gga aga agg att cgt atg cca atc att tgc gca gct cga gtt ttt caa
197
Gly Arg Arg Ile Arg Met Pro Ile Ile Cys Ala Ala Arg Val Phe Gln
            45                  50                  55

ttg acc aga gag tta ggt cac aag tcc gat ggt caa acc ata gag tgg
245
Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Gln Thr Ile Glu Trp
            60                  65                  70

ctt ctc cgt caa gct gag cct tct atc ata gcc gcc act gga act ggc
293
Leu Leu Arg Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly
        75                  80                  85

act act ccg gcg agt ttc tcc act gct tct ctc tcc act tct tct ccg
341
Thr Thr Pro Ala Ser Phe Ser Thr Ala Ser Leu Ser Thr Ser Ser Pro
90                  95                  100                 105
```

ttt act ctc ggg aaa cgt gtc gtc aga gcg gag gaa gga gaa tcc ggc
389
Phe Thr Leu Gly Lys Arg Val Val Arg Ala Glu Glu Gly Glu Ser Gly
                  110   115   120

ggc gga gga gga gga ggg tta aca gtg gga cac aca atg ggg act tcg
437
Gly Gly Gly Gly Gly Gly Leu Thr Val Gly His Thr Met Gly Thr Ser
                  125   130   135

tta atg ggt ggt ggt ggt tct ggt ggg ttt tgg gct gtt ccg gcg agg
485
Leu Met Gly Gly Gly Gly Ser Gly Gly Phe Trp Ala Val Pro Ala Arg
          140   145   150

ccg gat ttc gga caa gtc tgg agc ttt gca acc gga gct cca ccg gaa
533
Pro Asp Phe Gly Gln Val Trp Ser Phe Ala Thr Gly Ala Pro Pro Glu
      155   160   165

atg gtt ttt gcg cag cag cag caa cca gct aca ctc ttc gtc cgc cac
581
Met Val Phe Ala Gln Gln Gln Gln Pro Ala Thr Leu Phe Val Arg His
170   175   180   185

cag cag caa cag caa gct tcc gcc gcc gca gca gct gca atg ggt gag
629
Gln Gln Gln Gln Gln Ala Ser Ala Ala Ala Ala Ala Ala Met Gly Glu
              190   195   200

gct tca gca gct aga gtt ggg aat tat ctt ccg ggt cat cat ctc aat
677
Ala Ser Ala Ala Arg Val Gly Asn Tyr Leu Pro Gly His His Leu Asn
          205   210   215

ttg ctt gct tct ttg tct ggt gga gct aac ggg tcg ggt cgg agg gaa
725
Leu Leu Ala Ser Leu Ser Gly Gly Ala Asn Gly Ser Gly Arg Arg Glu
          220   225   230

gac gac cac gaa cca cgt tga gaaatggtat tgtctttttg gtaatgtata
776
Asp Asp His Glu Pro Arg
      235

gaaaaattcc tatgttttat gtcatcgaaa gtgtttagaa agtacctcta atttgcggtt
836

tcttttgctc cttttttact taatttaagc ttattgcttg tttgattagg gttttagggt
896

ttaagaatat ttggtctcgt taatttgttt cggagagtga tagaaagaga gagagattga
956

ttgattgttg tacctaaaac gctataaaag ctctgttttt actagcgaaa aaa
1009

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134

235

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Met Ala Asp Asn Asp Gly Ala Val Ser Asn Gly Ile Ile Val Glu Gln
1               5                   10                  15


Thr Ser Asn Lys Gly Pro Leu Asn Ala Val Lys Lys Pro Pro Ser Lys
            20                  25                  30


Asp Arg His Ser Lys Val Asp Gly Arg Gly Arg Arg Ile Arg Met Pro
        35                  40                  45


Ile Ile Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu Gly His
    50                  55                  60


Lys Ser Asp Gly Gln Thr Ile Glu Trp Leu Leu Arg Gln Ala Glu Pro
65                  70                  75                  80


Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Thr Pro Ala Ser Phe Ser
                85                  90                  95


Thr Ala Ser Leu Ser Thr Ser Ser Pro Phe Thr Leu Gly Lys Arg Val
            100                 105                 110


Val Arg Ala Glu Glu Gly Glu Ser Gly Gly Gly Gly Gly Gly Gly Leu
            115                 120                 125


Thr Val Gly His Thr Met Gly Thr Ser Leu Met Gly Gly Gly Gly Ser
    130                 135                 140


Gly Gly Phe Trp Ala Val Pro Ala Arg Pro Asp Phe Gly Gln Val Trp
145                 150                 155                 160


Ser Phe Ala Thr Gly Ala Pro Pro Glu Met Val Phe Ala Gln Gln Gln
            165                 170                 175


Gln Pro Ala Thr Leu Phe Val Arg His Gln Gln Gln Gln Gln Ala Ser
            180                 185                 190


Ala Ala Ala Ala Ala Ala Met Gly Glu Ala Ser Ala Ala Arg Val Gly
        195                 200                 205


Asn Tyr Leu Pro Gly His His Leu Asn Leu Leu Ala Ser Leu Ser Gly
    210                 215                 220


Gly Ala Asn Gly Ser Gly Arg Arg Glu Asp Asp His Glu Pro Arg
225                 230                 235
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236

<210> 135 <211> 1263 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (114)..(1139) <223> G804

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60

ttccattttc ttgtgtgttt ttttccccat aatttataaa ttttataagc aat atg
116
                                                                    Met
                                                                    1

gag tcc cac aac aac aac cag agc aac aac aac acc act ggt tcg gcc
164
Glu Ser His Asn Asn Asn Gln Ser Asn Asn Asn Thr Thr Gly Ser Ala
            5   10   15

cat ctg gtc cca tcc atg gga cca atc tcc ggt tca gtc tca tta acc
212
His Leu Val Pro Ser Met Gly Pro Ile Ser Gly Ser Val Ser Leu Thr
        20   25   30

acc act gct cca aac tcc act acc acc acc gtc acc gcc gct aaa aca
260
Thr Thr Ala Pro Asn Ser Thr Thr Thr Thr Val Thr Ala Ala Lys Thr
    35   40   45

ccc gca aaa cga ccg tcc aag gac cgt cac atc aaa gta gac gga cgt
308
Pro Ala Lys Arg Pro Ser Lys Asp Arg His Ile Lys Val Asp Gly Arg
50   55   60   65

ggc cgg agg ata cgt atg ccg gct atc tgc gca gca cgt gtc ttc caa
356
Gly Arg Arg Ile Arg Met Pro Ala Ile Cys Ala Ala Arg Val Phe Gln
                70   75   80

cta aca cgt gag tta caa cac aaa tcg gac ggc gag act ata gag tgg
404
Leu Thr Arg Glu Leu Gln His Lys Ser Asp Gly Glu Thr Ile Glu Trp
            85   90   95

ctg ctc caa caa gcg gag cca gct atc atc gca gcc acc gga act gga
452
Leu Leu Gln Gln Ala Glu Pro Ala Ile Ile Ala Ala Thr Gly Thr Gly
        100   105   110

acc ata ccg gcg aat atc tct act ttg aac atc tct ctt cga agc agt
500
Thr Ile Pro Ala Asn Ile Ser Thr Leu Asn Ile Ser Leu Arg Ser Ser
    115   120   125

ggc tct act ctt tca gct cca ctg tct aaa tct ttc cac atg gga aga
548
Gly Ser Thr Leu Ser Ala Pro Leu Ser Lys Ser Phe His Met Gly Arg
130   135   140   145

gcg gct caa aac gct gcc gtt ttt ggg ttc cag caa cag ctt tat cat
596
Ala Ala Gln Asn Ala Ala Val Phe Gly Phe Gln Gln Gln Leu Tyr His
                150   155   160

237

```
cct cat cat atc acg aca gat tct tct tct tct tct ctt ccc aaa aca
644
Pro His His Ile Thr Thr Asp Ser Ser Ser Ser Ser Leu Pro Lys Thr
            165             170             175

ttc cgt gaa gaa gat ctt ttt aaa gat cct aat ttt cta gat caa gaa
692
Phe Arg Glu Glu Asp Leu Phe Lys Asp Pro Asn Phe Leu Asp Gln Glu
        180             185             190

ccc ggt tca aga tca cct aaa ccg gga tcc gaa gct cct gat caa gat
740
Pro Gly Ser Arg Ser Pro Lys Pro Gly Ser Glu Ala Pro Asp Gln Asp
        195             200             205

ccg ggt tcg acc cgg tca aga aca caa aat atg ata ccg ccg atg tgg
788
Pro Gly Ser Thr Arg Ser Arg Thr Gln Asn Met Ile Pro Pro Met Trp
210             215             220             225

gca cta gcg cca acg cca gcc tcc aca aac gga ggt agt gct ttt tgg
836
Ala Leu Ala Pro Thr Pro Ala Ser Thr Asn Gly Gly Ser Ala Phe Trp
            230             235             240

atg tta cca gtc gga gga gga gga ggt ccg gct aac gtt cag gat cca
884
Met Leu Pro Val Gly Gly Gly Gly Gly Pro Ala Asn Val Gln Asp Pro
            245             250             255

tca cag cac atg tgg gcg ttt aat ccg ggt cat tac ccg ggt cga atc
932
Ser Gln His Met Trp Ala Phe Asn Pro Gly His Tyr Pro Gly Arg Ile
            260             265             270

ggg tcg gtt cag cta ggg tct atg tta gtg gga ggt caa cag tta ggg
980
Gly Ser Val Gln Leu Gly Ser Met Leu Val Gly Gly Gln Gln Leu Gly
        275             280             285

tta ggt gtt gca gaa aat aac aat ttg ggg cta ttt tcc ggc gga gga
1028
Leu Gly Val Ala Glu Asn Asn Asn Leu Gly Leu Phe Ser Gly Gly Gly
290             295             300             305

gga gac ggt ggt cgg gtt ggt ctc gga atg agt ctt gag caa aag cct
1076
Gly Asp Gly Gly Arg Val Gly Leu Gly Met Ser Leu Glu Gln Lys Pro
            310             315             320

caa cat caa gtg agt gat cat gct act aga gac caa aat cct act ata
1124
Gln His Gln Val Ser Asp His Ala Thr Arg Asp Gln Asn Pro Thr Ile
            325             330             335

gat ggt tct cct tga aagacttcat gatttctttg gtttttaaaa agtgtgaatg
1179
Asp Gly Ser Pro
            340
```

tgtgatttat tgcaactttt gttgaggact ccaatgttaa tatgggtttt agggttggct
1239

tttcgggatt gccaaattgt tatt
1263

<210> 136 <211> 341 <212> PRT <213> Arabidopsis thaliana <400>
136

Met Glu Ser His Asn Asn Asn Gln Ser Asn Asn Asn Thr Thr Gly Ser
1   5   10   15

Ala His Leu Val Pro Ser Met Gly Pro Ile Ser Gly Ser Val Ser Leu
            20   25   30

Thr Thr Thr Ala Pro Asn Ser Thr Thr Thr Thr Val Thr Ala Ala Lys
            35   40   45

Thr Pro Ala Lys Arg Pro Ser Lys Asp Arg His Ile Lys Val Asp Gly
        50   55   60

Arg Gly Arg Arg Ile Arg Met Pro Ala Ile Cys Ala Ala Arg Val Phe
65   70   75   80

Gln Leu Thr Arg Glu Leu Gln His Lys Ser Asp Gly Glu Thr Ile Glu
                85   90   95

Trp Leu Leu Gln Gln Ala Glu Pro Ala Ile Ile Ala Ala Thr Gly Thr
                100   105   110

Gly Thr Ile Pro Ala Asn Ile Ser Thr Leu Asn Ile Ser Leu Arg Ser
        115   120   125

Ser Gly Ser Thr Leu Ser Ala Pro Leu Ser Lys Ser Phe His Met Gly
    130   135   140

Arg Ala Ala Gln Asn Ala Ala Val Phe Gly Phe Gln Gln Gln Leu Tyr
145   150   155   160

His Pro His His Ile Thr Thr Asp Ser Ser Ser Ser Ser Leu Pro Lys
                165   170   175

Thr Phe Arg Glu Glu Asp Leu Phe Lys Asp Pro Asn Phe Leu Asp Gln
                180   185   190

Glu Pro Gly Ser Arg Ser Pro Lys Pro Gly Ser Glu Ala Pro Asp Gln
        195   200   205

```
Asp Pro Gly Ser Thr Arg Ser Arg Thr Gln Asn Met Ile Pro Pro Met
    210             215             220
```

```
Trp Ala Leu Ala Pro Thr Pro Ala Ser Thr Asn Gly Gly Ser Ala Phe
225             230             235             240
```

```
Trp Met Leu Pro Val Gly Gly Gly Gly Pro Ala Asn Val Gln Asp
            245             250             255
```

```
Pro Ser Gln His Met Trp Ala Phe Asn Pro Gly His Tyr Pro Gly Arg
            260             265             270
```

```
Ile Gly Ser Val Gln Leu Gly Ser Met Leu Val Gly Gly Gln Gln Leu
        275             280             285
```

```
Gly Leu Gly Val Ala Glu Asn Asn Asn Leu Gly Leu Phe Ser Gly Gly
    290             295             300
```

```
Gly Gly Asp Gly Gly Arg Val Gly Leu Gly Met Ser Leu Glu Gln Lys
305             310             315             320
```

```
Pro Gln His Gln Val Ser Asp His Ala Thr Arg Asp Gln Asn Pro Thr
            325             330             335
```

```
Ile Asp Gly Ser Pro
            340
```

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<210> 137 <211> 1231 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (107)..(1084) <223> G805
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<400> 137
tatagagaga ggaaaaaact atggctcaca taaagatcta acagagacag tagtatagtc
60

ccacttcccc cccaccaaag cttcgatcat catcatcatc atcatc atg gat ccg
115
                                            Met Asp Pro
                                             1

gat ccg gat cat aac cat cga ccc aac ttc cct ctc cag ctt ctt gat
163
Asp Pro Asp His Asn His Arg Pro Asn Phe Pro Leu Gln Leu Leu Asp
    5               10              15

tct tct acc tcc tcc tct tcc act tcc tta gcc atc atc tct act act
211
Ser Ser Thr Ser Ser Ser Ser Thr Ser Leu Ala Ile Ile Ser Thr Thr
20              25              30              35

tcc gaa cct aac tcc gaa cct aag aag cct cct cct aaa cga acc tct
259
```

240

Ser Glu Pro Asn Ser Glu Pro Lys Lys Pro Pro Pro Lys Arg Thr Ser
          40   45   50

act aaa gac cga cac acc aaa gtc gaa ggc cga ggc cgt cgg atc cgt
307
Thr Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile Arg
          55   60   65

atg cct gcc atg tgt gct gca cgt gtc ttt cag ctc aca cgt gag ctt
355
Met Pro Ala Met Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu
          70   75   80

ggt cac aaa tcc gac ggt gaa act att gag tgg cta ctc caa caa gca
403
Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln Ala
    85   90   95

gaa cca gcg gtt ata gcc gct aca ggg act gga acc att ccg gct aac
451
Glu Pro Ala Val Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Asn
100   105   110   115

ttc act tct tta aac atc tca ctt cgt agc tca aga tct tct ctc tct
499
Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Arg Ser Ser Leu Ser
              120   125   130

gct gct cat ctt cgt aca act cct agt agc tat tac ttt cat tca cca
547
Ala Ala His Leu Arg Thr Thr Pro Ser Ser Tyr Tyr Phe His Ser Pro
              135   140   145

cat cag tcc atg act cat cat ctt caa cat cag cat cag gtt cgt ccc
595
His Gln Ser Met Thr His His Leu Gln His Gln His Gln Val Arg Pro
          150   155   160

aag aac gag tca cat tct tcg tct tct tct tct tca cag ctt tta gat
643
Lys Asn Glu Ser His Ser Ser Ser Ser Ser Ser Ser Gln Leu Leu Asp
    165   170   175

cac aac caa atg ggt aac tat cta gta caa tca act gct gga tct tta
691
His Asn Gln Met Gly Asn Tyr Leu Val Gln Ser Thr Ala Gly Ser Leu
180   185   190   195

cct acg agt cag agt cct gca acg gca ccg ttt tgg agt agt ggt gac
739
Pro Thr Ser Gln Ser Pro Ala Thr Ala Pro Phe Trp Ser Ser Gly Asp
              200   205   210

aac aca cag aat ctt tgg gct ttt aat att aat cct cat cat tcc ggt
787
Asn Thr Gln Asn Leu Trp Ala Phe Asn Ile Asn Pro His His Ser Gly
              215   220   225

gtt gtc gcc gga gat gtt tac aac ccc aac agt ggt ggt agt ggc ggc
835
Val Val Ala Gly Asp Val Tyr Asn Pro Asn Ser Gly Gly Ser Gly Gly

241

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            230                    235                    240

ggt agt gga gtt cat ttg atg aat ttt gca gct cct att gct ttg ttt
883
Gly Ser Gly Val His Leu Met Asn Phe Ala Ala Pro Ile Ala Leu Phe
    245                    250                    255


tct gga cag cct ttg gct tct ggt tat gga gga gga gga ggt ggc ggt
931
Ser Gly Gln Pro Leu Ala Ser Gly Tyr Gly Gly Gly Gly Gly Gly Gly
260                    265                    270                275


gga gaa cat agc cat tat gga gtt tta gcg gcg ttg aat gct gct tac
979
Gly Glu His Ser His Tyr Gly Val Leu Ala Ala Leu Asn Ala Ala Tyr
                280                    285                    290


cga ccg gtg gcg gag acg ggg aac cat aac aac aac cag caa aac cgt
1027
Arg Pro Val Ala Glu Thr Gly Asn His Asn Asn Asn Gln Gln Asn Arg
                295                    300                    305


gac gga gat cat cat cac aac cat caa gaa gat gga agc acc agt cat
1075
Asp Gly Asp His His His Asn His Gln Glu Asp Gly Ser Thr Ser His
            310                    315                    320


cat tcc tag gcaaacatac acaaacaaat atattctgtg agatttattt
1124
His Ser
    325


ttcttttttt gtcctttcgt ttgtttgttt gttcttaaca agcgtgtttt ttttgcattg
1184


cttctttttc atatattttt atttatttct aaattctaat aaaaaaa
1231


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138


Met Asp Pro Asp Pro Asp His Asn His Arg Pro Asn Phe Pro Leu Gln
1                 5                  10                 15


Leu Leu Asp Ser Ser Thr Ser Ser Ser Thr Ser Leu Ala Ile Ile
            20                 25                 30


Ser Thr Thr Ser Glu Pro Asn Ser Glu Pro Lys Lys Pro Pro Pro Lys
        35                 40                 45


Arg Thr Ser Thr Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg
    50                 55                 60


Arg Ile Arg Met Pro Ala Met Cys Ala Ala Arg Val Phe Gln Leu Thr
65                 70                 75                 80
```

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Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu
             85                  90                  95


Gln Gln Ala Glu Pro Ala Val Ile Ala Ala Thr Gly Thr Gly Thr Ile
             100             105                 110


Pro Ala Asn Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Arg Ser
             115             120                 125


Ser Leu Ser Ala Ala His Leu Arg Thr Thr Pro Ser Ser Tyr Tyr Phe
     130             135                 140


His Ser Pro His Gln Ser Met Thr His His Leu Gln His Gln His Gln
145             150                 155                 160


Val Arg Pro Lys Asn Glu Ser His Ser Ser Ser Ser Ser Ser Ser Gln
             165             170                 175


Leu Leu Asp His Asn Gln Met Gly Asn Tyr Leu Val Gln Ser Thr Ala
             180             185                 190


Gly Ser Leu Pro Thr Ser Gln Ser Pro Ala Thr Ala Pro Phe Trp Ser
             195             200                 205


Ser Gly Asp Asn Thr Gln Asn Leu Trp Ala Phe Asn Ile Asn Pro His
     210             215                 220


His Ser Gly Val Val Ala Gly Asp Val Tyr Asn Pro Asn Ser Gly Gly
225             230                 235                 240


Ser Gly Gly Gly Ser Gly Val His Leu Met Asn Phe Ala Ala Pro Ile
             245             250                 255


Ala Leu Phe Ser Gly Gln Pro Leu Ala Ser Gly Tyr Gly Gly Gly Gly
             260             265                 270


Gly Gly Gly Gly Glu His Ser His Tyr Gly Val Leu Ala Ala Leu Asn
             275             280                 285


Ala Ala Tyr Arg Pro Val Ala Glu Thr Gly Asn His Asn Asn Asn Gln
     290             295                 300


Gln Asn Arg Asp Gly Asp His His His Asn His Gln Glu Asp Gly Ser
305             310                 315                 320
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243

Thr Ser His His Ser
                    325

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cagg atg atg aac ccg ttt ctc ccg gaa ggc tgc gat cca cca cca cca
109
     Met Met Asn Pro Phe Leu Pro Glu Gly Cys Asp Pro Pro Pro Pro
      1   5   10   15

cca caa cca atg gag ggt tta cac gaa aat gct cca cct cca ttt ctg
157
Pro Gln Pro Met Glu Gly Leu His Glu Asn Ala Pro Pro Pro Phe Leu
             20   25   30

acc aag aca ttt gag atg gtg gat gat cca aac act gac cac atc gta
205
Thr Lys Thr Phe Glu Met Val Asp Asp Pro Asn Thr Asp His Ile Val
            35   40   45

tct tgg aac aga gga gga aca agt ttt gtc gtc tgg gat ttg cat tct
253
Ser Trp Asn Arg Gly Gly Thr Ser Phe Val Val Trp Asp Leu His Ser
        50   55   60

ttc tcc acg att ctc ctt cct cgt cat ttc aaa cac agc aat ttc tca
301
Phe Ser Thr Ile Leu Leu Pro Arg His Phe Lys His Ser Asn Phe Ser
    65   70   75

agt ttc atc aga caa ctc aat act tat ggt ttc aga aag ata gaa gca
349
Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala
80   85   90   95

gag aga tgg gaa ttt gca aac gaa gag ttt ttg tta gga caa aga cag
397
Glu Arg Trp Glu Phe Ala Asn Glu Glu Phe Leu Leu Gly Gln Arg Gln
                100   105   110

ttg ttg aag aac atc aag agg aga aac cct ttt act cca tca tct tca
445
Leu Leu Lys Asn Ile Lys Arg Arg Asn Pro Phe Thr Pro Ser Ser Ser
            115   120   125

cca agc cat gac gct tgc aac gag ctt cgc aga gag aag caa gtg cta
493
Pro Ser His Asp Ala Cys Asn Glu Leu Arg Arg Glu Lys Gln Val Leu
        130   135   140

atg atg gag ata gtg agt cta aga cag cag caa caa aca acg aaa agc
541
Met Met Glu Ile Val Ser Leu Arg Gln Gln Gln Gln Thr Thr Lys Ser
    145   150   155

244

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tac atc aaa gct atg gaa cag agg ata gaa gga aca gag agg aaa cag
589
Tyr Ile Lys Ala Met Glu Gln Arg Ile Glu Gly Thr Glu Arg Lys Gln
160                 165                 170                 175

aga caa atg atg tcg ttt ctg gct aga gca atg cag agt cct tcg ttt
637
Arg Gln Met Met Ser Phe Leu Ala Arg Ala Met Gln Ser Pro Ser Phe
                180                 185                 190

ttg cat cag ttg ttg aaa caa aga gat aaa aaa att aag gag ctt gag
685
Leu His Gln Leu Leu Lys Gln Arg Asp Lys Lys Ile Lys Glu Leu Glu
                195                 200                 205

gat aat gag tca gca aag agg aaa aga ggt tct tct tcg atg tcg gaa
733
Asp Asn Glu Ser Ala Lys Arg Lys Arg Gly Ser Ser Ser Met Ser Glu
            210                 215                 220

ttg gaa gtt ttg gct ttg gag atg caa ggg cat gga aaa cag agg aat
781
Leu Glu Val Leu Ala Leu Glu Met Gln Gly His Gly Lys Gln Arg Asn
        225                 230                 235

atg ttg gaa gaa gag gat cat caa ctg gtg gta gag aga gag ttg gat
829
Met Leu Glu Glu Glu Asp His Gln Leu Val Val Glu Arg Glu Leu Asp
240                 245                 250                 255

gat ggt ttc tgg gaa gag ttg ctt agt gat gag agt ttg gct tcc acc
877
Asp Gly Phe Trp Glu Glu Leu Leu Ser Asp Glu Ser Leu Ala Ser Thr
                260                 265                 270

tcc taa ctagatggat ttctttttgg ttttgttttt agtttcttct actttcaagc
933
Ser
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tcattttctt ctgtcacaa
952
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140

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Met Met Asn Pro Phe Leu Pro Glu Gly Cys Asp Pro Pro Pro Pro Pro
1               5               10              15

Gln Pro Met Glu Gly Leu His Glu Asn Ala Pro Pro Pro Phe Leu Thr
            20                  25                  30

Lys Thr Phe Glu Met Val Asp Asp Pro Asn Thr Asp His Ile Val Ser
            35                  40                  45

Trp Asn Arg Gly Gly Thr Ser Phe Val Val Trp Asp Leu His Ser Phe
    50                  55                  60
```

245

Ser Thr Ile Leu Leu Pro Arg His Phe Lys His Ser Asn Phe Ser Ser
65   70   75   80

Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala Glu
                85   90   95

Arg Trp Glu Phe Ala Asn Glu Glu Phe Leu Leu Gly Gln Arg Gln Leu
            100   105   110

Leu Lys Asn Ile Lys Arg Arg Asn Pro Phe Thr Pro Ser Ser Ser Pro
        115   120   125

Ser His Asp Ala Cys Asn Glu Leu Arg Arg Glu Lys Gln Val Leu Met
    130   135   140

Met Glu Ile Val Ser Leu Arg Gln Gln Gln Gln Thr Thr Lys Ser Tyr
145   150   - 155   160

Ile Lys Ala Met Glu Gln Arg Ile Glu Gly Thr Glu Arg Lys Gln Arg
            165   170   175

Gln Met Met Ser Phe Leu Ala Arg Ala Met Gln Ser Pro Ser Phe Leu
        180   185   190

His Gln Leu Leu Lys Gln Arg Asp Lys Lys Ile Lys Glu Leu Glu Asp
.   195   200   205

Asn Glu Ser Ala Lys Arg Lys Arg Gly Ser Ser Ser Met Ser Glu Leu
    210   215   220

Glu Val Leu Ala Leu Glu Met Gln Gly His Gly Lys Gln Arg Asn Met
225   230   235   240

Leu Glu Glu Glu Asp His Gln Leu Val Val Glu Arg Glu Leu Asp Asp
            245   250   255

Gly Phe Trp Glu Glu Leu Leu Ser Asp Glu Ser Leu Ala Ser Thr Ser
        260   265   270

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<221> CDS <222> (218)..(2077) <223> G849

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60

246

tctaattttt cctttgtaca ttgtttttata tatacataaa acacacaaat cgggtatggg
120

ggaatttggg ttttaagata gcgtgatctg taataataag tggttcgcga tcgtgatcaa
180

gaaactggtg gctgatagtg atatgcatat ttgagag atg gtg ttc aag aga aag
235
                                        Met Val Phe Lys Arg Lys
                                         1   5

tta gat tgc ctt tcc gtg gga ttt gat ttt ccc aac att ccc aga gct
283
Leu Asp Cys Leu Ser Val Gly Phe Asp Phe Pro Asn Ile Pro Arg Ala
            10   15   20

cct cgt tca tgc agg agg aag gtt cta aac aag agg att gat cat gat
331
Pro Arg Ser Cys Arg Arg Lys Val Leu Asn Lys Arg Ile Asp His Asp
            25   30   35

gat gat aac act cag atc tgt gca att gac tta cta gct ttg gct gga
379
Asp Asp Asn Thr Gln Ile Cys Ala Ile Asp Leu Leu Ala Leu Ala Gly
        40   45   50

aag att cta cag gaa agc gag agt tcc tct gcg tct tct aat gca ttt
427
Lys Ile Leu Gln Glu Ser Glu Ser Ser Ser Ala Ser Ser Asn Ala Phe
55   60   65   70

gaa gaa att aag caa gag aaa gta gaa aat tgc aag act att aaa tct
475
Glu Glu Ile Lys Gln Glu Lys Val Glu Asn Cys Lys Thr Ile Lys Ser
            75   80   85

gag tct tct gac caa gga aac tct gtg tca aag cct act tat gat atc
523
Glu Ser Ser Asp Gln Gly Asn Ser Val Ser Lys Pro Thr Tyr Asp Ile
            90   95   100

tct act gag aag tgt gtg gtg aac agt tgt ttt tca ttt ccg gat agt
571
Ser Thr Glu Lys Cys Val Val Asn Ser Cys Phe Ser Phe Pro Asp Ser
            105   110   115

gac ggc gtt ttg gag cgg act ccg atg tct gat tac aag aag att cat
619
Asp Gly Val Leu Glu Arg Thr Pro Met Ser Asp Tyr Lys Lys Ile His
        120   125   130

ggt ttg atg gat gta ggg tgt gaa aac aag aat gta aat aat ggg ttc
667
Gly Leu Met Asp Val Gly Cys Glu Asn Lys Asn Val Asn Asn Gly Phe
135   140   145   150

gag caa gga gaa gca acc gat cgc gtg ggt gat gga ggc tta gtc act
715
Glu Gln Gly Glu Ala Thr Asp Arg Val Gly Asp Gly Gly Leu Val Thr
            155   160   165

247

gat act tgc aac tta gag gat gca act gcg tta ggt ctg cag ttt ccg
763
Asp Thr Cys Asn Leu Glu Asp Ala Thr Ala Leu Gly Leu Gln Phe Pro
        170   175   180

aaa tca gtc tgt gtg ggt ggt gat tta aaa tca cca tcc acc ttg gat
811
Lys Ser Val Cys Val Gly Gly Asp Leu Lys Ser Pro Ser Thr Leu Asp
        185   190   195

atg acc cct aat ggt tcc tat gct aga cat ggg aac cat act aac cta
859
Met Thr Pro Asn Gly Ser Tyr Ala Arg His Gly Asn His Thr Asn Leu
        200   205   210

ggt aga aaa gat gat gat gaa aaa ttc tat agt tac cat aaa ctt agc
907
Gly Arg Lys Asp Asp Asp Glu Lys Phe Tyr Ser Tyr His Lys Leu Ser
215   220   225   230

aat aaa ttt aag tcg tat agg tct cca aca att cga aga ata aga aag
955
Asn Lys Phe Lys Ser Tyr Arg Ser Pro Thr Ile Arg Arg Ile Arg Lys
                235   240   245

tcc atg tcg tcc aaa tac tgg aaa caa gtt cca aaa gat ttt gga tac
1003
Ser Met Ser Ser Lys Tyr Trp Lys Gln Val Pro Lys Asp Phe Gly Tyr
                250   255   260

agt aga gct gat gtg ggt gtg aag act ctt tat cgc aaa aga aaa tca
1051
Ser Arg Ala Asp Val Gly Val Lys Thr Leu Tyr Arg Lys Arg Lys Ser
                265   270   275

tgt tat ggt tac aac gca tgg cag cgt gag atc att tat aag aga aga
1099
Cys Tyr Gly Tyr Asn Ala Trp Gln Arg Glu Ile Ile Tyr Lys Arg Arg
        280   285   290

aga tca cct gac aga agc tcg gtc gta act tct gat gga gga ctc agt
1147
Arg Ser Pro Asp Arg Ser Ser Val Val Thr Ser Asp Gly Gly Leu Ser
295   300   305   310

agt gga agt gtt tcc aag tta ccc aag aag gga gat aca gta aag cta
1195
Ser Gly Ser Val Ser Lys Leu Pro Lys Lys Gly Asp Thr Val Lys Leu
                315   320   325

agc att aag tcc ttt agg att cca gag ctt ttt att gaa gtt cca gaa
1243
Ser Ile Lys Ser Phe Arg Ile Pro Glu Leu Phe Ile Glu Val Pro Glu
                330   335   340

act gca aca gta gga tca cta aag agg act gtg atg gag gct gtc agt
1291
Thr Ala Thr Val Gly Ser Leu Lys Arg Thr Val Met Glu Ala Val Ser
        345   350   355

248

gtt tta ctc agc gga gga ata cgt gtt ggg gtg tta atg cat ggg aag
1339
Val Leu Leu Ser Gly Gly Ile Arg Val Gly Val Leu Met His Gly Lys
    360   365   370

aag gtt aga gat gaa agg aaa act ctg tcc cag act ggg atc tca tgt
1387
Lys Val Arg Asp Glu Arg Lys Thr Leu Ser Gln Thr Gly Ile Ser Cys
375   380   385   390

gat gaa aat cta gac aac ctt ggg ttc acc ttg gag cct agt ccc agc
1435
Asp Glu Asn Leu Asp Asn Leu Gly Phe Thr Leu Glu Pro Ser Pro Ser
            395   400   405

aaa gtt ccc cta cct ttg tgt tct gaa gat cct gct gtg cca acc gac
1483
Lys Val Pro Leu Pro Leu Cys Ser Glu Asp Pro Ala Val Pro Thr Asp
        410   415   420

cct aca agt ttg tct gaa cgg tct gcg gcg tct cct atg cta gat tct
1531
Pro Thr Ser Leu Ser Glu Arg Ser Ala Ala Ser Pro Met Leu Asp Ser
        425   430   435

gga att cca cat gca gat gac gtg att gat tca aga aat att gtg gac
1579
Gly Ile Pro His Ala Asp Asp Val Ile Asp Ser Arg Asn Ile Val Asp
    440   445   450

agt aac ctc gaa tta gtt cca tat cag ggt gac ata tct gtt gat gaa
1627
Ser Asn Leu Glu Leu Val Pro Tyr Gln Gly Asp Ile Ser Val Asp Glu
455   460   465   470

cct tca tca gat tca aaa gag ctt gtc cca ctt cca gag ttg gaa gtc
1675
Pro Ser Ser Asp Ser Lys Glu Leu Val Pro Leu Pro Glu Leu Glu Val
            475   480   485

aag gcg ctt gcc ata gtt ccg ttg aac cag aaa cct aag cgt act gag
1723
Lys Ala Leu Ala Ile Val Pro Leu Asn Gln Lys Pro Lys Arg Thr Glu
            490   495   500

cta gcc cag agg aga act agg aga ccc ttc tct gtg aca gag gta gaa
1771
Leu Ala Gln Arg Arg Thr Arg Arg Pro Phe Ser Val Thr Glu Val Glu
        505   510   515

gct ctt gta caa gca gtt gag gaa ctc ggg act gga aga tgg cgt gat
1819
Ala Leu Val Gln Ala Val Glu Glu Leu Gly Thr Gly Arg Trp Arg Asp
    520   525   530

gta aaa ttg cgt gct ttc gag gat gca gat cat cgg act tac gtg gac
1867
Val Lys Leu Arg Ala Phe Glu Asp Ala Asp His Arg Thr Tyr Val Asp
535   540   545   550

ttg aag gac aaa tgg aag acg cta gtt cac aca gca agt ata tcc cca
1915
Leu Lys Asp Lys Trp Lys Thr Leu Val His Thr Ala Ser Ile Ser Pro
            555   560   565

cag caa cga aga gga gag ccg gtg cca caa gaa ctg cta gac aga gtc
1963
Gln Gln Arg Arg Gly Glu Pro Val Pro Gln Glu Leu Leu Asp Arg Val
            570   575   580

ttg agg gca tac ggg tat tgg tcg cag cac caa gga aaa cat cag gcg
2011
Leu Arg Ala Tyr Gly Tyr Trp Ser Gln His Gln Gly Lys His Gln Ala
            585   590   595

aga gga gcg tcc aaa gat cca gac atg aac aga ggt gga gct ttt gaa
2059
Arg Gly Ala Ser Lys Asp Pro Asp Met Asn Arg Gly Gly Ala Phe Glu
     600   605   610

tca ggt gtt tca gtg taa aaaaggaggt acgcattggt gggtgggtgt
2107
Ser Gly Val Ser Val
615

acagaagcaa acaacacaat aaatggacaa ctcaatttct gcaaagttta attgtcttta
2167

tttctcgttt tttttttttt ttctcctaca tacactttt tttttct
2214

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142

Met Val Phe Lys Arg Lys Leu Asp Cys Leu Ser Val Gly Phe Asp Phe
1   5   10   15

Pro Asn Ile Pro Arg Ala Pro Arg Ser Cys Arg Arg Lys Val Leu Asn
            20   25   30

Lys Arg Ile Asp His Asp Asp Asp Asn Thr Gln Ile Cys Ala Ile Asp
        35   40   45

Leu Leu Ala Leu Ala Gly Lys Ile Leu Gln Glu Ser Glu Ser Ser Ser
    50   55   60

Ala Ser Ser Asn Ala Phe Glu Glu Ile Lys Gln Glu Lys Val Glu Asn
65   70   75   80

Cys Lys Thr Ile Lys Ser Glu Ser Ser Asp Gln Gly Asn Ser Val Ser
                85   90   95

Lys Pro Thr Tyr Asp Ile Ser Thr Glu Lys Cys Val Val Asn Ser Cys
            100   105   110

```
Phe Ser Phe Pro Asp Ser Asp Gly Val Leu Glu Arg Thr Pro Met Ser
        115         120             125

Asp Tyr Lys Lys Ile His Gly Leu Met Asp Val Gly Cys Glu Asn Lys
    130         135             140

Asn Val Asn Asn Gly Phe Glu Gln Gly Glu Ala Thr Asp Arg Val Gly
145             150             155             160

Asp Gly Gly Leu Val Thr Asp Thr Cys Asn Leu Glu Asp Ala Thr Ala
            165             170             175

Leu Gly Leu Gln Phe Pro Lys Ser Val Cys Val Gly Gly Asp Leu Lys
        180             185             190

Ser Pro Ser Thr Leu Asp Met Thr Pro Asn Gly Ser Tyr Ala Arg His
        195             200             205

Gly Asn His Thr Asn Leu Gly Arg Lys Asp Asp Asp Glu Lys Phe Tyr
    210             215             220

Ser Tyr His Lys Leu Ser Asn Lys Phe Lys Ser Tyr Arg Ser Pro Thr
225             230             235             240

Ile Arg Arg Ile Arg Lys Ser Met Ser Ser Lys Tyr Trp Lys Gln Val
                245             250             255

Pro Lys Asp Phe Gly Tyr Ser Arg Ala Asp Val Gly Val Lys Thr Leu
            260             265             270

Tyr Arg Lys Arg Lys Ser Cys Tyr Gly Tyr Asn Ala Trp Gln Arg Glu
    275             280             285

Ile Ile Tyr Lys Arg Arg Arg Ser Pro Asp Arg Ser Ser Val Val Thr
    290             295             300

Ser Asp Gly Gly Leu Ser Ser Gly Ser Val Ser Lys Leu Pro Lys Lys
305             310             315             320

Gly Asp Thr Val Lys Leu Ser Ile Lys Ser Phe Arg Ile Pro Glu Leu
            325             330             335

Phe Ile Glu Val Pro Glu Thr Ala Thr Val Gly Ser Leu Lys Arg Thr
            340             345             350
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Val Met Glu Ala Val Ser Val Leu Leu Ser Gly Gly Ile Arg Val Gly
     355   360   365

Val Leu Met His Gly Lys Lys Val Arg Asp Glu Arg Lys Thr Leu Ser
   370   375   380

Gln Thr Gly Ile Ser Cys Asp Glu Asn Leu Asp Asn Leu Gly Phe Thr
385   390   395   400

Leu Glu Pro Ser Pro Ser Lys Val Pro Leu Pro Leu Cys Ser Glu Asp
          405   410   415

Pro Ala Val Pro Thr Asp Pro Thr Ser Leu Ser Glu Arg Ser Ala Ala
          420   425   430

Ser Pro Met Leu Asp Ser Gly Ile Pro His Ala Asp Asp Val Ile Asp
        435   440   445

Ser Arg Asn Ile Val Asp Ser Asn Leu Glu Leu Val Pro Tyr Gln Gly
        450   455   460

Asp Ile Ser Val Asp Glu Pro Ser Ser Asp Ser Lys Glu Leu Val Pro
465   470   475   480

Leu Pro Glu Leu Glu Val Lys Ala Leu Ala Ile Val Pro Leu Asn Gln
          485   490   495

Lys Pro Lys Arg Thr Glu Leu Ala Gln Arg Arg Thr Arg Arg Pro Phe
          500   505   510

Ser Val Thr Glu Val Glu Ala Leu Val Gln Ala Val Glu Glu Leu Gly
        515   520   525

Thr Gly Arg Trp Arg Asp Val Lys Leu Arg Ala Phe Glu Asp Ala Asp
        530   535   540

His Arg Thr Tyr Val Asp Leu Lys Asp Lys Trp Lys Thr Leu Val His
545   550   555   560

Thr Ala Ser Ile Ser Pro Gln Gln Arg Arg Gly Glu Pro Val Pro Gln
          565   570   575

Glu Leu Leu Asp Arg Val Leu Arg Ala Tyr Gly Tyr Trp Ser Gln His
          580   585   590

Gln Gly Lys His Gln Ala Arg Gly Ala Ser Lys Asp Pro Asp Met Asn
        595   600   605

Arg Gly Gly Ala Phe Glu Ser Gly Val Ser Val
       610   615

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<221> CDS <222> (108)..(806) <223> G913

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60

acaaacaaaa acacattgta acattagttt aagcattaag cttcttt atg tcg aat
116
                                                  Met Ser Asn
                                                  1

aat aat aat tct ccg acc acc gtg aat caa gaa acg acg acg tct cgt
164
Asn Asn Asn Ser Pro Thr Thr Val Asn Gln Glu Thr Thr Thr Ser Arg
    5   10   15

gaa gtc tca atc aca ttg cct act gat caa tct cct caa acc tca cca
212
Glu Val Ser Ile Thr Leu Pro Thr Asp Gln Ser Pro Gln Thr Ser Pro
20   25   30   35

gga tca tct tct tct cct tca ccg aga cct tcc ggt gga tca ccg gcg
260
Gly Ser Ser Ser Ser Pro Ser Pro Arg Pro Ser Gly Gly Ser Pro Ala
                40   45   50

aga aga acg gcg act gga tta tcc ggc aag cac tct att ttc agg ggg
308
Arg Arg Thr Ala Thr Gly Leu Ser Gly Lys His Ser Ile Phe Arg Gly
            55   60   65

att cga cta cgt aac gga aaa tgg gta tcg gag att aga gag cca cgt
356
Ile Arg Leu Arg Asn Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg
        70   75   80

aaa acg aca aga att tgg ctc ggg act tat ccg gta ccg gag atg gct
404
Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Val Pro Glu Met Ala
    85   90   95

gcc gcc gct tac gac gtg gct gcg tta gct tta aaa gga ccc gac gcc
452
Ala Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Pro Asp Ala
100   105   110   115

gtt ttg aat ttt cct ggt tta gct ttg act tac gtg gct ccg gtt tca
500
Val Leu Asn Phe Pro Gly Leu Ala Leu Thr Tyr Val Ala Pro Val Ser
            120   125   130

253

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aac tct gct gcg gat ata aga gcg gct gct agt aga gca gcg gag atg
548
Asn Ser Ala Ala Asp Ile Arg Ala Ala Ala Ser Arg Ala Ala Glu Met
            135             140             145

aag caa ccg gat cag ggt ggg gat gag aag gta ttg gaa ccg gtt caa
596
Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu Pro Val Gln
            150             155             160

ccc ggc aaa gag gaa gaa tta gaa gaa gtg tcg tgt aac tcg tgt tcg
644
Pro Gly Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn Ser Cys Ser
        165             170             175

ttg gag ttt atg gat gag gaa gcg atg ttg aat atg ccg act ttg ttg
692
Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro Thr Leu Leu
180             185             190             195

acg gag atg gct gaa ggg atg ttg atg agt cca ccg aga atg atg ata
740
Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg Met Met Ile
            200             205             210

cat ccg acg atg gaa gat gat tcg ccg gag aat cat gaa gga gat aat
788
His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu Gly Asp Asn
            215             220             225

ctt tgg agt tat aaa tga atccattgaa gctgctctct ttttattgt
836
Leu Trp Ser Tyr Lys
            230


tttccggtcg aatgagattt tccccctttt tttttttctt tttgggtcgc tgtt
890


<210>  144 <211>  232 <212>  PRT <213>  Arabidopsis thaliana <400>
144

Met Ser Asn Asn Asn Asn Ser Pro Thr Thr Val Asn Gln Glu Thr Thr
1               5               10              15

Thr Ser Arg Glu Val Ser Ile Thr Leu Pro Thr Asp Gln Ser Pro Gln
            20              25              30

Thr Ser Pro Gly Ser Ser Ser Ser Pro Ser Pro Arg Pro Ser Gly Gly
        35              40              45

Ser Pro Ala Arg Arg Thr Ala Thr Gly Leu Ser Gly Lys His Ser Ile
    50              55              60

Phe Arg Gly Ile Arg Leu Arg Asn Gly Lys Trp Val Ser Glu Ile Arg
65              70              75              80
```

254

Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Val Pro
                85   90   95

Glu Met Ala Ala Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly
            100   105   110

Pro Asp Ala Val Leu Asn Phe Pro Gly Leu Ala Leu Thr Tyr Val Ala
        115   120   125

Pro Val Ser Asn Ser Ala Ala Asp Ile Arg Ala Ala Ala Ser Arg Ala
        130   135   140

Ala Glu Met Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu
145   150   155   160

Pro Val Gln Pro Gly Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn
                165   170   175

Ser Cys Ser Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro
            180   185   190

Thr Leu Leu Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg
            195   200   205

Met Met Ile His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu
    210   215   220

Gly Asp Asn Leu Trp Ser Tyr Lys
225   230

<210> 145 <211> 1130 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (116)..(1024) <223> G921

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ccaagatcga ctcttacttc gaatctctct caactttctt cctcagctta cgggaacttc
60

cacacatata catccacaag aacccatatc gaagattcat cctacatata tttac atg
118
                                                                    Met
                                                                    1

gat cag tac tca tcc tct ttg gtc gat act tca tta gat ctc act att
166
Asp Gln Tyr Ser Ser Ser Leu Val Asp Thr Ser Leu Asp Leu Thr Ile
            5   10   15

ggc gtt act cgt atg cga gtt gaa gaa gat cca ccg aca agt gct ttg
214
Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala Leu

255

```
           20                      25                      30

gtg gaa gaa tta aac cga gtt agt gct gag aac aag aag ctc tcg gag
262
Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser Glu
    35                  40                  45

atg cta act ttg atg tgt gac aac tac aac gtc ttg agg aag caa ctt
310
Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln Leu
50                  55                  60                  65

atg gaa tat gtt aac aag agc aac ata acc gag agg gat caa atc agc
358
Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile Ser
                70                  75                  80

cct ccc aag aaa cgc aaa tcc ccg gcg aga gag gac gca ttc agc tgc
406
Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser Cys
                85                  90                  95

gcg gtt att ggc gga gtg tcg gag agt agc tca acg gat caa gat gag
454
Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp Glu
            100                 105                 110

tat ttg tgt aag aag cag aga gaa gag act gtc gtg aag gag aaa gtc
502
Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys Val
    115                 120                 125

tca agg gtc tat tac aag acc gaa gct tct gac act acc ctc gtt gtg
550
Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val Val
130                 135                 140                 145

aaa gat ggg tat caa tgg agg aaa tat gga cag aaa gtg act aga gac
598
Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg Asp
                150                 155                 160

aat cca tct cca aga gct tac ttc aaa tgt gct tgt gct cca agc tgt
646
Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser Cys
                165                 170                 175

tct gtc aaa aag aag gtt cag aga agt gtg gag gat cag tcc gtg tta
694
Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val Leu
            180                 185                 190

gtt gca act tat gag ggt gaa cac aac cat cca atg cca tcg cag atc
742
Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln Ile
    195                 200                 205

gat tca aac aat ggc tta aac cgc cac atc tct cat ggt ggt tca gct
790
Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser Ala
210                 215                 220                 225
```

256

```
tca aca ccc gtt gca gca aac aga aga agt agc ttg act gtg ccg gtg
838
Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro Val
            230             235             240

act acc gta gat atg att gaa tcg aag aaa gtg acg agc cca acg tca
886
Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr Ser
            245             250             255

aga atc gat ttt ccc caa gtt cag aaa ctt ttg gtg gag caa atg gct
934
Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met Ala
        260             265             270

tct tcc tta acc aaa gat cct aac ttt aca gca gct tta gca gca gct
982
Ser Ser Leu Thr Lys Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala Ala
    275             280             285

gtt acc gga aaa ttg tat caa cag aat cat acc gag aaa tag
1024
Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys
290             295             300

tttagcttca aattccgtta gagtttttag atttgaattt gtcatgagta agagaaagag
1084

agtagattat aatccattgt gatactgaaa aaaaaaaaaa aaaaaa
1130
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<210> 146 <211> 302 <212> PRT <213> Arabidopsis thaliana <400>
146

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Met Asp Gln Tyr Ser Ser Ser Leu Val Asp Thr Ser Leu Asp Leu Thr
1               5               10              15

Ile Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala
            20              25              30

Leu Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser
        35              40              45

Glu Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln
    50              55              60

Leu Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile
65              70.             75              80

Ser Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser
            85              90              95

Cys Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp
```

                    100   105   110

    Glu Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys
            115   120   125

    Val Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val
        130   135   140

    Val Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg
    145   150   155   160

    Asp Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser
                    165   170   175

    Cys Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val
                180   185   190

    Leu Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln
            195   200   205

    Ile Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser
        210   215   220

    Ala Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro
    225   230   235   240

    Val Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr
                    245   250   255

    Ser Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met
                260   265   270

    Ala Ser Ser Leu Thr Lys Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala
            275   280   285

    Ala Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys
        290   295   300

    <210> 147 <211> 1722 <212> DNA <213> Arabidopsis thaliana <220>
    <221> CDS <222> (9)..(1565) <223> G939

     <400> 147
    cagattct atg gat atg tat aac aac aat ata ggg atg ttc cgg agt tta
    50
             Met Asp Met Tyr Asn Asn Asn Ile Gly Met Phe Arg Ser Leu
             1   5   10

gtt tgt agc tcg gcg cct cca ttt aca gag gga cat atg tgt tct gat
98
Val Cys Ser Ser Ala Pro Pro Phe Thr Glu Gly His Met Cys Ser Asp
15   20   25   30

tcg cat acg gct ttg tgc gat gat ctg agt agt gat gag gaa atg gaa
146
Ser His Thr Ala Leu Cys Asp Asp Leu Ser Ser Asp Glu Glu Met Glu
              35   40   45

ata gag gag ctt gag aag aag atc tgg aga gac aag cag cgt tta aag
194
Ile Glu Glu Leu Glu Lys Lys Ile Trp Arg Asp Lys Gln Arg Leu Lys
              50   55   60

cgg ctc aag gaa atg gcg aag aac ggt cta gga aca aga ttg ttg ttg
242
Arg Leu Lys Glu Met Ala Lys Asn Gly Leu Gly Thr Arg Leu Leu Leu
              65   70   75

aag cag caa cat gat gat ttt cca gag cac tct agt aag aga acc atg
290
Lys Gln Gln His Asp Asp Phe Pro Glu His Ser Ser Lys Arg Thr Met
              80   85   90

tac aag gca caa gat ggg atc ttg aag tac atg tcg aag aca atg gag
338
Tyr Lys Ala Gln Asp Gly Ile Leu Lys Tyr Met Ser Lys Thr Met Glu
95   100   105   110

cga tat aaa gct caa ggt ttt gtt tat ggg att gtg tta gag aat ggg
386
Arg Tyr Lys Ala Gln Gly Phe Val Tyr Gly Ile Val Leu Glu Asn Gly
                  115   120   125

aaa acg gta gcg gga tct tct gat aat ctc cgt gaa tgg tgg aaa gac
434
Lys Thr Val Ala Gly Ser Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp
                  130   135   140

aaa gtg agg ttt gat agg aac ggc cca gct gct ata atc aag cac caa
482
Lys Val Arg Phe Asp Arg Asn Gly Pro Ala Ala Ile Ile Lys His Gln
                  145   150   155

agg gat atc aat ctt tct gat gga agt gat tca ggg tct gag gtt ggg
530
Arg Asp Ile Asn Leu Ser Asp Gly Ser Asp Ser Gly Ser Glu Val Gly
              160   165   170

gat tct acc gca cag aag ttg ctt gag ctt caa gat act act ctt gga
578
Asp Ser Thr Ala Gln Lys Leu Leu Glu Leu Gln Asp Thr Thr Leu Gly
175   180   185   190

gct ctg tta tcg gct ctg ttt cct cac tgc aac cct cct cag agg cgg
626
Ala Leu Leu Ser Ala Leu Phe Pro His Cys Asn Pro Pro Gln Arg Arg
                  195   200   205

```
ttt ccg ttg gag aaa ggc gtg aca ccg cca tgg tgg cca acg ggg aaa
674
Phe Pro Leu Glu Lys Gly Val Thr Pro Pro Trp Trp Pro Thr Gly Lys
        210                 215                 220

gaa gat tgg tgg gat caa ctg tct tta ccc gtt gat ttt cga ggt gtt
722
Glu Asp Trp Trp Asp Gln Leu Ser Leu Pro Val Asp Phe Arg Gly Val
        225                 230                 235

ccg cca cct tac aag aag cct cat gat ctc aag aag ctg tgg aaa att
770
Pro Pro Pro Tyr Lys Lys Pro His Asp Leu Lys Lys Leu Trp Lys Ile
        240                 245                 250

ggt gtt ttg att ggt gta atc aga cat atg gct tct gac att agc aac
818
Gly Val Leu Ile Gly Val Ile Arg His Met Ala Ser Asp Ile Ser Asn
255                 260                 265                 270

ata ccc aat ctc gtg aga cgg tct aga agt ttg cag gag aaa atg acg
866
Ile Pro Asn Leu Val Arg Arg Ser Arg Ser Leu Gln Glu Lys Met Thr
                275                 280                 285

tca aga gaa ggc gct tta tgg ctc gct gct ctt tac cga gaa aag gct
914
Ser Arg Glu Gly Ala Leu Trp Leu Ala Ala Leu Tyr Arg Glu Lys Ala
        290                 295                 300

att gtt gat caa ata gcc atg tct aga gaa aac aac aac act tct aac
962
Ile Val Asp Gln Ile Ala Met Ser Arg Glu Asn Asn Asn Thr Ser Asn
        305                 310                 315

ttt ctt gtt cct gca acc ggt gga gac cca gat gtt ttg ttt cct gaa
1010
Phe Leu Val Pro Ala Thr Gly Gly Asp Pro Asp Val Leu Phe Pro Glu
        320                 325                 330

tct aca gac tat gat gtt gaa ctg att ggt ggc act cat cgg acc aat
1058
Ser Thr Asp Tyr Asp Val Glu Leu Ile Gly Gly Thr His Arg Thr Asn
335                 340                 345                 350

cag cag tat cct gaa ttt gaa aac aac tac aac tgt gtt tac aag aga
1106
Gln Gln Tyr Pro Glu Phe Glu Asn Asn Tyr Asn Cys Val Tyr Lys Arg
                355                 360                 365

aag ttt gaa gaa gat ttt ggg atg cca atg cat cca aca ctc cta aca
1154
Lys Phe Glu Glu Asp Phe Gly Met Pro Met His Pro Thr Leu Leu Thr
        370                 375                 380

tgt gag aac agt ctc tgt cct tat agc caa cca cat atg gga ttt ctt
1202
Cys Glu Asn Ser Leu Cys Pro Tyr Ser Gln Pro His Met Gly Phe Leu
        385                 390                 395
```

260

```
gac agg aac tta aga gag aat cac caa atg act tgt cct tat aaa gtc
1250
Asp Arg Asn Leu Arg Glu Asn His Gln Met Thr Cys Pro Tyr Lys Val
    400                     405                     410

act tcc ttc tac caa cca act aaa ccc tat ggt atg acg ggt tta atg
1298
Thr Ser Phe Tyr Gln Pro Thr Lys Pro Tyr Gly Met Thr Gly Leu Met
415                     420                     425             430

gtt cct tgt ccg gat tat aac ggg atg cag cag cag gtt cag agc ttt
1346
Val Pro Cys Pro Asp Tyr Asn Gly Met Gln Gln Gln Val Gln Ser Phe
                435                     440                 445

caa gac cag ttt aat cat ccc aac gat ctc tac aga cca aaa gct cca
1394
Gln Asp Gln Phe Asn His Pro Asn Asp Leu Tyr Arg Pro Lys Ala Pro
                450                     455                 460

caa aga ggc aac gat gac ttg gtt gag gat ttg aat cct tct cct tcg
1442
Gln Arg Gly Asn Asp Asp Leu Val Glu Asp Leu Asn Pro Ser Pro Ser
            465                     470                 475

acg ctg aat cag aat ctt ggt tta gtc tta cct act gac ttc aat gga
1490
Thr Leu Asn Gln Asn Leu Gly Leu Val Leu Pro Thr Asp Phe Asn Gly
    480                     485                     490

ggt gag gaa aca gta gga aca gag aac aat ctg cat aat caa ggg caa
1538
Gly Glu Glu Thr Val Gly Thr Glu Asn Asn Leu His Asn Gln Gly Gln
495                     500                     505             510

gag ttg ccc aca tct tgg att cag taa agaaagcttc agagttttct
1585
Glu Leu Pro Thr Ser Trp Ile Gln
                515

ttttatgttt ctagtcttt atagctttgt ctcttgctta ttctctcatt aaacacagtt
1645

tttgatctct ccatttcata gcccatgtag caatggagaa gattaggttt cataataagt
1705

taataaccaa attcaaa
1722


<210> 148 .<211> 518 <212> PRT <213> Arabidopsis thaliana <400>
148

Met Asp Met Tyr Asn Asn Asn Ile Gly Met Phe Arg Ser Leu Val Cys
1               5                   10                  15


Ser Ser Ala Pro Pro Phe Thr Glu Gly His Met Cys Ser Asp Ser His
            20                  25                  30
```

Thr Ala Leu Cys Asp Asp Leu Ser Ser Asp Glu Glu Met Glu Ile Glu
        35   40   45

Glu Leu Glu Lys Lys Ile Trp Arg Asp Lys Gln Arg Leu Lys Arg Leu
    50   55   60

Lys Glu Met Ala Lys Asn Gly Leu Gly Thr Arg Leu Leu Leu Lys Gln
65   70   75   80

Gln His Asp Asp Phe Pro Glu His Ser Ser Lys Arg Thr Met Tyr Lys
            85   90   95

Ala Gln Asp Gly Ile Leu Lys Tyr Met Ser Lys Thr Met Glu Arg Tyr
            100   105   110

Lys Ala Gln Gly Phe Val Tyr Gly Ile Val Leu Glu Asn Gly Lys Thr
        115   120   125

Val Ala Gly Ser Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val
    130   135   140

Arg Phe Asp Arg Asn Gly Pro Ala Ala Ile Ile Lys His Gln Arg Asp
145   150   155   160

Ile Asn Leu Ser Asp Gly Ser Asp Ser Gly Ser Glu Val Gly Asp Ser
            165   170   175

Thr Ala Gln Lys Leu Leu Glu Leu Gln Asp Thr Thr Leu Gly Ala Leu
            180   185   190

Leu Ser Ala Leu Phe Pro His Cys Asn Pro Pro Gln Arg Arg Phe Pro
        195   200   205

Leu Glu Lys Gly Val Thr Pro Pro Trp Trp Pro Thr Gly Lys Glu Asp
    210   215   220

Trp Trp Asp Gln Leu Ser Leu Pro Val Asp Phe Arg Gly Val Pro Pro
225   230   235   240

Pro Tyr Lys Lys Pro His Asp Leu Lys Lys Leu Trp Lys Ile Gly Val
            245   250   255

Leu Ile Gly Val Ile Arg His Met Ala Ser Asp Ile Ser Asn Ile Pro
            260   265   270

Asn Leu Val Arg Arg Ser Arg Ser Leu Gln Glu Lys Met Thr Ser Arg

262

                275   ¡   280   285

        Glu Gly Ala Leu Trp Leu Ala Ala Leu Tyr Arg Glu Lys Ala Ile Val
            290   295   300

        Asp Gln Ile Ala Met Ser Arg Glu Asn Asn Asn Thr Ser Asn Phe Leu
        305   310   315   320

        Val Pro Ala Thr Gly Gly Asp Pro Asp Val Leu Phe Pro Glu Ser Thr
                    325   330   335

        Asp Tyr Asp Val Glu Leu Ile Gly Gly Thr His Arg Thr Asn Gln Gln
                    340   345   350

        Tyr Pro Glu Phe Glu Asn Asn Tyr Asn Cys Val Tyr Lys Arg Lys Phe
                355   360   365

        Glu Glu Asp Phe Gly Met Pro Met His Pro Thr Leu Leu Thr Cys Glu
            370   375   380

        Asn Ser Leu Cys Pro Tyr Ser Gln Pro His Met Gly Phe Leu Asp Arg
        385   390   395   400

        Asn Leu Arg Glu Asn His Gln Met Thr Cys Pro Tyr Lys Val Thr Ser
                    405   410   415

        Phe Tyr Gln Pro Thr Lys Pro Tyr Gly Met Thr Gly Leu Met Val Pro
                    420   425   430

        Cys Pro Asp Tyr Asn Gly Met Gln Gln Gln Val Gln Ser Phe Gln Asp
                435   440   445

        Gln Phe Asn His Pro Asn Asp Leu Tyr Arg Pro Lys Ala Pro Gln Arg
            450   455   460

        Gly Asn Asp Asp Leu Val Glu Asp Leu Asn Pro Ser Pro Ser Thr Leu
        465   470   475   480

        Asn Gln Asn Leu Gly Leu Val Leu Pro Thr Asp Phe Asn Gly Gly Glu
                    485   490   495

        Glu Thr Val Gly Thr Glu Asn Asn Leu His Asn Gln Gly Gln Glu Leu
                    500   505   510

        Pro Thr Ser Trp Ile Gln
            515

                                    263

<210> 149 <211> 2057 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (102)..(1805) <223> G940

<400> 149
ttccctgag aacgacagga gaaagaataa aaaccctaaa tttctttaat ttcggcgctt
60

cagattatcg ttgttaaagg tttttgattg attttgttta a atg ggc gat ctt gct
116
                                             Met Gly Asp Leu Ala
                                             1   5

atg tcc gta gca gac atc agg atg gag aat gag cct gat gat tta gct
164
Met Ser Val Ala Asp Ile Arg Met Glu Asn Glu Pro Asp Asp Leu Ala
            10   15   20

agt gat aat gtt gct gag att gat gtg agt gat gaa gag att gat gct
212
Ser Asp Asn Val Ala Glu Ile Asp Val Ser Asp Glu Glu Ile Asp Ala
            25   30   35

gac gac ctt gag aga cgg atg tgg aaa gat cgt gtc agg ctt aaa aga
260
Asp Asp Leu Glu Arg Arg Met Trp Lys Asp Arg Val Arg Leu Lys Arg
        40   45   50

atc aaa gag cga caa aaa gct ggc tct caa gga gct caa acg aag gag
308
Ile Lys Glu Arg Gln Lys Ala Gly Ser Gln Gly Ala Gln Thr Lys Glu
    55   60   65

aca cct aag aaa atc tct gat caa gct cag agg aag aaa atg tct aga
356
Thr Pro Lys Lys Ile Ser Asp Gln Ala Gln Arg Lys Lys Met Ser Arg
70   75   80   85

gct caa gat ggt atc ctt aag tac atg ttg aag ctt atg gaa gtc tgc
404
Ala Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Leu Met Glu Val Cys
                90   95   100

aaa gtt cgc ggg ttt gtc tat ggt ata ata ccg gaa aag ggc aag cct
452
Lys Val Arg Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro
            105   110   115

gtg agt ggt tcc tct gac aat ata aga gct tgg tgg aaa gag aaa gtg
500
Val Ser Gly Ser Ser Asp Asn Ile Arg Ala Trp Trp Lys Glu Lys Val
            120   125   130

aag ttt gat aag aac ggt cct gct gct att gct aaa tac gaa gag gag
548
Lys Phe Asp Lys Asn Gly Pro Ala Ala Ile Ala Lys Tyr Glu Glu Glu
        135   140   145

tgt tta gcg ttt ggg aaa tct gat ggg aat agg aat tca cag ttt gtt
596

264

```
Cys Leu Ala Phe Gly Lys Ser Asp Gly Asn Arg Asn Ser Gln Phe Val
150                155            160                165

ctc cag gat ttg caa gat gct act tta ggg tct ttg tta tct tct ttg
644
Leu Gln Asp Leu Gln Asp Ala Thr Leu Gly Ser Leu Leu Ser Ser Leu
                170            175                180

atg caa cat tgt gat cct cct caa agg aag tat ccg ttg gag aaa ggg
692
Met Gln His Cys Asp Pro Pro Gln Arg Lys Tyr Pro Leu Glu Lys Gly
            185            190                195

acg cct ccg cct tgg tgg cca acg ggg aat gaa gaa tgg tgg gtg aaa
740
Thr Pro Pro Pro Trp Trp Pro Thr Gly Asn Glu Glu Trp Trp Val Lys
        200            205                210

ctc ggt ctg cct aaa agc cag agt cct cct tac cga aaa cct cat gat
788
Leu Gly Leu Pro Lys Ser Gln Ser Pro Pro Tyr Arg Lys Pro His Asp
        215            220                225

ctc aag aag atg tgg aag gtt gga gtt tta acg gca gtg atc aat cat
836
Leu Lys Lys Met Trp Lys Val Gly Val Leu Thr Ala Val Ile Asn His
230                235            240                245

atg tta cct gat att gca aag att aag agg cat gtt cgt cag tcg aaa
884
Met Leu Pro Asp Ile Ala Lys Ile Lys Arg His Val Arg Gln Ser Lys
                250            255                260

tgt tta cag gac aag atg aca gct aaa gag agt gcg att tgg ttg gcg
932
Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Ile Trp Leu Ala
            265            270                275

gtt ttg aac caa gag gaa tct ttg att cag cag cct agc agt gac aat
980
Val Leu Asn Gln Glu Glu Ser Leu Ile Gln Gln Pro Ser Ser Asp Asn
            280            285                290

gga aac tcc aat gtg act gag aca cat cgt agg ggt aat aac gct gac
1028
Gly Asn Ser Asn Val Thr Glu Thr His Arg Arg Gly Asn Asn Ala Asp
        295            300                305

agg agg aaa cct gtg gtc aac agt gac agt gac tat gat gtt gat ggg
1076
Arg Arg Lys Pro Val Val Asn Ser Asp Ser Asp Tyr Asp Val Asp Gly
310            315                320                325

aca gag gaa gct tca ggt tca gtt tca tct aaa gac agt aga aga aat
1124
Thr Glu Glu Ala Ser Gly Ser Val Ser Ser Lys Asp Ser Arg Arg Asn
                330            335                340

cag att caa aaa gaa caa cca aca gcc atc tca cat tca gta aga gat
1172
Gln Ile Gln Lys Glu Gln Pro Thr Ala Ile Ser His Ser Val Arg Asp
```

265

                345   350   355

caa gat aaa gca gag aaa cat cgc aga agg aaa aga cct cga att aga
1220
Gln Asp Lys Ala Glu Lys His Arg Arg Arg Lys Arg Pro Arg Ile Arg
        360   365   370

tcc gga act gtc aat cga caa gag gaa gaa caa cct gaa gct caa caa
1268
Ser Gly Thr Val Asn Arg Gln Glu Glu Glu Gln Pro Glu Ala Gln Gln
        375   380   385

aga aac atc tta cct gat atg aat cat gtt gat gcc cct ctg cta gaa
1316
Arg Asn Ile Leu Pro Asp Met Asn His Val Asp Ala Pro Leu Leu Glu
390   395   400   405

tat aac atc aac ggt act cat caa gag gac gat gtt gtc gac cca aat
1364
Tyr Asn Ile Asn Gly Thr His Gln Glu Asp Asp Val Val Asp Pro Asn
                410   415   420

att gcc tta gga cca gag gat aat ggt ctg gaa cta gtg gtt cct gag
1412
Ile Ala Leu Gly Pro Glu Asp Asn Gly Leu Glu Leu Val Val Pro Glu
                425   430   435

ttc aat aac aac tat act tat ctt cca ctt gtt aat gaa caa act atg
1460
Phe Asn Asn Asn Tyr Thr Tyr Leu Pro Leu Val Asn Glu Gln Thr Met
                440   445   450

atg cct gta gac gaa agg cca atg ctt tat gga cca aac cct aac caa
1508
Met Pro Val Asp Glu Arg Pro Met Leu Tyr Gly Pro Asn Pro Asn Gln
        455   460   465

gag ctt caa ttt ggg tca ggg tac aac ttc tac aat ccc tct gca gtg
1556
Glu Leu Gln Phe Gly Ser Gly Tyr Asn Phe Tyr Asn Pro Ser Ala Val
470   475   480   485

ttt gta cat aac cag gaa gac gac att ctc cat aca cag ata gaa atg
1604
Phe Val His Asn Gln Glu Asp Asp Ile Leu His Thr Gln Ile Glu Met
                490   495   500

aat aca caa gca cca cct cac aac agt ggg ttc gag gag gcc cca gga
1652
Asn Thr Gln Ala Pro Pro His Asn Ser Gly Phe Glu Glu Ala Pro Gly
                505   510   515

gga gta ctt caa ccc ctt ggt tta ctc gga aat gaa gac ggt gta aca
1700
Gly Val Leu Gln Pro Leu Gly Leu Leu Gly Asn Glu Asp Gly Val Thr
        520   525   530

ggg agt gag ttg cct cag tat cag agt ggc att ctg tct cca ttg act
1748
Gly Ser Glu Leu Pro Gln Tyr Gln Ser Gly Ile Leu Ser Pro Leu Thr
        535   540   545

gac ttg gac ttt gac tat ggt ggt ttt ggt gat gat ttc tca tgg ttt
1796
Asp Leu Asp Phe Asp Tyr Gly Gly Phe Gly Asp Asp Phe Ser Trp Phe
550   555   560   565

gga gct tag tgtcttgcca tttttttttgg gagattacat agttcaaaag
1845
Gly Ala

gacatggcaa tagtctggct agtacagtta ctttctcttc ttcatttctt ctgatcttat
1905

attcttcctc tttttttttctt ataatatttt cttagatttg ttaagagaaa caattttcct
1965

tttgaataag ttgccagaag aactgctttg cccgttgtaa tggtctctag ggaaagcagt
2025

tagcgtatca tcatttgtaa atttactgtg ag
2057

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150

Met Gly Asp Leu Ala Met Ser Val Ala Asp Ile Arg Met Glu Asn Glu
1   5   10   15

Pro Asp Asp Leu Ala Ser Asp Asn Val Ala Glu Ile Asp Val Ser Asp
20   25   30

Glu Glu Ile Asp Ala Asp Asp Leu Glu Arg Arg Met Trp Lys Asp Arg
35   40   45

Val Arg Leu Lys Arg Ile Lys Glu Arg Gln Lys Ala Gly Ser Gln Gly
50   55   60

Ala Gln Thr Lys Glu Thr Pro Lys Lys Ile Ser Asp Gln Ala Gln Arg
65   70   75   80

Lys Lys Met Ser Arg Ala Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys
85   90   95

Leu Met Glu Val Cys Lys Val Arg Gly Phe Val Tyr Gly Ile Ile Pro
100   105   110

Glu Lys Gly Lys Pro Val Ser Gly Ser Ser Asp Asn Ile Arg Ala Trp
115   120   125

Trp Lys Glu Lys Val Lys Phe Asp Lys Asn Gly Pro Ala Ala Ile Ala
130   135   140

267

Lys Tyr Glu Glu Glu Cys Leu Ala Phe Gly Lys Ser Asp Gly Asn Arg
145   150   155   160

Asn Ser Gln Phe Val Leu Gln Asp Leu Gln Asp Ala Thr Leu Gly Ser
                165   170   175

Leu Leu Ser Ser Leu Met Gln His Cys Asp Pro Pro Gln Arg Lys Tyr
            180   185   190

Pro Leu Glu Lys Gly Thr Pro Pro Trp Trp Pro Thr Gly Asn Glu
        195   200   205

Glu Trp Trp Val Lys Leu Gly Leu Pro Lys Ser Gln Ser Pro Pro Tyr
    210   215   220

Arg Lys Pro His Asp Leu Lys Lys Met Trp Lys Val Gly Val Leu Thr
225   230   235   240

Ala Val Ile Asn His Met Leu Pro Asp Ile Ala Lys Ile Lys Arg His
            245   250   255

Val Arg Gln Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser
            260   265   270

Ala Ile Trp Leu Ala Val Leu Asn Gln Glu Glu Ser Leu Ile Gln Gln
        275   280   285

Pro Ser Ser Asp Asn Gly Asn Ser Asn Val Thr Glu Thr His Arg Arg
    290   295   300

Gly Asn Asn Ala Asp Arg Arg Lys Pro Val Val Asn Ser Asp Ser Asp
305   310   315   320

Tyr Asp Val Asp Gly Thr Glu Glu Ala Ser Gly Ser Val Ser Ser Lys
            325   330   335

Asp Ser Arg Arg Asn Gln Ile Gln Lys Glu Gln Pro Thr Ala Ile Ser
            340   345   350

His Ser Val Arg Asp Gln Asp Lys Ala Glu Lys His Arg Arg Arg Lys
    355   360   365

Arg Pro Arg Ile Arg Ser Gly Thr Val Asn Arg Gln Glu Glu Glu Gln
    370   375   380

268

```
Pro Glu Ala Gln Gln Arg Asn Ile Leu Pro Asp Met Asn His Val Asp
385                 390             395             400


Ala Pro Leu Leu Glu Tyr Asn Ile Asn Gly Thr His Gln Glu Asp Asp
                405             410             415


Val Val Asp Pro Asn Ile Ala Leu Gly Pro Glu Asp Asn Gly Leu Glu
            420             425             430


Leu Val Val Pro Glu Phe Asn Asn Asn Tyr Thr Tyr Leu Pro Leu Val
            435             440             445


Asn Glu Gln Thr Met Met Pro Val Asp Glu Arg Pro Met Leu Tyr Gly
    450             455             460


Pro Asn Pro Asn Gln Glu Leu Gln Phe Gly Ser Gly Tyr Asn Phe Tyr
465             470             475             480


Asn Pro Ser Ala Val Phe Val His Asn Gln Glu Asp Asp Ile Leu His
            485             490             495


Thr Gln Ile Glu Met Asn Thr Gln Ala Pro Pro His Asn Ser Gly Phe
            500             505             510


Glu Glu Ala Pro Gly Gly Val Leu Gln Pro Leu Gly Leu Leu Gly Asn
        515             520             525


Glu Asp Gly Val Thr Gly Ser Glu Leu Pro Gln Tyr Gln Ser Gly Ile
    530             535             540


Leu Ser Pro Leu Thr Asp Leu Asp Phe Asp Tyr Gly Gly Phe Gly Asp
545             550             555             560


Asp Phe Ser Trp Phe Gly Ala
            565
```

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<221>  CDS <222>  (46)..(591) <223>  G977
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caccaaactc acctgaaacc ctatttccat ttaccattca cacta atg gca cga cca
57
                                                 Met Ala Arg Pro
                                                  1


caa caa cgc ttt cga ggc gtt aga cag agg cat tgg ggc tct tgg gtc
105
Gln Gln Arg Phe Arg Gly Val Arg Gln Arg His Trp Gly Ser Trp Val
```

```
5                      10                    ·    15                      20 ·
    ·
tcc gaa att cgt cac cct ctc ttg aaa aca aga atc tgg cta ggg acg
153
Ser Glu Ile Arg His Pro Leu Leu Lys Thr Arg Ile Trp Leu Gly Thr
            25            30                35


ttt gag aca gcg gag gat gca gca agg gcc tac gac gag gcg gct agg
201
Phe Glu Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp Glu Ala Ala Arg
            40            45            50


cta atg tgt ggc ccg aga gct cgt act aat ttc cca tac aac cct aat
249
Leu Met Cys Gly Pro Arg Ala Arg Thr Asn Phe Pro Tyr Asn Pro Asn
            55        ·   60            65


gcc att cct act tcc tct tcc aag ctt cta tca gca act ctt acc gct
297
Ala Ile Pro Thr Ser Ser Ser Lys Leu Leu Ser Ala Thr Leu Thr Ala
    70                75            80


aaa ctc cac aaa tgc tac atg gct tct ctt caa atg acc aag caa acg
345                                      ─
Lys Leu His Lys Cys Tyr Met Ala Ser Leu Gln Met Thr Lys Gln Thr
85            90            95                100


caa aca caa acg caa acg cag acc gca aga tca caa tcc gcg gac agt
393
Gln Thr Gln Thr Gln Thr Gln Thr Ala Arg Ser Gln Ser Ala Asp Ser
            105           110           115


gac ggt gtg acg gct aac gaa agt cat ttg aac aga gga gta acg gag
441
Asp Gly Val Thr Ala Asn Glu Ser His Leu Asn Arg Gly Val Thr Glu
            120           125           130


acg aca gag atc aag tgg gaa gat gga aat gcg aat atg caa cag aat
489
Thr Thr Glu Ile Lys Trp Glu Asp Gly Asn Ala Asn Met Gln Gln Asn
            135       ·   140           145


ttt agg cca ttg gag gaa gat cat atc· gag caa atg att gag gag ctg
537
Phe Arg Pro Leu Glu Glu Asp His Ile Glu Gln Met Ile Glu Glu Leu
    150   ·               155           160


ctt cac tac ggt tcc att gag ctt tgc tct gtt tta cca act cag acg
585
Leu His Tyr Gly Ser Ile Glu Leu Cys Ser Val Leu Pro Thr Gln Thr
165               170           175           180


ctg tga gaaatggcct tgtcgtttta gcgtattctt ttcattttta ttttgtttc
641
Leu


cacaaaaacg gcgtcgtaag tgatgagagt agtagtgaga gaaggctaat ttcaagacat
701
```

270

tttgatctga attggcctct tttgaaacac tgattctagt ttctataaga gcaatcgatc
761

atatgctatg ttatgtatag tattataaaa aaatgttatt ttctgattaa aaaaaaaaaa
821

aaaaaaaaaa aa
·833

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152

Met Ala Arg Pro Gln Gln Arg Phe Arg Gly Val Arg Gln Arg His Trp
1   5   10   15

Gly Ser Trp Val Ser Glu Ile Arg His Pro Leu Leu Lys Thr Arg Ile
            20   25   30

Trp Leu Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp
            35   40   45

Glu Ala Ala Arg Leu Met Cys Gly Pro Arg Ala Arg Thr Asn Phe Pro
    50   55   60

Tyr Asn Pro Asn Ala Ile Pro Thr Ser Ser Ser Lys Leu Leu Ser Ala
65   70   75   80

Thr Leu Thr Ala Lys Leu His Lys Cys Tyr Met Ala Ser Leu Gln Met
            85   90   95

Thr Lys Gln Thr Gln Thr Gln Thr Gln Thr Gln Thr Ala Arg Ser Gln
            100   105   110

Ser Ala Asp Ser Asp Gly Val Thr Ala Asn Glu Ser His Leu Asn Arg
        115   120   125

Gly Val Thr Glu Thr Thr Glu Ile Lys Trp Glu Asp Gly Asn Ala Asn
    130   135   140

Met Gln Gln Asn Phe Arg Pro Leu Glu Glu Asp His Ile Glu Gln Met
145   150   155   160

Ile Glu Glu Leu Leu His Tyr Gly Ser Ile Glu Leu Cys Ser Val Leu
            165   170   175

Pro Thr Gln Thr Leu
            180

271

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<221> CDS <222> (60)..(1352) <223> G979

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59

atg aag aag cgc tta acc act tcc act tgt tct tct tct cca tct tcc
107
Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser
1   5   10   15

tct gtt tct tct tct act act act·tcc tct cct att cag tcg gag gct
155
Ser Val Ser Ser Ser Thr Thr Thr Ser Ser Pro Ile Gln Ser Glu Ala
            20   25   30

cca agg cct aaa cga gcc aaa agg gct aag aaa tct tct cct tct ggt
203
Pro Arg Pro Lys Arg Ala Lys Arg Ala Lys Lys Ser Ser Pro Ser Gly
        35,   40   45

gat aaa tct cat aac ccg aca agc cct gct tct acc cga cgc agc tct
251
Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser
    50   55   60

atc tac aga gga gtc act aga cat aga tgg act ggg aga ttc gag gct
299
Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala
65   70   75   80

cat ctt tgg gac aaa agc tct tgg aat tcg att cag aac aag aaa ggc
347
His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly
                85   90   95

aaa caa gtt tat ctg gga gca tat gac agt gaa gaa gca gca gca cat
395
Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His
            100   105   110

acg tac gat ctg gct gct ctc aag tac tgg gga ccc gac acc atc ttg
443
Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu
            115   120   125

aat ttt ccg gca gag acg tac aca aag gaa ttg gaa gaa atg cag aga
491
Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg
    130   135   140

gtg aca aag gaa gaa tat ttg gct tct ctc cgc cgc cag agc agt ggt
539
Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly
145   150   155   160

ttc tcc aga ggc gtc tct aaa tat cgc ggc gtc gct agg cat cac cac
587
Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His
                165   170   175

272

```
aac gga aga tgg gag gct cgg atc gga aga gtg ttt ggg aac aag tac
635
Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr
            180                 185                 190

ttg tac ctc ggc acc tat aat acg cag gag gaa gct gct gca gca tat
683
Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Ala Tyr
            195                 200                 205

gac atg gct gcg att gag tat cga ggc gca aac gcg gtt act aat ttc
731
Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe
        210                 215                 220

gac att agt aat tac att gac cgg tta aag aag aaa ggt gtt ttc ccg
779
Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro
225                 230                 235                 240

ttc cct gtg aac caa gct aac cat caa gag ggt att ctt gtt gaa gcc
827
Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala
                245                 250                 255

aaa caa gaa gtt gaa acg aga gaa gcg aag gaa gag cct aga gaa gaa
875
Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu
                260                 265                 270

gtg aaa caa cag tac gtg gaa gaa cca ccg caa gaa gaa gaa gag aag
923
Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Glu Lys
            275                 280                 285

gaa gaa gag aaa gca gag caa caa gaa gca gag att gta gga tat tca
971
Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser
        290                 295                 300

gaa gaa gca gca gtg gtc aat tgc tgc ata gac tct tca acc ata atg
1019
Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met
305                 310                 315                 320

gaa atg gat cgt tgt ggg gac aac aat gag ctg gct tgg aac ttc tgt
1067
Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys
                325                 330                 335

atg atg gat aca ggg ttt tct ccg ttt ttg act gat cag aat ctc gcg
1115
Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala
            340                 345                 350

aat gag aat ccc ata gag tat ccg gag cta ttc aat gag tta gca ttt
1163
Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe
            355                 360                 365
```

273

```
gag gac aac atc gac ttc atg ttc gat gat ggg aag cac gag tgc ttg
1211
Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu
    370             375             380

aac ttg gaa aat ctg gat tgt tgc gtg gtg gga aga gag agc cca ccc
1259
Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro
385             390             395             400

tct tct tct tca cca ttg tct tgc tta tct act gac tct gct tca tca
1307
Ser Ser Ser Ser Pro Leu Ser Cys Leu Ser Thr Asp Ser Ala Ser Ser
            405             410             415

aca aca aca aca aca acc tcg gtt tct tgt aac tat ttg gtc tga
1352
Thr Thr Thr Thr Thr Thr Ser Val Ser Cys Asn Tyr Leu Val
            420             425             430

gagagagagc tttgccttct agtttgaatt tctatttctt ccgcttcttc ttcttttttt
1412

tcttttgttg ggttctgctt agggtttgta tttcagtttc agggcttgtt cgttggttct
1472

gaataatcaa tgtctttgcc cctttttaaaa agatacaaga aaaaaaaaaa aaaaaaaa
1530
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Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser
1               5               10              15

Ser Val Ser Ser Ser Thr Thr Thr Ser Ser Pro Ile Gln Ser Glu Ala
            20              25              30

Pro Arg Pro Lys Arg Ala Lys Arg Ala Lys Lys Ser Ser Pro Ser Gly
        35              40              45

Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser
    50              55              60

Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala
65              70              75              80

His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly
            85              90              95

Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His
            100             105             110
```

274

```
Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu
        115             120             125


Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg
    130             135             140


Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly
145             150             155             160


Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His
            165             170             175


Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr
            180             185             190


Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Ala Tyr
        195             200             205


Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe
    210             215             220


Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro
225             230             235             240


Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala
            245             250             255


Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu
            260             265             270


Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Glu Lys
        275             280             285


Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser
    290             295             300


Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met
305             310             315             320


Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys
            325             330             335


Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala
            340             345             350


Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe
```

275

```
                355                      360                       365
```

```
       Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu
          370              375              380
```

```
       Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro
       385              390              395              400
```

```
       Ser Ser Ser Ser Pro Leu Ser Cys Leu Ser Thr Asp Ser Ala Ser Ser
                    405              410              415
```

```
       Thr Thr Thr Thr Thr Thr Ser Val Ser Cys Asn Tyr Leu Val
                    420              425              430
```

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<221> CDS <222> (1)..(954) <223> G1000

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48
Met Gly Arg Pro Pro Cys Cys Asp Lys Ser Asn Val Lys Lys Gly Leu
1               5               10               15
```

```
tgg acc gag gaa gaa gac gct aag atc ctt gct tat gtt gct atc cat
96
Trp Thr Glu Glu Glu Asp Ala Lys Ile Leu Ala Tyr Val Ala Ile His
          20               25               30
```

```
ggt gta gga aac tgg agc ttg atc ccc aaa aaa gca ggt ctg aat cga
144
Gly Val Gly Asn Trp Ser Leu Ile Pro Lys Lys Ala Gly Leu Asn Arg
          35               40               45
```

```
tgt gga aag agc tgt aga cta aga tgg act aat tac tta aga cct gac
192
Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
     50               55               60
```

```
ctt aaa cat gac agc ttc tct acc caa gaa gaa gag ctt atc att gag
240
Leu Lys His Asp Ser Phe Ser Thr Gln Glu Glu Glu Leu Ile Ile Glu
65               70               75               80
```

```
tgt cat aga gcc att ggc agc agg tgg tct tcc att gca cga aag ctt
288
Cys His Arg Ala Ile Gly Ser Arg Trp Ser Ser Ile Ala Arg Lys Leu
               85               90               95
```

```
cca gga aga acg gat aat gat gtg aag aat cac tgg aac aca aag ctg
336
Pro Gly Arg Thr Asp Asn Asp Val Lys Asn His Trp Asn Thr Lys Leu
          100              105              110
```

```
aag aag aag ctg atg aaa atg ggg ata gac ccg gtg act cat aaa ccg
384
Lys Lys Lys Leu Met Lys Met Gly Ile Asp Pro Val Thr His Lys Pro
```

```
              115                  120                  125

gtt tct caa ctc ctt gca gaa ttc aga aac att agc ggc cat gga aat
432
Val Ser Gln Leu Leu Ala Glu Phe Arg Asn Ile Ser Gly His Gly Asn
    130                  135                  140

gca tcc ttc aaa aca gaa cca tct aac aac tct ata ctc aca caa tcc
480
Ala Ser Phe Lys Thr Glu Pro Ser Asn Asn Ser Ile Leu Thr Gln Ser
145                  150                  155                  160

aac tca gct tgg gaa atg atg aga aac aca aca aac cat gag agt
528
Asn Ser Ala Trp Glu Met Met Arg Asn Thr Thr Thr Asn His Glu Ser
                165                  170                  175

tat tac acc aac tct cca atg atg ttt aca aat tcc tct gag tac caa
576
Tyr Tyr Thr Asn Ser Pro Met Met Phe Thr Asn Ser Ser Glu Tyr Gln
                180                  185                  190

act act cca ttt cat ttc tat agc cat cca aat cat ctg ctc aat gga
624
Thr Thr Pro Phe His Phe Tyr Ser His Pro Asn His Leu Leu Asn Gly
          195                  200                  205

acc aca tct tca tgc tct tcc tca tca tct tct act agt atc act cag
672
Thr Thr Ser Ser Cys Ser Ser Ser Ser Ser Ser Thr Ser Ile Thr Gln
    210                  215                  220

cca aac caa gta cct caa aca ccg gtt act aac ttc tac tgg agc gat
720
Pro Asn Gln Val Pro Gln Thr Pro Val Thr Asn Phe Tyr Trp Ser Asp
225                  230                  235                  240

ttc ctt ctc tcg gac ccg gtt cct caa gta gtg gga tcc tca gct act
768
Phe Leu Leu Ser Asp Pro Val Pro Gln Val Val Gly Ser Ser Ala Thr
                245                  250                  255

agc gac ctc act ttt acg cag aac gaa cat cat ttc aac atc gaa gcc
816
Ser Asp Leu Thr Phe Thr Gln Asn Glu His His Phe Asn Ile Glu Ala
                260                  265                  270

gaa tac atc tct caa aac atc gat tca aag gcc tcg gga aca tgt cat
864
Glu Tyr Ile Ser Gln Asn Ile Asp Ser Lys Ala Ser Gly Thr Cys His
                275                  280                  285

tcc gcg agt tcc ttc gtt gac gaa ata cta gat aaa gac caa gag atg
912
Ser Ala Ser Ser Phe Val Asp Glu Ile Leu Asp Lys Asp Gln Glu Met
    290                  295                  300

ttg tca cag ttt cct caa ctc ttg aat gat ttc gat tat tag
954
Leu Ser Gln Phe Pro Gln Leu Leu Asn Asp Phe Asp Tyr
305                  310                  315
```

277

<210> 156 <211> 317 <212> PRT <213> Arabidopsis thaliana <400>
156

Met Gly Arg Pro Pro Cys Cys Asp Lys Ser Asn Val Lys Lys Gly Leu
1   5   10   15

Trp Thr Glu Glu Glu Asp Ala Lys Ile Leu Ala Tyr Val Ala Ile His
            20   25   30

Gly Val Gly Asn Trp Ser Leu Ile Pro Lys Lys Ala Gly Leu Asn Arg
            35   40   45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
    50   55   60

Leu Lys His Asp Ser Phe Ser Thr Gln Glu Glu Glu Leu Ile Ile Glu
65   70   75   80

Cys His Arg Ala Ile Gly Ser Arg Trp Ser Ser Ile Ala Arg Lys Leu
                85   90   95

Pro Gly Arg Thr Asp Asn Asp Val Lys Asn His Trp Asn Thr Lys Leu
            100   105   110

Lys Lys Lys Leu Met Lys Met Gly Ile Asp Pro Val Thr His Lys Pro
            115   120   125

Val Ser Gln Leu Leu Ala Glu Phe Arg Asn Ile Ser Gly His Gly Asn
    130   135   140

Ala Ser Phe Lys Thr Glu Pro Ser Asn Asn Ser Ile Leu Thr Gln Ser
145   150   155   160

Asn Ser Ala Trp Glu Met Met Arg Asn Thr Thr Thr Asn His Glu Ser
            165   170   175

Tyr Tyr Thr Asn Ser Pro Met Met Phe Thr Asn Ser Ser Glu Tyr Gln
            180   185   190

Thr Thr Pro Phe His Phe Tyr Ser His Pro Asn His Leu Leu Asn Gly
            195   200   205

Thr Thr Ser Ser Cys Ser Ser Ser Ser Ser Ser Thr Ser Ile Thr Gln
    210   215   220

278

```
Pro Asn Gln Val Pro Gln Thr Pro Val Thr Asn Phe Tyr Trp Ser Asp
225                 230             235             240


Phe Leu Leu Ser Asp Pro Val Pro Gln Val Val Gly Ser Ser Ala Thr
            245             250             255


Ser Asp Leu Thr Phe Thr Gln Asn Glu His His Phe Asn Ile Glu Ala
        260             265             270


Glu Tyr Ile Ser Gln Asn Ile Asp Ser Lys Ala Ser Gly Thr Cys His
        275             280             285


Ser Ala Ser Ser Phe Val Asp Glu Ile Leu Asp Lys Asp Gln Glu Met
    290             295             300


Leu Ser Gln Phe Pro Gln Leu Leu Asn Asp Phe Asp Tyr
305             310             315
```

<210> 157 <211> 476 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (41)..(370) <223> G1012

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<400> 157
aacacacaat tcgttgattc atcatatctc ctcttcatta atg aat ggc ctc gtc
55
                                             Met Asn Gly Leu Val
                                             1               5


gac tct tct cga gat aag aag atg aaa aat ccg cga ttt tcg ttt cgc
103
Asp Ser Ser Arg Asp Lys Lys Met Lys Asn Pro Arg Phe Ser Phe Arg
              10              15              20


aca aag agt gat gca gat att ctc gat gat ggt tat cga tgg aga aag
151
Thr Lys Ser Asp Ala Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys
          25              30              35


tac ggt cag aaa tcc gtc aag aac agc ttg tat ccc agg agc tat tat
199
Tyr Gly Gln Lys Ser Val Lys Asn Ser Leu Tyr Pro Arg Ser Tyr Tyr
      40              45              50


aga tgc aca caa cac atg tgt aac gtg aag aag caa gtt cag agg ctg
247
Arg Cys Thr Gln His Met Cys Asn Val Lys Lys Gln Val Gln Arg Leu
    55              60              65


tcg aag gag acg agc att gtg gag aca act tat gaa gga atc cat aac
295
Ser Lys Glu Thr Ser Ile Val Glu Thr Thr Tyr Glu Gly Ile His Asn
70              75              80              85


cat cct tgt gag gag ctc atg caa acc cta act cct ctt ctt cat caa
343
His Pro Cys Glu Glu Leu Met Gln Thr Leu Thr Pro Leu Leu His Gln
```

                    90   95   100

ttg cag ttc ctc tct aag ttc acc taa ttatgtttgt atatatatta
390
Leu Gln Phe Leu Ser Lys Phe Thr
            105

acgttctaag agcatctcca atggaagtat ctcaatgaga tacctaacaa aagaaaaaaa
450

atttaaaaaa aaaaaaaaaa aaaaaa
476

<210> 158 <211> 109 <212> PRT <213> Arabidopsis thaliana <400>
158

Met Asn Gly Leu Val Asp Ser Ser Arg Asp Lys Lys Met Lys Asn Pro
1   5   10   15

Arg Phe Ser Phe Arg Thr Lys Ser Asp Ala Asp Ile Leu Asp Asp Gly
            20   25   30

Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys Asn Ser Leu Tyr
            35   40   45

Pro Arg Ser Tyr Tyr Arg Cys Thr Gln His Met Cys Asn Val Lys Lys
        50   55   60

Gln Val Gln Arg Leu Ser Lys Glu Thr Ser Ile Val Glu Thr Thr Tyr
65   70   75   80

Glu Gly Ile His Asn His Pro Cys Glu Glu Leu Met Gln Thr Leu Thr
                85   90   95

Pro Leu Leu His Gln Leu Gln Phe Leu Ser Lys Phe Thr
            100   105

<210> 159 <211> 1257 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (174)..(1112) <223> G1014

 <400> 159
cacaaaccac agtctctctt tctctctcta tctatcttct ctttctctct ctatctctat
60

cactgaaacc caaagagatc caccatttgt tctttttttcc ttcacacaga gaactgtttt
120

cttccacact tccttttttac taggcagtgt taaccaattg agagagaaaa atg atg
176
                                                          Met
                                                          1

```
gtt gat gaa aat gtg gaa acc aag gcc tct act tta gtg gca agt gtt
224
Val Asp Glu Asn Val Glu Thr Lys Ala Ser Thr Leu Val Ala Ser Val
            5                 10                15

gat cat ggg ttt gga tcc ggg tcg ggt cat gat cat cat ggg tta tcg
272
Asp His Gly Phe Gly Ser Gly Ser Gly His Asp His His Gly Leu Ser
        20             25                30

gcg tct gtg cct ctt ctt ggt gtt aac tgg aag aag aga agg atg cct
320
Ala Ser Val Pro Leu Leu Gly Val Asn Trp Lys Lys Arg Arg Met Pro
    35             40                45

aga cag aga cga tct tct tct tcc ttt aac ctt ctc tct ttc cct cct
368
Arg Gln Arg Arg Ser Ser Ser Ser Phe Asn Leu Leu Ser Phe Pro Pro
50             55                60                65

cct atg cct cct att tcc cac gtg cca act cct ctc ccc gca cgt aaa
416
Pro Met Pro Pro Ile Ser His Val Pro Thr Pro Leu Pro Ala Arg Lys
            70                75                80

att gac cca aga aag cta aga ttc ctc ttc caa aag gaa ctc aag aac
464
Ile Asp Pro Arg Lys Leu Arg Phe Leu Phe Gln Lys Glu Leu Lys Asn
            85                 90                95

agt gac gtc agc tct ctc cga cgt atg ata ctc ccg aag aaa gcc gcg
512
Ser Asp Val Ser Ser Leu Arg Arg Met Ile Leu Pro Lys Lys Ala Ala
        100               105               110

gag gct cac ttg ccg gca ctt gaa tgc aag gaa ggg att cct ata aga
560
Glu Ala His Leu Pro Ala Leu Glu Cys Lys Glu Gly Ile Pro Ile Arg
    115               120               125

atg gaa gat ttg gac ggt ttt cac gtt tgg acc ttc aag tat agg tac
608
Met Glu Asp Leu Asp Gly Phe His Val Trp Thr Phe Lys Tyr Arg Tyr
130               135               140               145

tgg cca aac aac aat agc aga atg tac gtg cta gaa aac aca ggc gat
656
Trp Pro Asn Asn Asn Ser Arg Met Tyr Val Leu Glu Asn Thr Gly Asp
            150               155               160

ttt gtg aat gct cat ggt ctg cag cta ggt gac ttc atc atg gtt tac
704
Phe Val Asn Ala His Gly Leu Gln Leu Gly Asp Phe Ile Met Val Tyr
            165               170               175

caa gat ctc tac tca aac aat tac gtt ata caa gca aga aaa gca tcg
752
Gln Asp Leu Tyr Ser Asn Asn Tyr Val Ile Gln Ala Arg Lys Ala Ser
        180               185               190
```

gaa gaa gaa gaa gta gac gta atc aat ctt gaa gaa gac gac gtt tac
800
Glu Glu Glu Glu Val Asp Val Ile Asn Leu Glu Glu Asp Asp Val Tyr
    195   200   205

aca aac tta aca agg atc gaa aac act gtg gtt aac gat ctt ctc ctc
848
Thr Asn Leu Thr Arg Ile Glu Asn Thr Val Val Asn Asp Leu Leu Leu
210   215   220   225

caa gat ttt aat cat cac aac aac aac aac aac aac aac agc aac agc
896
Gln Asp Phe Asn His His Asn Asn Asn Asn Asn Asn Asn Ser Asn Ser
            230   235   240

aac agc aac aaa tgt tct tac tat tat cca gtc ata gat gat gtc acc
944
Asn Ser Asn Lys Cys Ser Tyr Tyr Tyr Pro Val Ile Asp Asp Val Thr
            245   250   255

aca aac aca gag tct ttt gtc tac gac acg acg gct ctt acc tcc aac
992
Thr Asn Thr Glu Ser Phe Val Tyr Asp Thr Thr Ala Leu Thr Ser Asn
            260   265   --   270

gat act cct ctc gat ttt ttg ggt gga cat acg acg act act aat aat
1040
Asp Thr Pro Leu Asp Phe Leu Gly Gly His Thr Thr Thr Thr Asn Asn
    275   280   285

tat tac tcc aag ttc gga aca ttc gat ggt ttg ggc tcc gtt gag aat
1088
Tyr Tyr Ser Lys Phe Gly Thr Phe Asp Gly Leu Gly Ser Val Glu Asn
290   295   300   305

atc tct ctc gat gac ttc tac tag ataatcaatc gatgggctca tggtattctt
1142
Ile Ser Leu Asp Asp Phe Tyr
                310

gatggtgatc agctatttaa tatccttata atatatataa gaattaaatg caatttgcat
1202

atatattatc aagtgttgta atataacatt acagtttaaa aaaaaaaaa aaaaa
1257

<210> 160 <211> 312 <212> PRT <213> Arabidopsis thaliana <400>
160

Met Val Asp Glu Asn Val Glu Thr Lys Ala Ser Thr Leu Val Ala Ser
1   5   10   15

Val Asp His Gly Phe Gly Ser Gly Ser Gly His Asp His His Gly Leu
            20   25   30

Ser Ala Ser Val Pro Leu Leu Gly Val Asn Trp Lys Lys Arg Arg Met
        35   40   45

282

```
Pro Arg Gln Arg Arg Ser Ser Ser Ser Phe Asn Leu Leu Ser Phe Pro
    50              55              60


Pro Pro Met Pro Pro Ile Ser His Val Pro Thr Pro Leu Pro Ala Arg
65              70              75              80


Lys Ile Asp Pro Arg Lys Leu Arg Phe Leu Phe Gln Lys Glu Leu Lys
            85              90              95


Asn Ser Asp Val Ser Ser Leu Arg Arg Met Ile Leu Pro Lys Lys Ala
            100             105             110


Ala Glu Ala His Leu Pro Ala Leu Glu Cys Lys Glu Gly Ile Pro Ile
        115             120             125


Arg Met Glu Asp Leu Asp Gly Phe His Val Trp Thr Phe Lys Tyr Arg
    130             135             140


Tyr Trp Pro Asn Asn Asn Ser Arg Met Tyr Val Leu Glu Asn Thr Gly
145             150             155             160


Asp Phe Val Asn Ala His Gly Leu Gln Leu Gly Asp Phe Ile Met Val
            165             170             175


Tyr Gln Asp Leu Tyr Ser Asn Asn Tyr Val Ile Gln Ala Arg Lys Ala
            180             185             190


Ser Glu Glu Glu Glu Val Asp Val Ile Asn Leu Glu Glu Asp Asp Val
        195             200             205


Tyr Thr Asn Leu Thr Arg Ile Glu Asn Thr Val Val Asn Asp Leu Leu
    210             215             220


Leu Gln Asp Phe Asn His His Asn Asn Asn Asn Asn Asn Ser Asn
225             230             235             240


Ser Asn Ser Asn Lys Cys Ser Tyr Tyr Tyr Pro Val Ile Asp Asp Val
            245             250             255


Thr Thr Asn Thr Glu Ser Phe Val Tyr Asp Thr Thr Ala Leu Thr Ser
        260             265             270


Asn Asp Thr Pro Leu Asp Phe Leu Gly Gly His Thr Thr Thr Thr Asn
    275             280             285
```

Asn Tyr Tyr Ser Lys Phe Gly Thr Phe Asp Gly Leu Gly Ser Val Glu
    290   295   300

Asn Ile Ser Leu Asp Asp Phe Tyr
305   310

<210> 161 <211> 1057 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (51)..(863) <223> G1040

<400> 161
ctttgatctc cactatttaa gtagacaaga atcataaaga aaatagtgag atg atg
56
                                                        Met Met
                                                          1

atg tta gag tca aga aac agt atg aga gct tca aac tca gtc cca gat
104
Met Leu Glu Ser Arg Asn Ser Met Arg Ala Ser Asn Ser Val Pro Asp
        5   10   15

ctg tct ctt cag atc agt ctt cct aac tat cac gcc gga aaa cct ctt
152
Leu Ser Leu Gln Ile Ser Leu Pro Asn Tyr His Ala Gly Lys Pro Leu
    20   25   30

cac ggc ggt gac cgg agc tcc aca agc agt gat tct gga agc agc ctc
200
His Gly Gly Asp Arg Ser Ser Thr Ser Ser Asp Ser Gly Ser Ser Leu
35   40   45   50

agt gac ctg agc cat gag aac aac ttc ttc aac aaa cct ctc ttg agc
248
Ser Asp Leu Ser His Glu Asn Asn Phe Phe Asn Lys Pro Leu Leu Ser
                55   60   65

tta gga ttt gac cat cat cat caa agg cgc tca aac atg ttc caa cct
296
Leu Gly Phe Asp His His His Gln Arg Arg Ser Asn Met Phe Gln Pro
                70   75   80

caa atc tac ggt cga gat ttc aag aga agc tca tca tca atg gtt ggt
344
Gln Ile Tyr Gly Arg Asp Phe Lys Arg Ser Ser Ser Ser Met Val Gly
            85   90   95

ctt aaa cga agc att cgt gct cca aga atg aga tgg act tct act ctt
392
Leu Lys Arg Ser Ile Arg Ala Pro Arg Met Arg Trp Thr Ser Thr Leu
    100   105   110

cat gct cac ttc gtc cat gct gtt caa ctt ctt ggc ggc cat gaa aga
440
His Ala His Phe Val His Ala Val Gln Leu Leu Gly Gly His Glu Arg
115   120   125   130

gca acg cct aaa tca gtg ttg gag ctc atg aat gtg aag gat cta acc
488
Ala Thr Pro Lys Ser Val Leu Glu Leu Met Asn Val Lys Asp Leu Thr
                135   140   145

284

cta gct cat gtc aag agt cac ttg cag atg tat aga aca gtg aaa tgc
536
Leu Ala His Val Lys Ser His Leu Gln Met Tyr Arg Thr Val Lys Cys
            150   155   160

act gat aaa gga tca cca gga gaa gga aag gta gag aaa gag gca gag
584
Thr Asp Lys Gly Ser Pro Gly Glu Gly Lys Val Glu Lys Glu Ala Glu
            165   170   175

cag agg ata gag gac aat aat aat aat gaa gaa gct gat gaa gga act
632
Gln Arg Ile Glu Asp Asn Asn Asn Asn Glu Glu Ala Asp Glu Gly Thr
        180   185   190

gac aca aat tcg cca aac tca tca tct gtg caa aag acc caa aga gct
680
Asp Thr Asn Ser Pro Asn Ser Ser Ser Val Gln Lys Thr Gln Arg Ala
195   200   205   210

tca tgg tca tcg aca aag gaa gta tct agg agc ata tct aca caa gca
728
Ser Trp Ser Ser Thr Lys Glu Val Ser Arg Ser Ile Ser Thr Gln Ala
            215   220   225

tat tct cac ttg gga aca act cat cac act aag gcc aat gaa gag aaa
776
Tyr Ser His Leu Gly Thr Thr His His Thr Lys Ala Asn Glu Glu Lys
            230   235   240

gag gat acc aac att cat ctc aat ttg gat ttc aca ttg ggc ggc cta
824
Glu Asp Thr Asn Ile His Leu Asn Leu Asp Phe Thr Leu Gly Gly Leu
        245   250   255

gtt ggg gga tgg aat atg cgg aac cct cca gtg att taa cccttctcaa
873
Val Gly Gly Trp Asn Met Arg Asn Pro Pro Val Ile
    260   265   270

gtgctaattg ccttaagcta caacaaataa gtcagcttag gttaccagtt ttaacataat
933

tttaacttgt tttgatcata tgagcttcgg aagaatcata ttatcatcat atatgaactt
993

ctttccaaga atgttctatg agtttttttga tatgtataat caagagaatc gtttgaagta
1053

aaaa
1057

<210> 162 <211> 270 <212> PRT <213> Arabidopsis thaliana <400>
162

Met Met Met Leu Glu Ser Arg Asn Ser Met Arg Ala Ser Asn Ser Val
1   5   10   15

285

```
Pro Asp Leu Ser Leu Gln Ile Ser Leu Pro Asn Tyr His Ala Gly Lys
          20                  25                  30

Pro Leu His Gly Gly Asp Arg Ser Ser Thr Ser Ser Asp Ser Gly Ser
          35                  40                  45

Ser Leu Ser Asp Leu Ser His Glu Asn Asn Phe Phe Asn Lys Pro Leu
          50                  55                  60

Leu Ser Leu Gly Phe Asp His His His Gln Arg Arg Ser Asn Met Phe
65                  70                  75                  80

Gln Pro Gln Ile Tyr Gly Arg Asp Phe Lys Arg Ser Ser Ser Ser Met
                  85                  90                  95

Val Gly Leu Lys Arg Ser Ile Arg Ala Pro Arg Met Arg Trp Thr Ser
              100                 105                 110

Thr Leu His Ala His Phe Val His Ala Val Gln Leu Leu Gly Gly His
          115                 120                 125

Glu Arg Ala Thr Pro Lys Ser Val Leu Glu Leu Met Asn Val Lys Asp
    130                 135                 140

Leu Thr Leu Ala His Val Lys Ser His Leu Gln Met Tyr Arg Thr Val
145                 150                 155                 160

Lys Cys Thr Asp Lys Gly Ser Pro Gly Glu Gly Lys Val Glu Lys Glu
              165                 170                 175

Ala Glu Gln Arg Ile Glu Asp Asn Asn Asn Asn Glu Glu Ala Asp Glu
              180                 185                 190

Gly Thr Asp Thr Asn Ser Pro Asn Ser Ser Ser Val Gln Lys Thr Gln
          195                 200                 205

Arg Ala Ser Trp Ser Ser Thr Lys Glu Val Ser Arg Ser Ile Ser Thr
    210                 215                 220

Gln Ala Tyr Ser His Leu Gly Thr Thr His His Thr Lys Ala Asn Glu
225                 230                 235                 240

Glu Lys Glu Asp Thr Asn Ile His Leu Asn Leu Asp Phe Thr Leu Gly
              245                 250                 255

Gly Leu Val Gly Gly Trp Asn Met Arg Asn Pro Pro Val Ile
```

286

            260   265   270

<210> 163 <211> 1766 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (23)..(1582) <223> G1050

 <400> 163
ttccccattt cagaaaatca aa atg ggt ggt ggt ggt gat aca aca gat acc
52
                        Met Gly Gly Gly Gly Asp Thr Thr Asp Thr
                        1   5   10

aat atg atg cag aga gtt aat tct tct tct ggt aca tcg tct tct tcg
100
Asn Met Met Gln Arg Val Asn Ser Ser Ser Gly Thr Ser Ser Ser Ser
            15   20   25

atc cct aaa cac aat ctt cac ttg aat cct gct ctt atc cgc tct cac
148
Ile Pro Lys His Asn Leu His Leu Asn Pro Ala Leu Ile Arg Ser His
            30   35   40

cat cac ttc cgt cac cct ttc acc gga gct cct cca ccg ccg att cca
196
His His Phe Arg His Pro Phe Thr Gly Ala Pro Pro Pro Pro Ile Pro
            45   50   55

ccc att tct cct tac tct cag atc ccg gcg act tta caa cct aga cat
244
Pro Ile Ser Pro Tyr Ser Gln Ile Pro Ala Thr Leu Gln Pro Arg His
    60   65   70

tct cgc tct atg tcg caa ccg tct tct ttc ttc tcc ttt gat tca ttg
292
Ser Arg Ser Met Ser Gln Pro Ser Ser Phe Phe Ser Phe Asp Ser Leu
75   80.   85   90

ccg ccg tta aat cct tct gct ccg tcg gtt tcg gtg tcg gtg gag gag
340
Pro Pro Leu Asn Pro Ser Ala Pro Ser Val Ser Val Ser Val Glu Glu
            95   100   105

aaa acc ggt gcc gga ttt agt cct tcg ttg cct ccg tca ccg ttt acg
388
Lys Thr Gly Ala Gly Phe Ser Pro Ser Leu Pro Pro Ser Pro Phe Thr
            110   115   120

atg tgt cat tct tct agc tct agg aac gcc gga gat gga gag aat cta
436
Met Cys His Ser Ser Ser Ser Arg Asn Ala Gly Asp Gly Glu Asn Leu
        125   130   135

cct ccg aga aag tcg cat agg cgt tcg aat agt gat gtt act ttt ggg
484
Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Val Thr Phe Gly
        140   145   150

ttt agt tca atg atg tct cag aat caa aag tct cct cct ttg agt tct
532
Phe Ser Ser Met Met Ser Gln Asn Gln Lys Ser Pro Pro Leu Ser Ser
155   160   165   170

                              287

ttg gag aga tcg atc tct ggt gaa gat aca tca gat tgg tct aat ttg
580
Leu Glu Arg Ser Ile Ser Gly Glu Asp Thr Ser Asp Trp Ser Asn Leu
            175   180   185

gtg aag aaa gaa ccg aga gaa ggc ttc tac aag gga aga aaa cca gag
628
Val Lys Lys Glu Pro Arg Glu Gly Phe Tyr Lys Gly Arg Lys Pro Glu
            190   195   200

gtt gaa gca gct atg gac gat gtt ttc acg gct tat atg aat ctt gat
676
Val Glu Ala Ala Met Asp Asp Val Phe Thr Ala Tyr Met Asn Leu Asp
            205   210   215

aac att gat gtc ttg aat tct ttt gga ggt gaa gat ggc aag aat ggg
724
Asn Ile Asp Val Leu Asn Ser Phe Gly Gly Glu Asp Gly Lys Asn Gly
            220   225   230

aat gag aat gtg gag gag atg gag agt agt aga ggt agt ggt aca aag
772
Asn Glu Asn Val Glu Glu Met Glu Ser Ser Arg Gly Ser Gly Thr Lys
235   240   245   250

aag acg aat ggt gga agt agt agt gat tct gaa gga gat agc agt gcg
820
Lys Thr Asn Gly Gly Ser Ser Ser Asp Ser Glu Gly Asp Ser Ser Ala
            255   260   265

agt ggg aat gtg aag gtt gcg ttg agt tct tct tct tca ggc gtg aag
868
Ser Gly Asn Val Lys Val Ala Leu Ser Ser Ser Ser Ser Gly Val Lys
            270   275   280

aga aga gca ggt gga gat att gct cct act ggt aga cat tac agg agt
916
Arg Arg Ala Gly Gly Asp Ile Ala Pro Thr Gly Arg His Tyr Arg Ser
            285   290   295

gtt tct atg gac agt tgt ttc atg ggg aag ttg aat ttc ggc gac gaa
964
Val Ser Met Asp Ser Cys Phe Met Gly Lys Leu Asn Phe Gly Asp Glu
            300   305   310

tca tcg cta aag ctt ccg cct tct tca tca gct aaa gtt tcc cca acc
1012
Ser Ser Leu Lys Leu Pro Pro Ser Ser Ser Ala Lys Val Ser Pro Thr
315   320   325   330

aat tca ggt gaa ggg aat tca agt gct tat agt gtt gaa ttt gga aac
1060
Asn Ser Gly Glu Gly Asn Ser Ser Ala Tyr Ser Val Glu Phe Gly Asn
            335   340   345

agt gag ttt act gca gct gaa atg aag aag att gca gct gat gag aaa
1108
Ser Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Ala Ala Asp Glu Lys
            350   355   360

288

```
ctc gct gag att gta atg gct gac cct aag cgt gtt aaa aga atc ttg
1156
Leu Ala Glu Ile Val Met Ala Asp Pro Lys Arg Val Lys Arg Ile Leu
        365                     370                 375


gcg aac cgc gta tct gct gca cgt tca aag gag cgg aag acg cga tac
1204
Ala Asn Arg Val Ser Ala Ala Arg Ser Lys Glu Arg Lys Thr Arg Tyr
    380                     385                 390


atg gca gag ttg gaa cac aag gtg cag aca ctt cag act gaa gct act
1252
Met Ala Glu Leu Glu His Lys Val Gln Thr Leu Gln Thr Glu Ala Thr
395                 400                 405                 410


aca tta tcg gct cag ctc aca cat ttg cag aga gat tct atg ggg ttg
1300
Thr Leu Ser Ala Gln Leu Thr His Leu Gln Arg Asp Ser Met Gly Leu
                415                 420                 425


aca aac cag aac agt gag ctg aag ttt cgt ctt caa gct atg gag cag
1348
Thr Asn Gln Asn Ser Glu Leu Lys Phe Arg Leu Gln Ala Met Glu Gln
            430                 435                 440


caa gca caa ctc cgc gat gct ctg tca gag aaa ctg aat gaa gaa gtc
1396
Gln Ala Gln Leu Arg Asp Ala Leu Ser Glu Lys Leu Asn Glu Glu Val
        445                 450                 455


cag cgg ttg aaa ctg gtg ata ggg gag ccg aac cgc agg caa agt ggg
1444
Gln Arg Leu Lys Leu Val Ile Gly Glu Pro Asn Arg Arg Gln Ser Gly
    460                 465                 470


agc agc agc agc gaa tca aag atg tca cta aac ccg gag atg ttt cag
1492
Ser Ser Ser Ser Glu Ser Lys Met Ser Leu Asn Pro Glu Met Phe Gln
475                 480                 485                 490


cag ctt agc ata agt cag tta caa cac caa cag atg cag cat tcc aat
1540
Gln Leu Ser Ile Ser Gln Leu Gln His Gln Gln Met Gln His Ser Asn
                495                 500                 505


cag tgt agc aca atg aaa gca aag cac act tca aac gac tag
1582
Gln Cys Ser Thr Met Lys Ala Lys His Thr Ser Asn Asp
                510                 515


ggtaagtaaa actgcgatcc gcagttgtct agttacatat atgataagaa tcttttgtgc
1642


agagttctgt ttttggaagt tttaaagaaa catatataaa gattatgtcc gggaaatttg
1702


atcatatttc ctgaaacata cacacatata tatagtggta atggaggact ttctttctgg
1762


acca
1766
```

<210> 164 <211> 519 <212> PRT <213> Arabidopsis thaliana <400>
164

Met Gly Gly Gly Gly Asp Thr Thr Asp Thr Asn Met Met Gln Arg Val
1   5   10   15

Asn Ser Ser Ser Gly Thr Ser Ser Ser Ser Ile Pro Lys His Asn Leu
        20   25   30

His Leu Asn Pro Ala Leu Ile Arg Ser His His His Phe Arg His Pro
        35   40   45

Phe Thr Gly Ala Pro Pro Pro Ile Pro Pro Ile Ser Pro Tyr Ser
    50   55   60

Gln Ile Pro Ala Thr Leu Gln Pro Arg His Ser Arg Ser Met Ser Gln
65   70   75   80

Pro Ser Ser Phe Phe Ser Phe Asp Ser Leu Pro Pro Leu Asn Pro Ser
        85   90   95

Ala Pro Ser Val Ser Val Ser Val Glu Glu Lys Thr Gly Ala Gly Phe
        100   105   110

Ser Pro Ser Leu Pro Pro Ser Pro Phe Thr Met Cys His Ser Ser Ser
        115   120   125

Ser Arg Asn Ala Gly Asp Gly Glu Asn Leu Pro Pro Arg Lys Ser His
    130   135   140

Arg Arg Ser Asn Ser Asp Val Thr Phe Gly Phe Ser Ser Met Met Ser
145   150   155   160

Gln Asn Gln Lys Ser Pro Pro Leu Ser Ser Leu Glu Arg Ser Ile Ser
            165   170   175

Gly Glu Asp Thr Ser Asp Trp Ser Asn Leu Val Lys Lys Glu Pro Arg
            180   185   190

Glu Gly Phe Tyr Lys Gly Arg Lys Pro Glu Val Glu Ala Ala Met Asp
            195   200   205

Asp Val Phe Thr Ala Tyr Met Asn Leu Asp Asn Ile Asp Val Leu Asn
    210   215   220

290

Ser Phe Gly Gly Glu Asp Gly Lys Asn Gly Asn Glu Asn Val Glu Glu
225   230   235   240

Met Glu Ser Ser Arg Gly Ser Gly Thr Lys Lys Thr Asn Gly Gly Ser
                245   250   255

Ser Ser Asp Ser Glu Gly Asp Ser Ser Ala Ser Gly Asn Val Lys Val
                260   265   270

Ala Leu Ser Ser Ser Ser Ser Gly Val Lys Arg Arg Ala Gly Gly Asp
                275   280   285

Ile Ala Pro Thr Gly Arg His Tyr Arg Ser Val Ser Met Asp Ser Cys
    290   295   300

Phe Met Gly Lys Leu Asn Phe Gly Asp Glu Ser Ser Leu Lys Leu Pro
305   310   315   320

Pro Ser Ser Ser Ala Lys Val Ser Pro Thr Asn Ser Gly Glu Gly Asn
                325   330   335

Ser Ser Ala Tyr Ser Val Glu Phe Gly Asn Ser Glu Phe Thr Ala Ala
                340   345   350

Glu Met Lys Lys Ile Ala Ala Asp Glu Lys Leu Ala Glu Ile Val Met
                355   360   365

Ala Asp Pro Lys Arg Val Lys Arg Ile Leu Ala Asn Arg Val Ser Ala
    370   375   380

Ala Arg Ser Lys Glu Arg Lys Thr Arg Tyr Met Ala Glu Leu Glu His
385   390   395   400

Lys Val Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu
                405   410   415

Thr His Leu Gln Arg Asp Ser Met Gly Leu Thr Asn Gln Asn Ser Glu
                420   425   430

Leu Lys Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Gln Leu Arg Asp
                435   440   445

Ala Leu Ser Glu Lys Leu Asn Glu Glu Val Gln Arg Leu Lys Leu Val
    450   455   460

Ile Gly Glu Pro Asn Arg Arg Gln Ser Gly Ser Ser Ser Ser Glu Ser

291

465   470   475   480

Lys Met Ser Leu Asn Pro Glu Met Phe Gln Gln Leu Ser Ile Ser Gln
            485   490 ·   495

Leu Gln His Gln Gln Met Gln His Ser Asn Gln Cys Ser Thr Met Lys
            500   505   510

Ala Lys His Thr Ser Asn Asp
        515

<210> 165 <211> 1304 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (138)..(1127) <223> G1052

 <400> 165
tgatcatcta aaactttcaa tttctctctt gatcctcact tgaatttttt gttgtttctc
60

tcaaatcttt gatcctttcc tttgtttttc atttgacctc ttacaaaaaa atctggtgtg
120

ccattaaatc tttatta atg gca caa ctt cct ccg aaa atc cca acc atg
170
                     Met Ala Gln Leu Pro Pro Lys Ile Pro Thr Met
                     1   5   10

acg acg cca aat tgg cct gac ttc tcc tcc cag aaa ctc cct tcc ata
218
Thr Thr Pro Asn Trp Pro Asp Phe Ser Ser Gln Lys Leu Pro Ser Ile
            15   20   25

gcc gca acg gcg gca gcc gca gca acc gct gga cct caa caa caa aac
266
Ala Ala Thr Ala Ala Ala Ala Ala Thr Ala Gly Pro Gln Gln Gln Asn
            30   35   40

cct tca tgg atg gat gag ttt ctc gac ttc tca gcg act cgc cgt ggg
314
Pro Ser Trp Met Asp Glu Phe Leu Asp Phe Ser Ala Thr Arg Arg Gly
        45   50   55

act cac cgt cgt tct ata agc gac tcc att gct ttc ctt gaa cca cct
362
Thr His Arg Arg Ser Ile Ser Asp Ser Ile Ala Phe Leu Glu Pro Pro
60   65   70   75

tcc tcc ggc gtc gga aac cac cac ttc gat agg ttt gac gac gag caa
410
Ser Ser Gly Val Gly Asn His His Phe Asp Arg Phe Asp Asp Glu Gln
                80   85   90

ttc atg tcc atg ttc aac gac gac gta cac aac aat aac cac aat cat
458
Phe Met Ser Met Phe Asn Asp Asp Val His Asn Asn Asn His Asn His
                95   100   105

292

cat cat cat cac agc atc aac ggc aat gtg ggt ccc acg cgt tca tcc
506
His His His His Ser Ile Asn Gly Asn Val Gly Pro Thr Arg Ser Ser
        110   115   120

tcc aac acc tcc acg ccg tcc gat cat aat agc ctt agc gac gac gac
554
Ser Asn Thr Ser Thr Pro Ser Asp His Asn Ser Leu Ser Asp Asp Asp
    125   130   135

aac aac aaa gaa gca cca ccg tcc gat cat gat cat cac atg gac aat
602
Asn Asn Lys Glu Ala Pro Pro Ser Asp His Asp His His Met Asp Asn
140   145   150   155

aat gta gcc aat caa aac aac gcc gcc ggt aac aat tac aac gaa tca
650
Asn Val Ala Asn Gln Asn Asn Ala Ala Gly Asn Asn Tyr Asn Glu Ser
            160   165   170

gac gag gtc caa agc cag tgc aag acg gag cca caa gat ggt ccg tcg
698
Asp Glu Val Gln Ser Gln Cys Lys Thr Glu Pro Gln Asp Gly Pro Ser
        175   180   185

gcg aat caa aac tcc ggt gga agc tcc ggt aat cgt att cac gac cct
746
Ala Asn Gln Asn Ser Gly Gly Ser Ser Gly Asn Arg Ile His Asp Pro
        190   195   200

aaa agg gta aaa aga att tta gca aat agg caa tca gca cag aga tca
794
Lys Arg Val Lys Arg Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser
        205   210   215

agg gtg agg aaa ttg caa tac ata tca gag ctt gaa agg agc gtt act
842
Arg Val Arg Lys Leu Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr
220   225   230   235

tca ttg cag act gaa gtg tca gtg tta tcg cca aga gtt gcg ttt ttg
890
Ser Leu Gln Thr Glu Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu
            240   245   250

gat cat cag cga ttg ctt ctc aac gtc gac aat agt gct atc aag caa
938
Asp His Gln Arg Leu Leu Leu Asn Val Asp Asn Ser Ala Ile Lys Gln
        255   260   265

cga atc gca gct tta gca caa gat aag att ttc aaa gac gct cat caa
986
Arg Ile Ala Ala Leu Ala Gln Asp Lys Ile Phe Lys Asp Ala His Gln
        270   275   280

gaa gca ttg aag aga gaa ata gag aga ctt cga caa gta tat cat caa
1034
Glu Ala Leu Lys Arg Glu Ile Glu Arg Leu Arg Gln Val Tyr His Gln
        285   290   295

293

```
caa agc ctc aag aag atg gag aat aat gtc tcc gat caa tct ccg gcc
1082
Gln Ser Leu Lys Lys Met Glu Asn Asn Val Ser Asp Gln Ser Pro Ala
300             305             310             315

gat atc aaa ccg tcc gtt gag aag gaa cag ctc ctc aat gtc taa
1127
Asp Ile Lys Pro Ser Val Glu Lys Glu Gln Leu Leu Asn Val
            320             325

agctgttcgt tcactaagat ctttcttttc atggcgaaaa gattcttgac tataaaacct
1187

ctttgtgtca agaaattaat ttatcaaaga agatggcctt ttttatttga tctaatcaca
1247

tttttttaag ttgtgatgaa tttgcttttg atgtatctgt tttttttttt ttttttt
1304
```

<210> 166 <211> 329 <212> PRT <213> Arabidopsis thaliana <400>
166

```
Met Ala Gln Leu Pro Pro Lys Ile Pro Thr Met Thr Thr Pro Asn Trp
1               5               10              15


Pro Asp Phe Ser Ser Gln Lys Leu Pro Ser Ile Ala Ala Thr Ala Ala
            20              25              30


Ala Ala Ala Thr Ala Gly Pro Gln Gln Gln Asn Pro Ser Trp Met Asp
            35              40              45


Glu Phe Leu Asp Phe Ser Ala Thr Arg Arg Gly Thr His Arg Arg Ser
    50              55              60


Ile Ser Asp Ser Ile Ala Phe Leu Glu Pro Pro Ser Ser Gly Val Gly
65              70              75              80


Asn His His Phe Asp Arg Phe Asp Asp Glu Gln Phe Met Ser Met Phe
                85              90              95


Asn Asp Asp Val His Asn Asn Asn His Asn His His His His Ser
            100             105             110


Ile Asn Gly Asn Val Gly Pro Thr Arg Ser Ser Ser Asn Thr Ser Thr
            115             120             125


Pro Ser Asp His Asn Ser Leu Ser Asp Asp Asp Asn Asn Lys Glu Ala
    130             135             140


Pro Pro Ser Asp His Asp His His Met Asp Asn Asn Val Ala Asn Gln
145             150             155             160
```

294

```
Asn Asn Ala Ala Gly Asn Asn Tyr Asn Glu Ser Asp Glu Val Gln Ser
            165                 170                 175


Gln Cys Lys Thr Glu Pro Gln Asp Gly Pro Ser Ala Asn Gln Asn Ser
            180                 185                 190


Gly Gly Ser Ser Gly Asn Arg Ile His Asp Pro Lys Arg Val Lys Arg
            195                 200                 205


Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser Arg Val Arg Lys Leu
        210                 215                 220


Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr Ser Leu Gln Thr Glu
225                 230                 235                 240


Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu Asp His Gln Arg Leu
            245                 250                 255


Leu Leu Asn Val Asp Asn Ser Ala Ile Lys Gln Arg Ile Ala Ala Leu
            260                 265                 270


Ala Gln Asp Lys Ile Phe Lys Asp Ala His Gln Glu Ala Leu Lys Arg
            275                 280                 285


Glu Ile Glu Arg Leu Arg Gln Val Tyr His Gln Gln Ser Leu Lys Lys
        290                 295                 300


Met Glu Asn Asn Val Ser Asp Gln Ser Pro Ala Asp Ile Lys Pro Ser
305                 310                 315                 320


Val Glu Lys Glu Gln Leu Leu Asn Val
            325
```

<210> 167 <211> 1148 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (241)..(966) <223> G1063

 <400> 167
gttaaagaag atggatgggc cacaagttgc tatataaatc cttccacttc ttgttgtata
60

ctattgcttg agttctgatt gggcacagta gtaccattgc catttctctc acacataccg
120

tctctttctc tcatcatcaa tcatcaatca tccaaaagaa aaaccctaa aatttcactt
180

gtaagctttt caccagtttc tctccatacc cattttatca gcttctccat atctttctct
240

atg gat tct gac ata atg aac atg atg atg cat cag atg gag aag ctt
288
Met Asp Ser Asp Ile Met Asn Met Met Met His Gln Met Glu Lys Leu
1   5   10   15

cct gag ttt tgt aac cct aat tcc tct ttc ttc tct ccc gac cac aac
336
Pro Glu Phe Cys Asn Pro Asn Ser Ser Phe Phe Ser Pro Asp His Asn
                20   25   30

aac act tac cct ttt ctc ttt aac tcc act cat tac cag tcc gat cac
384
Asn Thr Tyr Pro Phe Leu Phe Asn Ser Thr His Tyr Gln Ser Asp His
            35   40   45

tca atg acc aac gaa cca ggt ttc cgc tac ggt tcc ggt tta ctc act
432
Ser Met Thr Asn Glu Pro Gly Phe Arg Tyr Gly Ser Gly Leu Leu Thr
        50   55   60

aac cct tct tct atc tct ccc aac aca gct tac tct tcc gtt ttt ctt
480
Asn Pro Ser Ser Ile Ser Pro Asn Thr Ala Tyr Ser Ser Val Phe Leu
65   70   75   80

gac aaa aga aac aac agt aac aac aac aat aat ggc acg aac atg gca
528
Asp Lys Arg Asn Asn Ser Asn Asn Asn Asn Asn Gly Thr Asn Met Ala
                85   90   95

gct atg cga gag atg atc ttc cgt atc gcc gtg atg caa ccg atc cat
576
Ala Met Arg Glu Met Ile Phe Arg Ile Ala Val Met Gln Pro Ile His
            100   105   110

atc gat ccc gag gcg gtt aag cca ccg aag agg agg aac gtc agg atc
624
Ile Asp Pro Glu Ala Val Lys Pro Pro Lys Arg Arg Asn Val Arg Ile
            115   120   125

tct aaa gat cct caa agc gtg gcg gct agg cat aga agg gag aga ata
672
Ser Lys Asp Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile
        130   135   140

agc gag agg att cgg att ttg caa cgg ctt gtt cct ggt ggg acg aag
720
Ser Glu Arg Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys
145   150   155   160

atg gat aca gct tcg atg ctc gat gaa gca att cat tat gtg aag ttt
768
Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile His Tyr Val Lys Phe
                165   170   175

tta aag aaa cag gtg cag tct ctg gag gag cag gcg gtg gtt act ggc
816
Leu Lys Lys Gln Val Gln Ser Leu Glu Glu Gln Ala Val Val Thr Gly
                180   185   190

gga ggg gga gga gga gga gga agg gtt ttg atc ggt gga ggt gga atg
864
Gly Gly Gly Gly Gly Gly Gly Arg Val Leu Ile Gly Gly Gly Gly Met
        195   200   205

acg gcg gcg agt ggt ggt ggt ggc ggc ggg gga gtg gtt atg aaa ggg
912
Thr Ala Ala Ser Gly Gly Gly Gly Gly Gly Gly Val Val Met Lys Gly
    210   215   220

tgt gga aca gtg ggg act cat cag atg gtg ggc aat gca cag att ctt
960
Cys Gly Thr Val Gly Thr His Gln Met Val Gly Asn Ala Gln Ile Leu
225   :   230   235   240

aga tga tgatgatttt taattttatt attattatat taatgttgga gaaaaagaga
1016
Arg

aaaatgattc tggagaggga agccaagtaa tttatgtgag agtctttaat ttaactttat
1076

tttcttgttt agataatgtg taatgatggt ttttaaagcc aaagactctc catggttgtt
1136

ggagcgagtt tg
1148

<210> 168 <211> 241 <212> PRT <213> Arabidopsis thaliana <400>
168

Met Asp Ser Asp Ile Met Asn Met Met Met His Gln Met Glu Lys Leu
1   5   10   15

Pro Glu Phe Cys Asn Pro Asn Ser Ser Phe Phe Ser Pro Asp His Asn
            20   25   30

Asn Thr Tyr Pro Phe Leu Phe Asn Ser Thr His Tyr Gln Ser Asp His
        35   ·   40   45

Ser Met Thr Asn Glu Pro Gly Phe Arg Tyr Gly Ser Gly Leu Leu Thr
    50   55   60

Asn Pro Ser Ser Ile Ser Pro Asn Thr Ala Tyr Ser Ser Val Phe Leu
65   70   75   80

Asp Lys Arg Asn Asn Ser Asn Asn Asn Asn Gly Thr Asn Met Ala
            85   90   95

Ala Met Arg Glu Met Ile Phe Arg Ile Ala Val Met Gln Pro Ile His
            100   105   .   110

```
Ile Asp Pro Glu Ala Val Lys Pro Pro Lys Arg Arg Asn Val Arg Ile
        115                 120                 125

Ser Lys Asp Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile
    130                 135                 140

Ser Glu Arg Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys
145                 150                 155                 160

Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile His Tyr Val Lys Phe
    ·             165                 170                 175

Leu Lys Lys Gln Val Gln Ser Leu Glu Glu Gln Ala Val Val Thr Gly
            180                 185                 190

Gly Gly Gly Gly Gly Gly Gly Arg Val Leu Ile Gly Gly Gly Gly Met
        195                 200                 205

Thr Ala Ala Ser Gly Gly Gly Gly Gly Gly Val Val Met Lys Gly
    210                 215                 220

Cys Gly Thr Val Gly Thr His Gln Met Val Gly Asn Ala Gln Ile Leu
225                 230                 235                 240

Arg
```

```
<210> 169 <211> 1728 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (106)..(1575) <223> G1064

<400> 169
ctttattttt tttcccctct tgtcgaaaac atcacatata aataaaaaac caaaaaccct
60

aatttataaa atatatataa aatagttata gctccccact tatat atg caa aag cca
117
                                                   Met Gln Lys Pro
                                                   1

aca tca agt atc tta aat gtc ata atg gac ggt gga gac agc gtc gga
165
Thr Ser Ser Ile Leu Asn Val Ile Met Asp Gly Gly Asp Ser Val Gly
5                 10                15                 20

gga gga gga gga gat gat cac cac cgt cac ctc cac cat cac cac cgc
213
Gly Gly Gly Gly Asp Asp His His Arg His Leu His His His Arg
                25                 30                 35

cct act ttc cct ttt caa cta ctc gga aaa cac gac ccc gac gac aac
261
Pro Thr Phe Pro Phe Gln Leu Leu Gly Lys His Asp Pro Asp Asp Asn
```

298

              40   45   50

cat caa caa caa cct tcc cct tcc tcc tcc tcc tct cta ttt tct ctc
309
His Gln Gln Gln Pro Ser Pro Ser Ser Ser Ser Ser Leu Phe Ser Leu
        55   60   65

cat caa cac caa caa tta tct caa tcg caa cct caa tcg caa tcg caa
357
His Gln His Gln Gln Leu Ser Gln Ser Gln Pro Gln Ser Gln Ser Gln
        70   75   80

aag tca caa ccg cag aca acg caa aaa gag tta tta caa acg caa gag
405
Lys Ser Gln Pro Gln Thr Thr Gln Lys Glu Leu Leu Gln Thr Gln Glu
85   90   95   100

gaa tct gcg gtg gtg gca gct aaa aag cca ccg ttg aaa cga gcg tcg
453
Glu Ser Ala Val Val Ala Ala Lys Lys Pro Pro Leu Lys Arg Ala Ser
            105   110   115

acg aaa gac cga cac acg aaa gta gac gga aga ggg agg aga ata agg
501
Thr Lys Asp Arg His Thr Lys Val Asp Gly Arg Gly Arg Arg Ile Arg
            120   125   130

atg ccg gcg tta tgt gca gct agg gtt ttt cag cta acg cga gag cta
549
Met Pro Ala Leu Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu
            135   140   145

ggt cat aaa tcc gac ggt gag aca ata gag tgg ctt ctt caa caa gct
597
Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln Ala
            150   155   160

gaa cca tct gta atc gcc gcc acc gga acc gga aca atc ccg gcg aat
645
Glu Pro Ser Val Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Asn
165   170   175   180

ttc act tct tta aac atc tct ctc cgt tct tca ggc tct tcc atg tct
693
Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Gly Ser Ser Met Ser
                185   190   195

ctt cct tct cat ttc cgc tcc gcc gct tcc act ttt agc cct aat aac
741
Leu Pro Ser His Phe Arg Ser Ala Ala Ser Thr Phe Ser Pro Asn Asn
            200   205   210

ata ttt tct ccg gcg atg ctt caa caa caa caa caa caa caa cgt ggt
789
Ile Phe Ser Pro Ala Met Leu Gln Gln Gln Gln Gln Gln Gln Arg Gly
            215   220   225

ggt ggt gtt ggg ttt cat cat ccc cat cta cag gga cgt gca cct acg
837
Gly Gly Val Gly Phe His His Pro His Leu Gln Gly Arg Ala Pro Thr
    230   235   240

```
tcg tct ttg ttt cct ggt att gat aac ttc aca cca acg acg tcg ttt
885
Ser Ser Leu Phe Pro Gly Ile Asp Asn Phe Thr Pro Thr Thr Ser Phe
245             250         255             260

ttg aac ttt cat aat cca aca aag caa gaa gga gat caa gat tct gaa
933
Leu Asn Phe His Asn Pro Thr Lys Gln Glu Gly Asp Gln Asp Ser Glu
                265             270             275

gag tta aac tcg gag aag aaa aga aga atc caa acg acg tcg gat ttg
981
Glu Leu Asn Ser Glu Lys Lys Arg Arg Ile Gln Thr Thr Ser Asp Leu
            280             285             290

cat caa caa caa caa caa cac caa cat gat caa atc gga gga tat aca
1029
His Gln Gln Gln Gln Gln His Gln His Asp Gln Ile Gly Gly Tyr Thr
        295             300             305

ctt caa tct agc aac agt gga tct acg gcc acc gca gcc gcc gcg caa
1077
Leu Gln Ser Ser Asn Ser Gly Ser Thr Ala Thr Ala Ala Ala Ala Gln
    310             315             320

caa ata ccg gga aat ttc tgg atg gtt gcg gcg gct gcg gct gca ggt
1125
Gln Ile Pro Gly Asn Phe Trp Met Val Ala Ala Ala Ala Ala Ala Gly
325             330             335             340

ggt ggt ggt ggt aat aac aac caa aca ggt ggt ctt atg aca gct tct
1173
Gly Gly Gly Gly Asn Asn Asn Gln Thr Gly Gly Leu Met Thr Ala Ser
            345             350             355

att ggt act ggt ggc ggc ggt gga gag cct gtt tgg acg ttt cct tcc
1221
Ile Gly Thr Gly Gly Gly Gly Glu Pro Val Trp Thr Phe Pro Ser
            360             365             370

att aac acg gca gcg gca gcg tta tat aga agt ggc gtt tcg ggc gtt
1269
Ile Asn Thr Ala Ala Ala Ala Leu Tyr Arg Ser Gly Val Ser Gly Val
            375             380             385

cca agc ggc gcg gtt tct agc ggt tta cat ttt atg aat ttc gca gcg
1317
Pro Ser Gly Ala Val Ser Ser Gly Leu His Phe Met Asn Phe Ala Ala
    390             395             400

cca atg gca ttt ctt act gga caa caa cag cta gca aca act agt aat
1365
Pro Met Ala Phe Leu Thr Gly Gln Gln Gln Leu Ala Thr Thr Ser Asn
405             410             415             420

cat gag att aat gaa gat agt aat aat aat gaa gga gga aga agt gac
1413
His Glu Ile Asn Glu Asp Ser Asn Asn Asn Glu Gly Gly Arg Ser Asp
            425             430             435
```

300

```
ggt ggt ggt gat cat cat aat aca cag aga cat cat cat cat caa caa
1461
Gly Gly Gly Asp His His Asn Thr Gln Arg His His His His Gln Gln
        440                     445              450

caa cat cat cat aat att ctc tcc ggc ttg aac cag tac gga cgg caa
1509
Gln His His His Asn Ile Leu Ser Gly Leu Asn Gln Tyr Gly Arg Gln
        455                     460              465

gtt tcc ggc gac tct caa gct agt gga tca ctt gga ggt ggt gat gag
1557
Val Ser Gly Asp Ser Gln Ala Ser Gly Ser Leu Gly Gly Gly Asp Glu
     470                     475              480

gag gat cag caa gat tag acacacacaa aaacatttta atggtgggat
1605
Glu Asp Gln Gln Asp
485

tttctgccga cggcggtagc ggtgacggcg ttcggcggct gtgtaaaact tttgttttca
1665

ccgttaattt tttttatttt ctgtagtaat ttttttgct aagtaaaaaa aaaaaaaaaa
1725

aaa
1728
```

`<210>` 170 `<211>` 489 `<212>` PRT `<213>` Arabidopsis thaliana `<400>`
170

```
Met Gln Lys Pro Thr Ser Ser Ile Leu Asn Val Ile Met Asp Gly Gly
1               5                   10                  15

Asp Ser Val Gly Gly Gly Gly Gly Asp Asp His His Arg His Leu His
            20                  25                  30

His His His Arg Pro Thr Phe Pro Phe Gln Leu Leu Gly Lys His Asp
        35                  40                  45

Pro Asp Asp Asn His Gln Gln Gln Pro Ser Pro Ser Ser Ser Ser Ser
     50                  55                  60

Leu Phe Ser Leu His Gln His Gln Gln Leu Ser Gln Ser Gln Pro Gln
65                  70                  75                  80

Ser Gln Ser Gln Lys Ser Gln Pro Gln Thr Thr Gln Lys Glu Leu Leu
                85                  90                  95

Gln Thr Gln Glu Glu Ser Ala Val Val Ala Ala Lys Lys Pro Pro Leu
            100                 105                 110
```

301

```
Lys Arg Ala Ser Thr Lys Asp Arg His Thr Lys Val Asp Gly Arg Gly
        115             120             125

Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Val Phe Gln Leu
    130             135             140

Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu
145             150             155                 160

Leu Gln Gln Ala Glu Pro Ser Val Ile Ala Ala Thr Gly Thr Gly Thr
                165             170             175

Ile Pro Ala Asn Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Gly
            180             185             190

Ser Ser Met Ser Leu Pro Ser His Phe Arg Ser Ala Ala Ser Thr Phe
        195             200             205

Ser Pro Asn Asn Ile Phe Ser Pro Ala Met Leu Gln Gln Gln Gln Gln
    210             215             220

Gln Gln Arg Gly Gly Gly Val Gly Phe His His Pro His Leu Gln Gly
225             230             235                 240

Arg Ala Pro Thr Ser Ser Leu Phe Pro Gly Ile Asp Asn Phe Thr Pro
            245             250             255

Thr Thr Ser Phe Leu Asn Phe His Asn Pro Thr Lys Gln Glu Gly Asp
            260             265             270

Gln Asp Ser Glu Glu Leu Asn Ser Glu Lys Lys Arg Arg Ile Gln Thr
        275             280             285

Thr Ser Asp Leu His Gln Gln Gln Gln His Gln His Asp Gln Ile
    290             295             300

Gly Gly Tyr Thr Leu Gln Ser Ser Asn Ser Gly Ser Thr Ala Thr Ala
305             310             315                 320

Ala Ala Ala Gln Gln Ile Pro Gly Asn Phe Trp Met Val Ala Ala Ala
            325             330             335

Ala Ala Ala Gly Gly Gly Gly Gly Asn Asn Asn Gln Thr Gly Gly Leu
            340             345             350

Met Thr Ala Ser Ile Gly Thr Gly Gly Gly Gly Gly Glu Pro Val Trp
```

302

```
        355                    360                    365
```

Thr Phe Pro Ser Ile Asn Thr Ala Ala Ala Ala Leu Tyr Arg Ser Gly
   370   .   375   380

Val Ser Gly Val Pro Ser Gly Ala Val Ser Ser Gly Leu His Phe Met
385   390   395   400

Asn Phe Ala Ala Pro Met Ala Phe Leu Thr Gly Gln Gln Gln Leu Ala
             405   410   415

Thr Thr Ser Asn His Glu Ile Asn Glu Asp Ser Asn Asn Asn Glu Gly
         420   425   430

Gly Arg Ser Asp Gly Gly Gly Asp His His Asn Thr Gln Arg His His
      435   440   445

His His Gln Gln Gln His His His Asn Ile Leu Ser Gly Leu Asn Gln
   450   455   460

Tyr Gly Arg Gln Val Ser Gly Asp Ser Gln Ala Ser Gly Ser Leu Gly
465   470   475   480

Gly Gly Asp Glu Glu Asp Gln Gln Asp
             485

<210> 171 <211> 1473 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (436)..(1371) <223> G1067

<400> 171
tctcaagctt ctctctcctt ttttttcccat agcacatcag aatcgctaaa tacgactcct
60

atgcaaagaa gaagctactt ctttctcttg ccctaattaa tctacctaac tagggtttcc
120

tcttaccttt catgagagag atcatttaac ataagtcacc tttttttatat cttttgcttc
180

gtctttaatt tagttctgtt cttggtctgt ttctatattt tgtcggcttg cgtaaccgat
240

cacaccttaa tgctttagct attgtttcct caaaatcatg agttttgact tctcgatctg
300

agttttcttt ttctctcttt acgctcttct tcacctagct accaatatat gaacgagcag
360

gatcaagaat cgagaaattg atttgagctg gcgaataagc agtggtggga tagggaatta
420

```
gtagatgcgg cggcg atg gaa ggc ggt tac gag caa ggc ggt gga gct tct
471
                Met Glu Gly Gly Tyr Glu Gln Gly Gly Gly Ala Ser
                 1               5                    10
```

```
aga tac ttc cat aac ctc ttt aga ccg gag att cac cac caa cag ctt
519
Arg Tyr Phe His Asn Leu Phe Arg Pro Glu Ile His His Gln Gln Leu
         15              20                  25
```

```
caa ccg cag ggc ggg atc aat ctt atc gac cag cat cat cat cag cac
567
Gln Pro Gln Gly Gly Ile Asn Leu Ile Asp Gln His His His Gln His
     30              35                  40
```

```
cag caa cat caa caa caa caa caa ccg tcg gat gat tca aga gaa tct
615
Gln Gln His Gln Gln Gln Gln Gln Pro Ser Asp Asp Ser Arg Glu Ser
45              50                  55                  60
```

```
gac cat tca aac aaa gat cat cat caa cag ggt cga ccc gat tca gac
663
Asp His Ser Asn Lys Asp His His Gln Gln Gly Arg Pro Asp Ser Asp
                 65              70                  75
```

```
ccg aat aca tca agc tca gca ccg gga aaa cgt cca cgt gga cgt cca
711
Pro Asn Thr Ser Ser Ser Ala Pro Gly Lys Arg Pro Arg Gly Arg Pro
             80              85                  90
```

```
cca gga tct aag aac aaa gcc aag cca ccg atc ata gta act cgt gat
759
Pro Gly Ser Lys Asn Lys Ala Lys Pro Pro Ile Ile Val Thr Arg Asp
             95             100                 105
```

```
agc ccc aac gcg ctt aga tct cac gtt ctt gaa gta tct cct gga gct
807
Ser Pro Asn Ala Leu Arg Ser His Val Leu Glu Val Ser Pro Gly Ala
        110             115                 120
```

```
gac ata gtt gag agt gtt tcc acg tac gct agg agg aga ggg aga ggc
855
Asp Ile Val Glu Ser Val Ser Thr Tyr Ala Arg Arg Arg Gly Arg Gly
125             130                 135                 140
```

```
gtc tcc gtt tta gga gga aac ggc acc gta tct aac gtc act ctc cgt
903
Val Ser Val Leu Gly Gly Asn Gly Thr Val Ser Asn Val Thr Leu Arg
                145                 150                 155
```

```
cag cca gtc act cct gga aat ggc ggt ggt gtg tcc gga gga gga gga
951
Gln Pro Val Thr Pro Gly Asn Gly Gly Gly Val Ser Gly Gly Gly Gly
             160                 165                 170
```

```
gtt gtg act tta cat gga agg ttt gag att ctt tcg cta acg ggg act
999
Val Val Thr Leu His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Thr
             175                 180                 185
```

gtt ttg cca cct cct gca ccg cct ggt gcc ggt ggt ttg tct ata ttt
1047
Val Leu Pro Pro Pro Ala Pro Pro Gly Ala Gly Gly Leu Ser Ile Phe
    190   195   200

tta gcc gga ggg caa ggt cag gtg gtc gga gga agc gtt gtg gct ccc
1095
Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Ala Pro
205   210   215   220

ctt att gca tca gct ccg gtt ata cta atg gcg gct tcg ttc tca aat
1143
Leu Ile Ala Ser Ala Pro Val Ile Leu Met Ala Ala Ser Phe Ser Asn
            225   230   235

gcg gtt ttc gag aga cta ccg att gag gag gag gaa gaa gaa ggt ggt
1191
Ala Val Phe Glu Arg Leu Pro Ile Glu Glu Glu Glu Glu Glu Gly Gly
            240   245   250

ggt ggc gga gga gga gga gga gga ggg cca ccg cag atg caa caa gct
1239
Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro Pro Gln Met Gln Gln Ala
            255   260   265

cca tca gca tct ccg ccg tct gga gtg acc ggt cag gga cag tta gga
1287
Pro Ser Ala Ser Pro Pro Ser Gly Val Thr Gly Gln Gly Gln Leu Gly
    270   275   280

ggt aat gtg ggt ggt tat ggg ttt tct ggt gat cct cat ttg ctt gga
1335
Gly Asn Val Gly Gly Tyr Gly Phe Ser Gly Asp Pro His Leu Leu Gly
285   290   295   300

tgg gga gct gga aca cct tca aga cca cct ttt taa ttgaatttta
1381
Trp Gly Ala Gly Thr Pro Ser Arg Pro Pro Phe
            305   310

atgtccggaa atttatgtgt ttttatcatc ttgaggagtc gtctttcctt tgggatattt
1441

ggtgtttaat gtttagttga tatgcatatt tt
1473

<210> 172 <211> 311 <212> PRT <213> Arabidopsis thaliana <400>
172

Met Glu Gly Gly Tyr Glu Gln Gly Gly Gly Ala Ser Arg Tyr Phe His
1   5   10   15

Asn Leu Phe Arg Pro Glu Ile His His Gln Gln Leu Gln Pro Gln Gly
            20   25   30

Gly Ile Asn Leu Ile Asp Gln His His His Gln His Gln Gln His Gln
            35   40   45

305

```
Gln Gln Gln Gln Pro Ser Asp Asp Ser Arg Glu Ser Asp His Ser Asn
    50              55                  60

Lys Asp His His Gln Gln Gly Arg Pro Asp Ser Asp Pro Asn Thr Ser
65              70                  75                  80

Ser Ser Ala Pro Gly Lys Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys
            85                  90                  95

Asn Lys Ala Lys Pro Pro Ile Ile Val Thr Arg Asp Ser Pro Asn Ala
            100             105                 110

Leu Arg Ser His Val Leu Glu Val Ser Pro Gly Ala Asp Ile Val Glu
        115                 120                 125

Ser Val Ser Thr Tyr Ala Arg Arg Arg Gly Arg Gly Val Ser Val Leu
    130             135                 140

Gly Gly Asn Gly Thr Val Ser Asn Val Thr Leu Arg Gln Pro Val Thr
145             150                 155                 160

Pro Gly Asn Gly Gly Gly Val Ser Gly Gly Gly Gly Val Val Thr Leu
            165                 170                 175

His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Thr Val Leu Pro Pro
            180                 185                 190

Pro Ala Pro Pro Gly Ala Gly Gly Leu Ser Ile Phe Leu Ala Gly Gly
        195                 200                 205

Gln Gly Gln Val Val Gly Gly Ser Val Val Ala Pro Leu Ile Ala Ser
    210                 215                 220

Ala Pro Val Ile Leu Met Ala Ala Ser Phe Ser Asn Ala Val Phe Glu
225                 230                 235                 240

Arg Leu Pro Ile Glu Glu Glu Glu Glu Glu Gly Gly Gly Gly Gly Gly
            245                 250                 255

Gly Gly Gly Gly Gly Pro Pro Gln Met Gln Gln Ala Pro Ser Ala Ser
            260                 265                 270

Pro Pro Ser Gly Val Thr Gly Gln Gly Gln Leu Gly Gly Asn Val Gly
            275                 280                 285
```

Gly Tyr Gly Phe Ser Gly Asp Pro His Leu Leu Gly Trp Gly Ala Gly
    290   295   300

Thr Pro Ser Arg Pro Pro Phe
305   310

<210> 173 <211> 1295 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (170)..(1144) <223> G1070

<400> 173
tcgaccagct tggatttcgt tgttcatcat tactactctc tttcttcttc tagctagcta
60

gttttgacag caaaataaga agcaaaaaaa aggtcaacta aaaaagatct gttcttagat
120

cactctcttc ttctttttttt gatccaattc caccattgaa tcatagatc atg gat cca
178
                                                        Met Asp Pro
                                                          1

gta caa tct cat gga tca caa agc tct cta cct cct cct ttc cac gca
226
Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro Phe His Ala
      5   10   15

aga gac ttt caa tta cat ctt caa caa cag caa caa gag ttc ttc ctc
274
Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Glu Phe Phe Leu
20   25   30   35

cac cat cac cag caa caa aga aac caa acc gat ggt gac caa caa gga
322
His His His Gln Gln Gln Arg Asn Gln Thr Asp Gly Asp Gln Gln Gly
              40   45   50

gga tca gga gga aac cga caa atc aag atg gat cgt gaa gag aca agc
370
Gly Ser Gly Gly Asn Arg Gln Ile Lys Met Asp Arg Glu Glu Thr Ser
            55   60   65

gac aac ata gac aac ata gct aac aac agc ggt agt gaa ggt aaa gac
418
Asp Asn Ile Asp Asn Ile Ala Asn Asn Ser Gly Ser Glu Gly Lys Asp
            70   75   80

ata gat ata cac ggt ggt tca gga gaa gga ggt ggt ggc tcc gga gga
466
Ile Asp Ile His Gly Gly Ser Gly Glu Gly Gly Gly Gly Ser Gly Gly
      85   90   95

gat cat cag atg aca aga aga cca aga gga aga cca gcg gga tcc aag
514
Asp His Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys
100   105   110   115

aac aaa cca aaa cca ccg att atc atc aca cgg gac agc gca aac gcg
562
Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala

307

                    120   125   130

ctt aga acc cac gtg atg gag atc gga gat ggc tgc gac tta gtc gaa
610
Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp Leu Val Glu
        135   140   145

agc gtt gcc act ttt gca cga aga cgc caa cgc ggc gtt tgc gtt atg
658
Ser Val Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Met
        150   155   160

agc ggt act gga aat gtt act aac gtc act ata cgt cag cct gga tct
706
Ser Gly Thr Gly Asn Val Thr Asn Val Thr Ile Arg Gln Pro Gly Ser
        165   170   175

cat cct tct cct ggc tcg gta gtt agt ctt cac gga agg ttc gag att
754
His Pro Ser Pro Gly Ser Val Val Ser Leu His Gly Arg Phe Glu Ile
180   185   190   195

cta tct ctc tca gga tct ttt ctc cct cct ccg gct cct cct aca gcc
802
Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Thr Ala
                200   205   210

acc gga ttg agt gtt tac ctc gct gga gga caa gga cag gtg gtt gga
850
Thr Gly Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly
                215   220   225

gga agc gta gtt ggt ccg ttg tta tgt gct ggt cct gtc gtt gtc atg
898
Gly Ser Val Val Gly Pro Leu Leu Cys Ala Gly Pro Val Val Val Met
            230   235   240

gct gcg tct ttt agc aat gcg gcg tac gaa agg ttg cct tta gag gaa
946
Ala Ala Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu Glu
        245   250   255

gat gag atg cag acg ccg gtt cat ggc gga gga gga gga gga tca ttg
994
Asp Glu Met Gln Thr Pro Val His Gly Gly Gly Gly Gly Gly Ser Leu
260   265   270   275

gag tcg ccg cca atg atg gga caa caa ctg caa cat cag caa caa gct
1042
Glu Ser Pro Pro Met Met Gly Gln Gln Leu Gln His Gln Gln Gln Ala
                280   285   290

atg tca ggt cat caa ggg tta cca cct aat ctt ctt ggt tcg gtt cag
1090
Met Ser Gly His Gln Gly Leu Pro Pro Asn Leu Leu Gly Ser Val Gln
            295   300   305

ttg cag cag caa cat gat cag tct tat tgg tca acg gga cga cca ccg
1138
Leu Gln Gln Gln His Asp Gln Ser Tyr Trp Ser Thr Gly Arg Pro Pro
        310   315   320

308

tat tga tcaaatatac acacacactc ataatcgttg ctagctagct aacgatgaat
1194
Tyr

catgagttta gtggatatat atatgattaa aagaggttag cttatgaaca ttaataagag
1254

tttggattct atcgagcttc attatgtttg ggtcatcgtt c
1295

<210> 174 <211> 324 <212> PRT <213> Arabidopsis thaliana <400>
174

Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro
1   5   10   15

Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Gln Glu
            20   25   30

Phe Phe Leu His His His Gln Gln Gln Arg Asn Gln Thr Asp Gly Asp
        35   40   45

Gln Gln Gly Gly Ser Gly Gly Asn Arg Gln Ile Lys Met Asp Arg Glu
    50   55   60

Glu Thr Ser Asp Asn Ile Asp Asn Ile Ala Asn Asn Ser Gly Ser Glu
65   70   75   80

Gly Lys Asp Ile Asp Ile His Gly Gly Ser Gly Glu Gly Gly Gly Gly
                85   90   95

Ser Gly Gly Asp His Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala
            100   105   110

Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser
            115   120   125

Ala Asn Ala Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp
    130   135   140

Leu Val Glu Ser Val Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val
145   150   155   160

Cys Val Met Ser Gly Thr Gly Asn Val Thr Asn Val Thr Ile Arg Gln
                165   170   175

Pro Gly Ser His Pro Ser Pro Gly Ser Val Val Ser Leu His Gly Arg

309

```
        180                    185                    190
```

Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro
        195   200   205

Pro Thr Ala Thr Gly Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln
        210   215   220

Val Val Gly Gly Ser Val Val Gly Pro Leu Leu Cys Ala Gly Pro Val
225   230   235   240

Val Val Met Ala Ala Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro
                245   250   255

Leu Glu Glu Asp Glu Met Gln Thr Pro Val His Gly Gly Gly Gly Gly
            260   265   270

Gly Ser Leu Glu Ser Pro Pro Met Met Gly Gln Gln Leu Gln His Gln
        275   280   285

Gln Gln Ala Met Ser Gly His Gln Gly Leu Pro Pro Asn Leu Leu Gly
        290   295   300

Ser Val Gln Leu Gln Gln Gln His, Asp Gln Ser Tyr Trp Ser Thr Gly
305   310   315   320

Arg Pro Pro Tyr

<210> 175 <211> 1084 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (19)..(876) <223> G1075

<400> 175
tttgtgtttg gtgctggc atg gct ggt ctc gat cta ggc aca act tct cgc
51
                Met Ala Gly Leu Asp Leu Gly Thr Thr Ser Arg
                1   5   10

tac gtc cac aac gtc gat ggt ggc ggc ggc gga cag ttc acc acc gac
99
Tyr Val His Asn Val Asp Gly Gly Gly Gly Gln Phe Thr Thr Asp
            15   20   25

aac cac cac gaa gat gac ggt ggc gct gga gga aac cac cat cat cac
147
Asn His His Glu Asp Asp Gly Gly Ala Gly Gly Asn His His His
            30   35   40

cat cat aat cat aat cac cat caa ggt tta gat tta ata gct tct aat
195
His His Asn His Asn His His Gln Gly Leu Asp Leu Ile Ala Ser Asn

310

```
        45                    50                    55

gat aac tct gga cta ggc ggc ggt gga gga gga ggg agc ggt gac ctc
243
Asp Asn Ser Gly Leu Gly Gly Gly Gly Gly Gly Ser Gly Asp Leu
60              65                  70                  75

gtc atg cgt cgg cca cgt ggc cgt cca gct gga tcg aag aac aaa ccg
291
Val Met Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro
            80                  85                  90

aag ccg ccg gtg att gtc acg cgc gag agc gca aac act ctt agg gct
339
Lys Pro Pro Val Ile Val Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala
            95                  100                 105

cac att ctt gaa gtt gga agt ggc tgc gac gtt ttc gaa tgt atc tcc
387
His Ile Leu Glu Val Gly Ser Gly Cys Asp Val Phe Glu Cys Ile Ser
        110                 115                 120

act tac gct cgt cgg aga cag cgc ggg att tgc gtt tta tcc ggg acg
435
Thr Tyr Ala Arg Arg Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Thr
        125                 130                 135

gga acc gtc act aac gtc agc atc cgt cag cct acg gcg gcc gga gct
483
Gly Thr Val Thr Asn Val Ser Ile Arg Gln Pro Thr Ala Ala Gly Ala
140             145                 150                     155

gtt gtg act ctg cgg ggt act ttt gag att ctt tcc ctc tcc gga tct
531
Val Val Thr Leu Arg Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser
            160                 165                 170

ttt ctt ccg cca cct gct cct cca ggg gcg act agc ttg acg ata ttc
579
Phe Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe
            175                 180                 185

ctc gct gga gct caa gga cag gtc gtc gga ggt aac gta gtt ggt gag
627
Leu Ala Gly Ala Gln Gly Gln Val Val Gly Gly Asn Val Val Gly Glu
        190                 195                 200

tta atg gcg gcg ggg ccg gta atg gtc atg gca gcg tct ttt aca aac
675
Leu Met Ala Ala Gly Pro Val Met Val Met Ala Ala Ser Phe Thr Asn
        205                 210                 215

gtg gct tac gaa agg ttg cct ttg gac gag cat gag gag cac ttg caa
723
Val Ala Tyr Glu Arg Leu Pro Leu Asp Glu His Glu Glu His Leu Gln
220                 225                 230                 235

agt ggc ggc ggc gga ggt gga ggg aat atg tac tcg gaa gcc act ggc
771
Ser Gly Gly Gly Gly Gly Gly Gly Asn Met Tyr Ser Glu Ala Thr Gly
            240                 245                 250
```

311

ggt ggc gga ggg ttg cct ttc ttt aat ttg ccg atg agt atg cct cag
819
Gly Gly Gly Gly Leu Pro Phe Phe Asn Leu Pro Met Ser Met Pro Gln
            255   260   265

att gga gtt gaa agt tgg cag ggg aat cac gcc ggc gcc ggt agg gct
867
Ile Gly Val Glu Ser Trp Gln Gly Asn His Ala Gly Ala Gly Arg Ala
            270   275   280

ccg ttt tag caatttaaga aactttaatt gttttttcca cttttttgtt
916
Pro Phe
    285

tttctccgaa ttttatgaaa ttatgattta agaaaaaaaa cgatattgtt catgtattga
976

ccctcttact gcatggtttc ttctattggg ttaattggct agctcataag aattgtttaa
1036

tttggttatt gtcatcaaat ttgcccacat ataaagcttc tagcaaat
1084   −

<210> 176 <211> 285 <212> PRT <213> Arabidopsis thaliana <400>
176

Met Ala Gly Leu Asp Leu Gly Thr Thr Ser Arg Tyr Val His Asn Val
1   5   10   15

Asp Gly Gly Gly Gly Gly Gln Phe Thr Thr Asp Asn His His Glu Asp
            20   25   30

Asp Gly Gly Ala Gly Gly Asn His His His His His His Asn His Asn
        35   40   45

His His Gln Gly Leu Asp Leu Ile Ala Ser Asn Asp Asn Ser Gly Leu
    50   55   60

Gly Gly Gly Gly Gly Gly Gly Ser Gly Asp Leu Val Met Arg Arg Pro
65   70   75   80

Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro Pro Val Ile
            85   90   95

Val Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala His Ile Leu Glu Val
        100   105   110

Gly Ser Gly Cys Asp Val Phe Glu Cys Ile Ser Thr Tyr Ala Arg Arg
        115   120   125

312

```
Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Thr Gly Thr Val Thr Asn
    130                 135                 140


Val Ser Ile Arg Gln Pro Thr Ala Ala Gly Ala Val Val Thr Leu Arg
145                 150                 155                 160


Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro
                165                 170                 175


Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe Leu Ala Gly Ala Gln
            180                 185                 190


Gly Gln Val Val Gly Gly Asn Val Val Gly Glu Leu Met Ala Ala Gly
        195                 200                 205


Pro Val Met Val Met Ala Ala Ser Phe Thr Asn Val Ala Tyr Glu Arg
    210                 215                 220


Leu Pro Leu Asp Glu His Glu Glu His Leu Gln Ser Gly Gly Gly Gly
225                 230                 235                 240


Gly Gly Gly Asn Met Tyr Ser Glu Ala Thr Gly Gly Gly Gly Gly Leu
                245                 250                 255


Pro Phe Phe Asn Leu Pro Met Ser Met Pro Gln Ile Gly Val Glu Ser
            260                 265                 270


Trp Gln Gly Asn His Ala Gly Ala Gly Arg Ala Pro Phe
            275                 280                 285
```

<210> 177 <211> 2663 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (31)..(2427) <223> G1089

<400> 177
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aagtaagaga gcttcttaag gaagaagaag atg ggt tgt gct caa tca aag atc
54
                                    Met Gly Cys Ala Gln Ser Lys Ile
                                    1                   5


gag aac gaa gaa gca gtt act cgt tgc aaa gaa cga aaa caa ttg atg
102
Glu Asn Glu Glu Ala Val Thr Arg Cys Lys Glu Arg Lys Gln Leu Met
    10                  15                  20


aaa gac gcc gtc act gct cgt aac gct ttc gcc gcc gct cac tca gct
150
Lys Asp Ala Val Thr Ala Arg Asn Ala Phe Ala Ala Ala His Ser Ala
25                  30                  35                  40


tac gct atg gct ctt aaa aac acc gga gct gct ctt tcc gat tac tct
198
```

```
Tyr Ala Met Ala Leu Lys Asn Thr Gly Ala Ala Leu Ser Asp Tyr Ser
                45                  50                  55

cac ggc gag ttt tta gtc tct aat cac tcg tct tcc tcc gca gct gca
246
His Gly Glu Phe Leu Val Ser Asn His Ser Ser Ser Ser Ala Ala Ala
                60                  65                  70

gca atc gct tct act tct tct ctt ccc act gct ata tct cct cct ctt
294
Ala Ile Ala Ser Thr Ser Ser Leu Pro Thr Ala Ile Ser Pro Pro Leu
                75                  80                  85

cct tct tcc acc gct ccg gtt tct aat tca acc gct tct tct tcc tcc
342
Pro Ser Ser Thr Ala Pro Val Ser Asn Ser Thr Ala Ser Ser Ser Ser
                90                  95                  100

gct gcg gtt cct cag ccg att cct gat act ctt cct cct cct cct cct
390
Ala Ala Val Pro Gln Pro Ile Pro Asp Thr Leu Pro Pro Pro Pro Pro
105                  110                 115                 120

cca cca ccg ctt cct ctt caa cgt gct gct act atg ccg gag atg aac
438
Pro Pro Pro Leu Pro Leu Gln Arg Ala Ala Thr Met Pro Glu Met Asn
                125                 130         •           135

ggt aga tcc ggt ggt ggt cat gct ggt agt gga ctc aac gga att gaa
486
Gly Arg Ser Gly Gly Gly His Ala Gly Ser Gly Leu Asn Gly Ile Glu
                140                 145                 150

gaa gat gga gcc cta gat aac gat gat gat gac gat gat gat gat gat
534
Glu Asp Gly Ala Leu Asp Asn Asp Asp Asp Asp Asp Asp Asp Asp Asp
                155                 160                 165

gac tct gaa atg gag aat cgt gat cgt ttg att agg aaa tcg aga agc
582
Asp Ser Glu Met Glu Asn Arg Asp Arg Leu Ile Arg Lys Ser Arg Ser
        170                 175                 180

cgt gga ggt agt act aga gga aat agg acg acg att gaa gat cat cat
630
Arg Gly Gly Ser Thr Arg Gly Asn Arg Thr Thr Ile Glu Asp His His
185                 190                 195                 200

ctt cag gag gag aaa gct ccg cca cct ccc cct ttg gcg aat tcg cgg
678
Leu Gln Glu Glu Lys Ala Pro Pro Pro Pro Leu Ala Asn Ser Arg
                205                 210                 215

cca att ccg ccg cca cgt cag cat cag cat caa cat cag caa cag caa
726
Pro Ile Pro Pro Pro Arg Gln His Gln His Gln His Gln Gln Gln Gln
                220                 225                 230

caa caa cct ttc tac gat tac ttc ttc cct aat gtt gag aat atg cct
774
Gln Gln Pro Phe Tyr Asp Tyr Phe Phe Pro Asn Val Glu Asn Met Pro
```

```
                 235                      240                      245

gga act act tta gaa gat act cct cca caa cca caa cca caa cca aca
822
Gly Thr Thr Leu Glu Asp Thr Pro Pro Gln Pro Gln Pro Gln Pro Thr
    250                      255                      260

agg cct gtg cct cct caa cca cat tca cca gtc gtt act gag gat gac
870
Arg Pro Val Pro Pro Gln Pro His Ser Pro Val Val Thr Glu Asp Asp
265                      270                      275                      280

gaa gat gag gag gag gaa gag gag gaa gag gag gag gaa gag gag acg
918
Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Thr
                285                      290                      295

gtg att gaa cgg aaa cca ctg gtg gag gaa aga ccg aag aga gta gag
966
Val Ile Glu Arg Lys Pro Leu Val Glu Glu Arg Pro Lys Arg Val Glu
                300                      305                      310

gaa gtg acg att gaa ttg gaa aaa gtt act aat ttg aga ggg atg aag
1014
Glu Val Thr Ile Glu Leu Glu Lys Val Thr Asn Leu Arg Gly Met Lys
            315                      320                      325

aag agt aaa ggg ata ggg att ccc gga gag agg aga gga atg cga atg
1062
Lys Ser Lys Gly Ile Gly Ile Pro Gly Glu Arg Arg Gly Met Arg Met
        330                      335                      340

ccg gtg act gcg acg cat ttg gcg aat gta ttc att gag ctt gat gat
1110
Pro Val Thr Ala Thr His Leu Ala Asn Val Phe Ile Glu Leu Asp Asp
345                      350                      355                      360

aat ttc ttg aaa gct tct gaa agt gct cat gat gtt tct aag atg ctt
1158
Asn Phe Leu Lys Ala Ser Glu Ser Ala His Asp Val Ser Lys Met Leu
                365                      370                      375

gaa gct act agg ctc cat tac cat tct aat ttt gca gat aac cga gga
1206
Glu Ala Thr Arg Leu His Tyr His Ser Asn Phe Ala Asp Asn Arg Gly
                380                      385                      390

cat att gat cac tct gct aga gtg atg cgt gta att aca tgg aat aga
1254
His Ile Asp His Ser Ala Arg Val Met Arg Val Ile Thr Trp Asn Arg
            395                      400                      405

tca ttt aga gga ata cca aat gct gat gat ggg aaa gat gat gtt gat
1302
Ser Phe Arg Gly Ile Pro Asn Ala Asp Asp Gly Lys Asp Asp Val Asp
        410                      415                      420

ttg gaa gag aat gaa act cat gct act gtt ctt gac aaa ttg cta gca
1350
Leu Glu Glu Asn Glu Thr His Ala Thr Val Leu Asp Lys Leu Leu Ala
425                      430                      435                      440
```

315

```
tgg gaa aag aag ctc tat gac gaa gtc aag gct ggc gaa ctc atg aaa
1398
Trp Glu Lys Lys Leu Tyr Asp Glu Val Lys Ala Gly Glu Leu Met Lys
                  445             450                 455

atc gag tac cag aaa aag gtt gct cat tta aat cgg gtg aag aaa cga
1446
Ile Glu Tyr Gln Lys Lys Val Ala His Leu Asn Arg Val Lys Lys Arg
              460             465                 470

ggt ggc cac tcg gat tca tta gag aga gct aaa gca gca gta agt cat
1494
Gly Gly His Ser Asp Ser Leu Glu Arg Ala Lys Ala Ala Val Ser His
          475             480                 485

ttg cat aca aga tat ata gtt gat atg caa tcc atg gac tcc aca gtt
1542
Leu His Thr Arg Tyr Ile Val Asp Met Gln Ser Met Asp Ser Thr Val
       490                 495             500

tca gaa atc aat cgt ctt agg gat gaa caa cta tac cta aag ctc gtt
1590
Ser Glu Ile Asn Arg Leu Arg Asp Glu Gln Leu Tyr Leu Lys Leu Val
505             510             515                 520

cac ctt gtt gag gcg atg ggg aag atg tgg gaa atg atg caa ata cat
1638
His Leu Val Glu Ala Met Gly Lys Met Trp Glu Met Met Gln Ile His
              525             530                 535

cat caa aga caa gct gag atc tca aag gtg ttg aga tct cta gat gtt
1686
His Gln Arg Gln Ala Glu Ile Ser Lys Val Leu Arg Ser Leu Asp Val
              540             545                 550

tca caa gcg gtg aaa gaa aca aat gat cat cat cac gaa cgc acc atc
1734
Ser Gln Ala Val Lys Glu Thr Asn Asp His His His Glu Arg Thr Ile
          555             560                 565

cag ctc ttg gca gtg gtt caa gaa tgg cac acg cag ttt tgc agg atg
1782
Gln Leu Leu Ala Val Val Gln Glu Trp His Thr Gln Phe Cys Arg Met
       570             575             580

ata gat cat cag aaa gaa tac ata aaa gca ctt ggc gga tgg cta aag
1830
Ile Asp His Gln Lys Glu Tyr Ile Lys Ala Leu Gly Gly Trp Leu Lys
585             590             595                 600

cta aat ctc atc cct atc gaa agc aca ctc aag gag aaa gta tct tcg
1878
Leu Asn Leu Ile Pro Ile Glu Ser Thr Leu Lys Glu Lys Val Ser Ser
              605             610                 615

cct cct cga gtt ccc aat ccc gca atc caa aaa ctc ctc cac gct tgg
1926
Pro Pro Arg Val Pro Asn Pro Ala Ile Gln Lys Leu Leu His Ala Trp
          620             625                 630
```

316

tat gac cgt tta gac aaa atc ccc gac gaa atg gct aaa agt gcc ata
1974
Tyr Asp Arg Leu Asp Lys Ile Pro Asp Glu Met Ala Lys Ser Ala Ile
        635   640   645

atc aat ttc gca gcg gtt gta agc acg ata atg cag cag caa gaa gac
2022
Ile Asn Phe Ala Ala Val Val Ser Thr Ile Met Gln Gln Gln Glu Asp
    650   655   660

gag ata agt ctc aga aac aaa tgc gaa gag aca aga aaa gaa ttg gga
2070
Glu Ile Ser Leu Arg Asn Lys Cys Glu Glu Thr Arg Lys Glu Leu Gly
665   670   675   680

aga aaa att aga cag ttt gag gat tgg tac cac aaa tac atc cag aag
2118
Arg Lys Ile Arg Gln Phe Glu Asp Trp Tyr His Lys Tyr Ile Gln Lys
            685   690   695

aga gga ccg gag ggg atg aat ccg gat gaa gcg gat aac gat cat aat
2166
Arg Gly Pro Glu Gly Met Asn Pro Asp Glu Ala Asp Asn Asp His Asn
        700   705   710

gat gag gtc gct gtg agg caa ttc aat gta gaa caa att aag aag agg
2214
Asp Glu Val Ala Val Arg Gln Phe Asn Val Glu Gln Ile Lys Lys Arg
        715   720   725

ttg gaa gaa gaa gaa gaa gct tac cat aga caa agc cat caa gtt aga
2262
Leu Glu Glu Glu Glu Glu Ala Tyr His Arg Gln Ser His Gln Val Arg
    730   735   740

gag aag tca ctg gct agt ctt cga act cgc ctc ccc gag ctt ttt cag
2310
Glu Lys Ser Leu Ala Ser Leu Arg Thr Arg Leu Pro Glu Leu Phe Gln
745   750   755   760

gca atg tcc gag gtt gcg tat tca tgt tcg gat atg tat aga gct ata
2358
Ala Met Ser Glu Val Ala Tyr Ser Cys Ser Asp Met Tyr Arg Ala Ile
                765   770   775

acg tat gcg agt aag cgg caa agc caa agc gaa cgg cat cag aaa cct
2406
Thr Tyr Ala Ser Lys Arg Gln Ser Gln Ser Glu Arg His Gln Lys Pro
            780   785   790

agc cag gga cag agt tcg taa gaactaatgt aagatcagag taatgtcttc
2457
Ser Gln Gly Gln Ser Ser
            795

ttcttctttg atcttgaata tttaagcaca cacatacata caacgtatag ctaaatcttt
2517

atcattgctt tcttatatta aggttttggc ttttgtaaga aggtttctta catatgagat
2577

tcatatagtg tttgattctt aaggaactgt tctgttgagt aataagaaag ttgtgtattg
2637

aaatagagtt gcatttgtta attttg
2663

<210> 178 <211> 798 <212> PRT <213> Arabidopsis thaliana <400>
178

Met Gly Cys Ala Gln Ser Lys Ile Glu Asn Glu Glu Ala Val Thr Arg
1   5   10   15

Cys Lys Glu Arg Lys Gln Leu Met Lys Asp Ala Val Thr Ala Arg Asn
            20   25   30

Ala Phe Ala Ala Ala His Ser Ala Tyr Ala Met Ala Leu Lys Asn Thr
            35   40   45

Gly Ala Ala Leu Ser Asp Tyr Ser His Gly Glu Phe Leu Val Ser Asn
    50   55   --   60

His Ser Ser Ser Ser Ala Ala Ala Ala Ile Ala Ser Thr Ser Ser Leu
65   70   75   80

Pro Thr Ala Ile Ser Pro Pro Leu Pro Ser Ser Thr Ala Pro Val Ser
                85   90   95

Asn Ser Thr Ala Ser Ser Ser Ser Ala Ala Val Pro Gln Pro Ile Pro
            100   105   110

Asp Thr Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro Leu Gln Arg
            115   120   125

Ala Ala Thr Met Pro Glu Met Asn Gly Arg Ser Gly Gly Gly His Ala
    130   135   140

Gly Ser Gly Leu Asn Gly Ile Glu Glu Asp Gly Ala Leu Asp Asn Asp
145   150   155   160

Asp Asp Asp Asp Asp Asp Asp Asp Asp Ser Glu Met Glu Asn Arg Asp
                165   170   175

Arg Leu Ile Arg Lys Ser Arg Ser Arg Gly Gly Ser Thr Arg Gly Asn
            180   185   190

Arg Thr Thr Ile Glu Asp His His Leu Gln Glu Glu Lys Ala Pro Pro
    195   200   205

```
Pro Pro Pro Leu Ala Asn Ser Arg Pro Ile Pro Pro Pro Arg Gln His
    210             215             220

Gln His Gln His Gln Gln Gln Gln Gln Gln Pro Phe Tyr Asp Tyr Phe
225             230             235             240

Phe Pro Asn Val Glu Asn Met Pro Gly Thr Thr Leu Glu Asp Thr Pro
            245             250             255

Pro Gln Pro Gln Pro Gln Pro Thr Arg Pro Val Pro Pro Gln Pro His
            260             265             270

Ser Pro Val Val Thr Glu Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu
        275             280             285

Glu Glu Glu Glu Glu Glu Glu Thr Val Ile Glu Arg Lys Pro Leu Val
    290             295             300

Glu Glu Arg Pro Lys Arg Val Glu Glu Val Thr Ile Glu Leu Glu Lys
305             310             315             320

Val Thr Asn Leu Arg Gly Met Lys Lys Ser Lys Gly Ile Gly Ile Pro
            325             330             335

Gly Glu Arg Arg Gly Met Arg Met Pro Val Thr Ala Thr His Leu Ala
            340             345             350

Asn Val Phe Ile Glu Leu Asp Asp Asn Phe Leu Lys Ala Ser Glu Ser
        355             360             365

Ala His Asp Val Ser Lys Met Leu Glu Ala Thr Arg Leu His Tyr His
    370             375             380

Ser Asn Phe Ala Asp Asn Arg Gly His Ile Asp His Ser Ala Arg Val
385             390             395             400

Met Arg Val Ile Thr Trp Asn Arg Ser Phe Arg Gly Ile Pro Asn Ala
            405             410             415

Asp Asp Gly Lys Asp Asp Val Asp Leu Glu Glu Asn Glu Thr His Ala
            420             425             430

Thr Val Leu Asp Lys Leu Leu Ala Trp Glu Lys Lys Leu Tyr Asp Glu
        435             440             445
```

Val Lys Ala Gly Glu Leu Met Lys Ile Glu Tyr Gln Lys Lys Val Ala
    450   455   460

His Leu Asn Arg Val Lys Lys Arg Gly Gly His Ser Asp Ser Leu Glu
465   470   475   480

Arg Ala Lys Ala Ala Val Ser His Leu His Thr Arg Tyr Ile Val Asp
                485   490   495

Met Gln Ser Met Asp Ser Thr Val Ser Glu Ile Asn Arg Leu Arg Asp
                500   505   510

Glu Gln Leu Tyr Leu Lys Leu Val His Leu Val Glu Ala Met Gly Lys
        515   520   525

Met Trp Glu Met Met Gln Ile His His Gln Arg Gln Ala Glu Ile Ser
    530   535   540

Lys Val Leu Arg Ser Leu Asp Val Ser Gln Ala Val Lys Glu Thr Asn
545   550   555   560

Asp His His His Glu Arg Thr Ile Gln Leu Leu Ala Val Val Gln Glu
            565   570   575

Trp His Thr Gln Phe Cys Arg Met Ile Asp His Gln Lys Glu Tyr Ile
            580   585   590

Lys Ala Leu Gly Gly Trp Leu Lys Leu Asn Leu Ile Pro Ile Glu Ser
        595   600   605

Thr Leu Lys Glu Lys Val Ser Ser Pro Pro Arg Val Pro Asn Pro Ala
    610   615   620

Ile Gln Lys Leu Leu His Ala Trp Tyr Asp Arg Leu Asp Lys Ile Pro
625   630   635   640

Asp Glu Met Ala Lys Ser Ala Ile Ile Asn Phe Ala Ala Val Val Ser
            645   650   655

Thr Ile Met Gln Gln Gln Glu Asp Glu Ile Ser Leu Arg Asn Lys Cys
            660   665   670

Glu Glu Thr Arg Lys Glu Leu Gly Arg Lys Ile Arg Gln Phe Glu Asp
        675   680   685

Trp Tyr His Lys Tyr Ile Gln Lys Arg Gly Pro Glu Gly Met Asn Pro

320

```
         690                  695                  700
```

```
Asp Glu Ala Asp Asn Asp His Asn Asp Glu Val Ala Val Arg Gln Phe
705                 710                 715                 720


Asn Val Glu Gln Ile Lys Lys Arg Leu Glu Glu Glu Glu Glu Ala Tyr
                725                 730                 735


His Arg Gln Ser His Gln Val Arg Glu Lys Ser Leu Ala Ser Leu Arg
            740                 745                 750


Thr Arg Leu Pro Glu Leu Phe Gln Ala Met Ser Glu Val Ala Tyr Ser
            755                 760                 765


Cys Ser Asp Met Tyr Arg Ala Ile Thr Tyr Ala Ser Lys Arg Gln Ser
        770                 775                 780


Gln Ser Glu Arg His Gln Lys Pro Ser Gln Gly Gln Ser Ser
785                 790                 795
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<221> CDS <222> (1)..(1146) <223> G1095
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atg gat cta aca gac cgt cgt aac cct ttt aac aat ctt gtt ttt ccg
48
Met Asp Leu Thr Asp Arg Arg Asn Pro Phe Asn Asn Leu Val Phe Pro
1               5                   10                  15


ccg ccg cct ccg ccg cca tcc acg acc ttc aca agc cct ata ttc cca
96
Pro Pro Pro Pro Pro Pro Ser Thr Thr Phe Thr Ser Pro Ile Phe Pro
                20                  25                  30


cga aca agc tct tcc ggc acc aat ttc ccc att ctg gcc atc gca gtg
144
Arg Thr Ser Ser Ser Gly Thr Asn Phe Pro Ile Leu Ala Ile Ala Val
            35                  40                  45


att gga atc tta gcc act gcg ttc tta ctt gta agt tac tac atc ttc
192
Ile Gly Ile Leu Ala Thr Ala Phe Leu Leu Val Ser Tyr Tyr Ile Phe
        50                  55                  60


gtg atc aaa tgc tgt ctt aat tgg cac caa atc gac atc ttt cgc cgc
240
Val Ile Lys Cys Cys Leu Asn Trp His Gln Ile Asp Ile Phe Arg Arg
65                  70                  75                  80


cgc aga cga agc agt gac caa aac cct cta atg att tac tct cct cat
288
Arg Arg Arg Ser Ser Asp Gln Asn Pro Leu Met Ile Tyr Ser Pro His
                85                  90                  95
```

```
gag gta aac aga gga cta gac gaa tcc gcc att aga gct atc cca gtc
336
Glu Val Asn Arg Gly Leu Asp Glu Ser Ala Ile Arg Ala Ile Pro Val
            100             105             110

ttc aaa ttc aag aag aga gac gtt gtt gca gga gaa gaa gat cag agt
384
Phe Lys Phe Lys Lys Arg Asp Val Val Ala Gly Glu Glu Asp Gln Ser
            115             120             125

aag aac tct caa gaa tgc tct gtt tgt tta aac gag ttt caa gaa gac
432
Lys Asn Ser Gln Glu Cys Ser Val Cys Leu Asn Glu Phe Gln Glu Asp
        130             135             140

gag aag cta agg att att cct aac tgc tgc cac gtg ttt cac att gat
480
Glu Lys Leu Arg Ile Ile Pro Asn Cys Cys His Val Phe His Ile Asp
145             150             155             160

tgc att gat atc tgg ctt cag ggc aac gca aat tgt ccc ttg tgc aga
528
Cys Ile Asp Ile Trp Leu Gln Gly Asn Ala Asn Cys Pro Leu Cys Arg
            165             170             175

acc agc gtt tct tgc gaa gca agt ttc act ctt gac cta atc tct gca
576
Thr Ser Val Ser Cys Glu Ala Ser Phe Thr Leu Asp Leu Ile Ser Ala
            180             185             190

ccg agc tct cct cgg gag aat agc cct cat tct cgg aac agg aat ctc
624
Pro Ser Ser Pro Arg Glu Asn Ser Pro His Ser Arg Asn Arg Asn Leu
            195             200             205

gaa ccc ggc ctg gtt cta gga ggc gat gat gac ttc gtc gtc ata gag
672
Glu Pro Gly Leu Val Leu Gly Gly Asp Asp Asp Phe Val Val Ile Glu
        210             215             220

ctt ggg gcc agt aat ggt aac aac aga gaa agc gtg aga aac ata gac
720
Leu Gly Ala Ser Asn Gly Asn Asn Arg Glu Ser Val Arg Asn Ile Asp
225             230             235             240

ttc ctt acg gag caa gaa agg gtt acc tcg aat gag gtc tcg acc gga
768
Phe Leu Thr Glu Gln Glu Arg Val Thr Ser Asn Glu Val Ser Thr Gly
            245             250             255

aac agc ccg aaa tcg gtg agt cct ttg cct ata aag ttt ggt aat cgg
816
Asn Ser Pro Lys Ser Val Ser Pro Leu Pro Ile Lys Phe Gly Asn Arg
            260             265             270

gga atg tat aag aaa gaa agg aaa ttt cac aaa gtg acg agt atg gga
864
Gly Met Tyr Lys Lys Glu Arg Lys Phe His Lys Val Thr Ser Met Gly
            275             280             285
```

gac gaa tgt atc gat act aga ggc aaa gat ggt cat ttt ggt gaa att
912
Asp Glu Cys Ile Asp Thr Arg Gly Lys Asp Gly His Phe Gly Glu Ile
    290   295   300

cag ccc ata aga aga tcg atc tcg atg gat tca tca gtg gat cgt cag
960
Gln Pro Ile Arg Arg Ser Ile Ser Met Asp Ser Ser Val Asp Arg Gln
305   310   315   320

ctg tac ttg gcg gtc caa gag gaa atc agc cgg aga aac agg cag att
1008
Leu Tyr Leu Ala Val Gln Glu Glu Ile Ser Arg Arg Asn Arg Gln Ile
                325   330   335

ccg gta gct gga gac ggt gaa gat agt agc agt agt ggt ggt ggt aat
1056
Pro Val Ala Gly Asp Gly Glu Asp Ser Ser Ser Ser Gly Gly Gly Asn
                340   345   350

agc aga gtc atg aag aga tgt ttc ttc tct ttt gga agt agt aga act
1104
Ser Arg Val Met Lys Arg Cys Phe Phe Ser Phe Gly Ser Ser Arg Thr
            355   360   365

tca aaa agt tct tca ata tta cct gtt tat ttg gaa ccc taa
1146
Ser Lys Ser Ser Ser Ile Leu Pro Val Tyr Leu Glu Pro
    370   375   380

<210> 180 <211> 381 <212> PRT <213> Arabidopsis thaliana <400>
180

Met Asp Leu Thr Asp Arg Arg Asn Pro Phe Asn Asn Leu Val Phe Pro
1   5   10   15

Pro Pro Pro Pro Pro Pro Ser Thr Thr Phe Thr Ser Pro Ile Phe Pro
            20   25   30

Arg Thr Ser Ser Ser Gly Thr Asn Phe Pro Ile Leu Ala Ile Ala Val
            35   40   45

Ile Gly Ile Leu Ala Thr Ala Phe Leu Leu Val Ser Tyr Tyr Ile Phe
    50   55   60

Val Ile Lys Cys Cys Leu Asn Trp His Gln Ile Asp Ile Phe Arg Arg
65   70   75   80

Arg Arg Arg Ser Ser Asp Gln Asn Pro Leu Met Ile Tyr Ser Pro His
            85   90   95

Glu Val Asn Arg Gly Leu Asp Glu Ser Ala Ile Arg Ala Ile Pro Val
            100   105   110

323

```
Phe Lys Phe Lys Lys Arg Asp Val Val Ala Gly Glu Glu Asp Gln Ser
        115                 120                 125

Lys Asn Ser Gln Glu Cys Ser Val Cys Leu Asn Glu Phe Gln Glu Asp
    130                 135                 140

Glu Lys Leu Arg Ile Ile Pro Asn Cys Cys His Val Phe His Ile Asp
145                 150                 155                 160

Cys Ile Asp Ile Trp Leu Gln Gly Asn Ala Asn Cys Pro Leu Cys Arg
                165                 170                 175

Thr Ser Val Ser Cys Glu Ala Ser Phe Thr Leu Asp Leu Ile Ser Ala
            180                 185                 190

Pro Ser Ser Pro Arg Glu Asn Ser Pro His Ser Arg Asn Arg Asn Leu
        195                 200                 205

Glu Pro Gly Leu Val Leu Gly Gly Asp Asp Asp Phe Val Val Ile Glu
    210                 215                 220

Leu Gly Ala Ser Asn Gly Asn Asn Arg Glu Ser Val Arg Asn Ile Asp
225                 230                 235                 240

Phe Leu Thr Glu Gln Glu Arg Val Thr Ser Asn Glu Val Ser Thr Gly
                245                 250                 255

Asn Ser Pro Lys Ser Val Ser Pro Leu Pro Ile Lys Phe Gly Asn Arg
            260                 265                 270

Gly Met Tyr Lys Lys Glu Arg Lys Phe His Lys Val Thr Ser Met Gly
        275                 280                 285

Asp Glu Cys Ile Asp Thr Arg Gly Lys Asp Gly His Phe Gly Glu Ile
    290                 295                 300

Gln Pro Ile Arg Arg Ser Ile Ser Met Asp Ser Ser Val Asp Arg Gln
305                 310                 315                 320

Leu Tyr Leu Ala Val Gln Glu Glu Ile Ser Arg Arg Asn Arg Gln Ile
            325                 330                 335

Pro Val Ala Gly Asp Gly Glu Asp Ser Ser Ser Ser Gly Gly Gly Asn
        340                 345                 350
```

324

```
Ser Arg Val Met Lys Arg Cys Phe Phe Ser Phe Gly Ser Ser Arg Thr
        355                 360                 365
```

```
Ser Lys Ser Ser Ser Ile Leu Pro Val Tyr Leu Glu Pro
        370                 375                 380
```

<210> 181 <211> 1064 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (61)..(849) <223> G1134

<400> 181

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taaagaaaga gaaaaaaagc tttcgtagtg tctattgaaa ccagagaaaa gccaaagggg
60
```

```
atg caa cca aca tcc gtc ggt agt agc ggc ggt ggt gac gac gga gga
108
Met Gln Pro Thr Ser Val Gly Ser Ser Gly Gly Gly Asp Asp Gly Gly
1                5                  10                  15
```

```
ggc aga gga gga gga gga ggg cta agt aga agt gga cta tct cgg atc
156
Gly Arg Gly Gly Gly Gly Gly Leu Ser Arg Ser Gly Leu Ser Arg Ile
            20                  25                  30
```

```
cgt tca gct cca gcg act tgg ctt gaa gct tta ctt gag gaa gat gaa
204
Arg Ser Ala Pro Ala Thr Trp Leu Glu Ala Leu Leu Glu Glu Asp Glu
        35                  40                  45
```

```
gaa gag tct ttg aaa cct aat ctt ggt ctc acc gat ttg ctt acc ggg
252
Glu Glu Ser Leu Lys Pro Asn Leu Gly Leu Thr Asp Leu Leu Thr Gly
    50                  55                  60
```

```
aac tcg aac gat tta ccg aca agt cgc ggc tcg ttc gag ttc ccg att
300
Asn Ser Asn Asp Leu Pro Thr Ser Arg Gly Ser Phe Glu Phe Pro Ile
65                  70                  75                  80
```

```
cct gtt gag caa ggg ttg tat caa caa ggt ggg ttt cac cga cag aat
348
Pro Val Glu Gln Gly Leu Tyr Gln Gln Gly Gly Phe His Arg Gln Asn
                85                  90                  95
```

```
agt act ccg gcg gat ttt ctt agt ggt tct gat gga ttt atc caa agc
396
Ser Thr Pro Ala Asp Phe Leu Ser Gly Ser Asp Gly Phe Ile Gln Ser
            100                 105                 110
```

```
ttt ggg att cag gcg aat tac gat tac tta tcg ggg aat atc gat gtt
444
Phe Gly Ile Gln Ala Asn Tyr Asp Tyr Leu Ser Gly Asn Ile Asp Val
            115                 120                 125
```

```
tct ccg gga agt aag cgg tct aga gaa atg gaa gca ctc ttc tct tct
492
Ser Pro Gly Ser Lys Arg Ser Arg Glu Met Glu Ala Leu Phe Ser Ser
        130                 135                 140
```

```
cct gag ttt act tct caa atg aaa gga gag caa agc agc ggt caa gtt
540
Pro Glu Phe Thr Ser Gln Met Lys Gly Glu Gln Ser Ser Gly Gln Val
145             150             155             160

cct acc gga gta tca agc atg tcg gat atg aac atg gag aac ctt atg
588
Pro Thr Gly Val Ser Ser Met Ser Asp Met Asn Met Glu Asn Leu Met
                165             170             175

gag gac tct gtt gct ttt agg gtt cgg gct aaa cgt ggt tgc gca act
636
Glu Asp Ser Val Ala Phe Arg Val Arg Ala Lys Arg Gly Cys Ala Thr
            180             185             190

cat ccc cgc agc att gcc gag agg gta cga agg acg cgg att agt gat
684
His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp
        195             200             205

cgg ata agg aag cta caa gag ctt gta cct aac atg gac aag caa acc
732
Arg Ile Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr
    210             215             220

aac act gca gac atg tta gaa gaa gca gta gaa tac gtg aaa gtt ctt
780
Asn Thr Ala Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Val Leu
225             230             235             240

caa agg cag atc cag gag tta aca gaa gaa cag aag agg tgc aca tgc
828
Gln Arg Gln Ile Gln Glu Leu Thr Glu Glu Gln Lys Arg Cys Thr Cys
                245             250             255

ata cct aag gaa gaa caa taa ggtttgctcc tgatttgttt tatatttgct
879
Ile Pro Lys Glu Glu Gln
                260

taacggcaat gatctgatcg aaaaattcga aagatgatct tagcttgaat ttagatggat
939

gtcatgttga aaagtatatt atttgataaa tggatgtagg tgtaatataa aatttttgta
999

caataatgaa gaaagttaaa aagaattaat gaaacatat attctttatg atataaaaaa
1059

aaaaa
1064


<210> 182 <211> 262 <212> PRT <213> Arabidopsis thaliana <400>
182

Met Gln Pro Thr Ser Val Gly Ser Ser Gly Gly Gly Asp Asp Gly Gly
1           5               10              15


Gly Arg Gly Gly Gly Gly Gly Leu Ser Arg Ser Gly Leu Ser Arg Ile
```

           20   25   30

```
Arg Ser Ala Pro Ala Thr Trp Leu Glu Ala Leu Leu Glu Glu Asp Glu
        35                  40                  45

Glu Glu Ser Leu Lys Pro Asn Leu Gly Leu Thr Asp Leu Leu Thr Gly
        50                  55                  60

Asn Ser Asn Asp Leu Pro Thr Ser Arg Gly Ser Phe Glu Phe Pro Ile
65                  70                  75                  80

Pro Val Glu Gln Gly Leu Tyr Gln Gln Gly Gly Phe His Arg Gln Asn
                85                  90                  95

Ser Thr Pro Ala Asp Phe Leu Ser Gly Ser Asp Gly Phe Ile Gln Ser
                100                 105                 110

Phe Gly Ile Gln Ala Asn Tyr Asp Tyr Leu Ser Gly Asn Ile Asp Val
                115                 120                 125

Ser Pro Gly Ser Lys Arg Ser Arg Glu Met Glu Ala Leu Phe Ser Ser
        130                 135                 140

Pro Glu Phe Thr Ser Gln Met Lys Gly Glu Gln Ser Ser Gly Gln Val
145                 150                 155                 160

Pro Thr Gly Val Ser Ser Met Ser Asp Met Asn Met Glu Asn Leu Met
                165                 170                 175

Glu Asp Ser Val Ala Phe Arg Val Arg Ala Lys Arg Gly Cys Ala Thr
                180                 185                 190

His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp
        195                 200                 205

Arg Ile Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr
        210                 215                 220

Asn Thr Ala Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Val Leu
225                 230                 235                 240

Gln Arg Gln Ile Gln Glu Leu Thr Glu Glu Gln Lys Arg Cys Thr Cys
                245                 250                 255

Ile Pro Lys Glu Glu Gln
        260
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<221> CDS <222> (46)..(807) <223> G1142

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attaattaac aaaaaaccaa aagaaggcgg cgcaaacaaa agata atg caa cca gag
57
                                                      Met Gln Pro Glu
                                                      1

acc tca gat cag atg ttg tac tcg ttt ctt gcc gga aac gaa gtc ggc
105
Thr Ser Asp Gln Met Leu Tyr Ser Phe Leu Ala Gly Asn Glu Val Gly
5   10   15   20

ggt gga ggg tac tgc gtc tcc ggc gac tac atg acg act atg cag agc
153
Gly Gly Gly Tyr Cys Val Ser Gly Asp Tyr Met Thr Thr Met Gln Ser
                25   30   35

tta tgt ggg tct tcg tcg tcg acg tca tcg tat tac cca ctg gcg atc
201
Leu Cys Gly Ser Ser Ser Ser Thr Ser Ser Tyr Tyr Pro Leu Ala Ile
            40   45   50

tcc ggc atc gga gaa acg atg gct caa gac aga gct tta gct gct ttg
249
Ser Gly Ile Gly Glu Thr Met Ala Gln Asp Arg Ala Leu Ala Ala Leu
        55   60   65

agg aac cac aaa gaa gct gag aga aga agg aga gag agg atc aat tct
297
Arg Asn His Lys Glu Ala Glu Arg Arg Arg Arg Glu Arg Ile Asn Ser
    70   75   80

cat ctc aac aag ctt cgt aac gta ctc tct tgt aat tct aag acc gat
345
His Leu Asn Lys Leu Arg Asn Val Leu Ser Cys Asn Ser Lys Thr Asp
85   90   95   100

aaa gcc aca ctg ctc gcc aaa gta gtt caa cga gtc aga gaa ctt aaa
393
Lys Ala Thr Leu Leu Ala Lys Val Val Gln Arg Val Arg Glu Leu Lys
            105   110   115

cag caa acc cta gag acc tcc gac tcc gac caa aca tta tta cca tca
441
Gln Gln Thr Leu Glu Thr Ser Asp Ser Asp Gln Thr Leu Leu Pro Ser
        120   125   130

gag acc gac gaa att agt gtt cta cac ttt gga gac tat tca aac gac
489
Glu Thr Asp Glu Ile Ser Val Leu His Phe Gly Asp Tyr Ser Asn Asp
        135   140   145

ggt cat ata atc ttc aaa gcc tct cta tgt tgt gaa gat aga tca gat
537
Gly His Ile Ile Phe Lys Ala Ser Leu Cys Cys Glu Asp Arg Ser Asp
    150   155   160

```
ctc ttg ccg gac ctt atg gag att ctc aag tct ctt aac atg aag act
585
Leu Leu Pro Asp Leu Met Glu Ile Leu Lys Ser Leu Asn Met Lys Thr
165             170             175             180

ctc cga gct gag atg gta acc att ggt ggt cgg aca aga agt gtt ctt
633
Leu Arg Ala Glu Met Val Thr Ile Gly Gly Arg Thr Arg Ser Val Leu
                185             190             195

gtc gta gct gct gac aaa gag atg cac ggc gtc gag tct gtg cat ttt
681
Val Val Ala Ala Asp Lys Glu Met His Gly Val Glu Ser Val His Phe
                200             205             210

ttg caa aat gct ctc aag tcg ctg ctt gag cgg tca agc aag tcg ttg
729
Leu Gln Asn Ala Leu Lys Ser Leu Leu Glu Arg Ser Ser Lys Ser Leu
            215             220             225

atg gaa cgt agt tct ggt ggt gga gga gga gaa cgg tca aag cgg cgt
777
Met Glu Arg Ser Ser Gly Gly Gly Gly Gly Glu Arg Ser Lys Arg Arg
        230             235             240

cgt gcg ctg gat cac atc ata atg gtg tga aatgatgaga attgagcaca
827
Arg Ala Leu Asp His Ile Ile Met Val
245             250

ctaaaaagtc tataattgat taatatatat agggtatgat cataattaac ttggttataa
887

ttaccaaaac cttttttatt cctctttaat aatatatatg ttatatggtt ttagttacta
947

agtcttggga gtgtaagcaa atgttgtaag taggtttggt gtgttctttt tcttttcttt
1007

ttttttttctt tttcaaaaaa aaaaaaaaaa
1037


<210> 184 <211> 253 <212> PRT <213> Arabidopsis thaliana <400>
184

Met Gln Pro Glu Thr Ser Asp Gln Met Leu Tyr Ser Phe Leu Ala Gly
1           5               10              15

Asn Glu Val Gly Gly Gly Gly Tyr Cys Val Ser Gly Asp Tyr Met Thr
            20              25              30

Thr Met Gln Ser Leu Cys Gly Ser Ser Ser Thr Ser Ser Tyr Tyr
        35              40              45

Pro Leu Ala Ile Ser Gly Ile Gly Glu Thr Met Ala Gln Asp Arg Ala
    50              55              60
```

329

```
Leu Ala Ala Leu Arg Asn His Lys Glu Ala Glu Arg Arg Arg Arg Glu
65                  70                  75                      80


Arg Ile Asn Ser His Leu Asn Lys Leu Arg Asn Val Leu Ser Cys Asn
                85                  90                  95


Ser Lys Thr Asp Lys Ala Thr Leu Leu Ala Lys Val Val Gln Arg Val
            100                 105                 110


Arg Glu Leu Lys Gln Gln Thr Leu Glu Thr Ser Asp Ser Asp Gln Thr
        115                 120                 125


Leu Leu Pro Ser Glu Thr Asp Glu Ile Ser Val Leu His Phe Gly Asp
    130                 135                 140


Tyr Ser Asn Asp Gly His Ile Ile Phe Lys Ala Ser Leu Cys Cys Glu
145                 150                 155                 160


Asp Arg Ser Asp Leu Leu Pro Asp Leu Met Glu Ile Leu Lys Ser Leu
            165                 170                 175


Asn Met Lys Thr Leu Arg Ala Glu Met Val Thr Ile Gly Gly Arg Thr
            180                 185                 190


Arg Ser Val Leu Val Val Ala Ala Asp Lys Glu Met His Gly Val Glu
        195                 200                 205


Ser Val His Phe Leu Gln Asn Ala Leu Lys Ser Leu Leu Glu Arg Ser
    210                 215                 220


Ser Lys Ser Leu Met Glu Arg Ser Ser Gly Gly Gly Gly Gly Glu Arg
225                 230                 235                 240


Ser Lys Arg Arg Arg Ala Leu Asp His Ile Ile Met Val
            245                 250


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<221>  CDS <222>   (56)..(1957) <223>  G1202

 <400> 185
caaatcacat attttgtgaa atcccaaaga aagttttttgc tttcaccggc cagtc atg          58
                                                                     Met
                                                                     1


gga aac tat cgg tgg ccg tca aag cta tca aag tta tca ctc aga gca          106
Gly Asn Tyr Arg Trp Pro Ser Lys Leu Ser Lys Leu Ser Leu Arg Ala
```

                    5   10   15

aaa caa acg aat ctg tac cgc gtc att cta atc gcg atc ctc tgc gtc
154
Lys Gln Thr Asn Leu Tyr Arg Val Ile Leu Ile Ala Ile Leu Cys Val
        20   25   30

acc ttt tac ttc gtc gga gta tgg caa cac tcc ggc aga gga atc tca
202
Thr Phe Tyr Phe Val Gly Val Trp Gln His Ser Gly Arg Gly Ile Ser
        35   40   45

cgc tct tcc att tct aac cac gag ctc acg tcc gtg ccc tgc acg ttt
250
Arg Ser Ser Ile Ser Asn His Glu Leu Thr Ser Val Pro Cys Thr Phe
50   55   60   65

cct cac caa acc aca ccg att ctc aac ttc gcc tcc cgt cac aca gcc
298
Pro His Gln Thr Thr Pro Ile Leu Asn Phe Ala Ser Arg His Thr Ala
                70   75   80

cct gac ctt cct ccg acg ata acg gac gcg cgt gtt gtt caa atc ccg
346
Pro Asp Leu Pro Pro Thr Ile Thr Asp Ala Arg Val Val Gln Ile Pro
                85   90   95

tcg tgc ggc gtt gaa ttc tcg gag tac acg ccc tgc gag ttc gtg aat
394
Ser Cys Gly Val Glu Phe Ser Glu Tyr Thr Pro Cys Glu Phe Val Asn
        100   105   110

cgg tct ttg aat ttc cca aga gag agg ctt ata tac aga gag aga cac
442
Arg Ser Leu Asn Phe Pro Arg Glu Arg Leu Ile Tyr Arg Glu Arg His
        115   120   125

tgt ccg gaa aaa cac gag ata gtc agg tgt cgg att cca gcg ccg tac
490
Cys Pro Glu Lys His Glu Ile Val Arg Cys Arg Ile Pro Ala Pro Tyr
130   135   140   145

ggt tac agt tta cct ttt cgg tgg ccg gag agc cgt gac gtg gcg tgg
538
Gly Tyr Ser Leu Pro Phe Arg Trp Pro Glu Ser Arg Asp Val Ala Trp
                150   155   160

ttt gct aac gtg ccg cat acg gaa cta acg gtg gag aag aag aat cag
586
Phe Ala Asn Val Pro His Thr Glu Leu Thr Val Glu Lys Lys Asn Gln
                165   170   175

aac tgg gta agg tat gag aag gat agg ttt tta ttt cct ggt ggt ggt
634
Asn Trp Val Arg Tyr Glu Lys Asp Arg Phe Leu Phe Pro Gly Gly Gly
        180   185   190

acg atg ttt cca cgt gga gct gat gct tac atc gac gag atc gga cgg
682
Thr Met Phe Pro Arg Gly Ala Asp Ala Tyr Ile Asp Glu Ile Gly Arg
        195   200   205

                                   331

ttg ata aat ctc aaa gat gga tca att cgg aca gcc att gat act gga
730
Leu Ile Asn Leu Lys Asp Gly Ser Ile Arg Thr Ala Ile Asp Thr Gly
210   215   220   225

tgt ggg gta gcg agc ttt ggg gcg tat cta atg tcg agg aac ata gta
778
Cys Gly Val Ala Ser Phe Gly Ala Tyr Leu Met Ser Arg Asn Ile Val
                   230   235   240

acg atg tcg ttt gca cca aga gac aca cac gaa gct cag gtt cag ttc
826
Thr Met Ser Phe Ala Pro Arg Asp Thr His Glu Ala Gln Val Gln Phe
                   245   250   255

gca ctt gag aga gga gtc cct gcc atc ata gga gtg tta gcc tct att
874
Ala Leu Glu Arg Gly Val Pro Ala Ile Ile Gly Val Leu Ala Ser Ile
           260   265   270

agg ctc cca ttt ccg gcc aga gcc ttc gac att gct cat tgc tct cga
922
Arg Leu Pro Phe Pro Ala Arg Ala Phe Asp Ile Ala His Cys Ser Arg
    275   280   285

tgt ctc att cct tgg ggc caa tac aac ggg acg tat ctc ata gaa gtg
970
Cys Leu Ile Pro Trp Gly Gln Tyr Asn Gly Thr Tyr Leu Ile Glu Val
290   295   300   305

gat agg gta ctg aga ccg ggg ggg tat tgg att ttg tcg gga ccg ccg
1018
Asp Arg Val Leu Arg Pro Gly Gly Tyr Trp Ile Leu Ser Gly Pro Pro
               310   315   320

att aac tgg cag aga cac tgg aag ggt tgg gaa aga act aga gac gat
1066
Ile Asn Trp Gln Arg His Trp Lys Gly Trp Glu Arg Thr Arg Asp Asp
               325   330   335

ctc aac tcg gag cag tct cag atc gag agg gtg gct agg agc ttg tgt
1114
Leu Asn Ser Glu Gln Ser Gln Ile Glu Arg Val Ala Arg Ser Leu Cys
           340   345   350

tgg agg aaa ttg gtg cag aga gag gat ctt gcg gtt tgg cag aaa cct
1162
Trp Arg Lys Leu Val Gln Arg Glu Asp Leu Ala Val Trp Gln Lys Pro
    355   360   365

acc aac cat gtt cac tgt aag cgc aat cgg ata gct tta gga cgc cct
1210
Thr Asn His Val His Cys Lys Arg Asn Arg Ile Ala Leu Gly Arg Pro
370   375   380   385

ccg ttc tgc cac cgg aca cta ccc aac cag ggc tgg tac act aag ctt
1258
Pro Phe Cys His Arg Thr Leu Pro Asn Gln Gly Trp Tyr Thr Lys Leu
               390   395   400

gaa acc tgt ttg acg ccg ttg ccg gaa gta aca gga tct gag atc aaa
1306
Glu Thr Cys Leu Thr Pro Leu Pro Glu Val Thr Gly Ser Glu Ile Lys
            405   410   415

gaa gta gcg ggt gga cag ttg gcg aga tgg cct gag aga ttg aat gct
1354
Glu Val Ala Gly Gly Gln Leu Ala Arg Trp Pro Glu Arg Leu Asn Ala
            420   425   430

ctt cct ccg agg atc aaa agt gga agc ttg gaa ggg atc act gag gat
1402
Leu Pro Pro Arg Ile Lys Ser Gly Ser Leu Glu Gly Ile Thr Glu Asp
            435   440   445

gaa ttt gtc agc aac aca gag aaa tgg cag aga aga gtg tct tac tac
1450
Glu Phe Val Ser Asn Thr Glu Lys Trp Gln Arg Arg Val Ser Tyr Tyr
450   455   460   465

aag aaa tat gac caa cag cta gcg gag acg gga aga tac aga aac ttt
1498
Lys Lys Tyr Asp Gln Gln Leu Ala Glu Thr Gly Arg Tyr Arg Asn Phe
            470   475   480

ctc gac atg aac gct cat ctt gga ggt ttc gcc tca gcc tta gtc gat
1546
Leu Asp Met Asn Ala His Leu Gly Gly Phe Ala Ser Ala Leu Val Asp
            485   490   495

gat cct gta tgg gtc atg aat gtt gtc ccc gtg gag gcc agt gtt aac
1594
Asp Pro Val Trp Val Met Asn Val Val Pro Val Glu Ala Ser Val Asn
            500   505   510

acc ctt gga gtt atc tat gag cga gga ttg att gga acg tat caa aac
1642
Thr Leu Gly Val Ile Tyr Glu Arg Gly Leu Ile Gly Thr Tyr Gln Asn
            515   520   525

tgg tgt gaa gca atg tca act tac cca agg aca tac gat ttc atc cat
1690
Trp Cys Glu Ala Met Ser Thr Tyr Pro Arg Thr Tyr Asp Phe Ile His
530   535   540   545

gcc gat tcg gtg ttc agt ctg tac aaa gac aga tgt gac atg gaa gat
1738
Ala Asp Ser Val Phe Ser Leu Tyr Lys Asp Arg Cys Asp Met Glu Asp
            550   555   560

atc ttg cta gaa atg gac agg att cta aga cca aag gga agc gtg atc
1786
Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Lys Gly Ser Val Ile
            565   570   575

atc aga gac gac att gat gtg cta acc aaa gtg aag aag att aca gat
1834
Ile Arg Asp Asp Ile Asp Val Leu Thr Lys Val Lys Lys Ile Thr Asp
            580   585   590

```
gcg atg caa tgg gaa ggg agg ata gga gat cat gaa aac gga cct ctt
1882
Ala Met Gln Trp Glu Gly Arg Ile Gly Asp His Glu Asn Gly Pro Leu
    595             600             605

gaa aga gag aag att ttg ttt ctt gtg aag gag tac tgg acc gca cct
1930
Glu Arg Glu Lys Ile Leu Phe Leu Val Lys Glu Tyr Trp Thr Ala Pro
610             615             620             625

gcg cct gat cag tca tca gat cct tga tcaagcttgg aataattcat
1977
Ala Pro Asp Gln Ser Ser Asp Pro
                630

aaaatttgta gctccattct tttttcttca aatgttttgt acacactaat cgactttggg
2037

ggaaagaaga acaaacacc cgctaaattg tttcaaaccg gagattcatt gcgactttgt
2097

gagaaaatga actagagagt ttactacaaa
2127


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186

Met Gly Asn Tyr Arg Trp Pro Ser Lys Leu Ser Lys Leu Ser Leu Arg
1               5               10              15

Ala Lys Gln Thr Asn Leu Tyr Arg Val Ile Leu Ile Ala Ile Leu Cys
            20              25              30

Val Thr Phe Tyr Phe Val Gly Val Trp Gln His Ser Gly Arg Gly Ile
        35              40              45

Ser Arg Ser Ser Ile Ser Asn His Glu Leu Thr Ser Val Pro Cys Thr
    50              55              60

Phe Pro His Gln Thr Thr Pro Ile Leu Asn Phe Ala Ser Arg His Thr
65              70              75              80

Ala Pro Asp Leu Pro Pro Thr Ile Thr Asp Ala Arg Val Val Gln Ile
            85              90              95

Pro Ser Cys Gly Val Glu Phe Ser Glu Tyr Thr Pro Cys Glu Phe Val
            100             105             110

Asn Arg Ser Leu Asn Phe Pro Arg Glu Arg Leu Ile Tyr Arg Glu Arg
        115             120             125

His Cys Pro Glu Lys His Glu Ile Val Arg Cys Arg Ile Pro Ala Pro
```

334

130   135   140

Tyr Gly Tyr Ser Leu Pro Phe Arg Trp Pro Glu Ser Arg Asp Val Ala
145   150   155   160

Trp Phe Ala Asn Val Pro His Thr Glu Leu Thr Val Glu Lys Lys Asn
                 165   170   175

Gln Asn Trp Val Arg Tyr Glu Lys Asp Arg Phe Leu Phe Pro Gly Gly
            180   185   190

Gly Thr Met Phe Pro Arg Gly Ala Asp Ala Tyr Ile Asp Glu Ile Gly
            195   200   205

Arg Leu Ile Asn Leu Lys Asp Gly Ser Ile Arg Thr Ala Ile Asp Thr
    210   215   220

Gly Cys Gly Val Ala Ser Phe Gly Ala Tyr Leu Met Ser Arg Asn Ile
225   230   235   240

Val Thr Met Ser Phe Ala Pro Arg Asp Thr His Glu Ala Gln Val Gln
                 245   250   255

Phe Ala Leu Glu Arg Gly Val Pro Ala Ile Ile Gly Val Leu Ala Ser
            260   265   270

Ile Arg Leu Pro Phe Pro Ala Arg Ala Phe Asp Ile Ala His Cys Ser
            275   280   285

Arg Cys Leu Ile Pro Trp Gly Gln Tyr Asn Gly Thr Tyr Leu Ile Glu
    290   295   300

Val Asp Arg Val Leu Arg Pro Gly Gly Tyr Trp Ile Leu Ser Gly Pro
305   310   315   320

Pro Ile Asn Trp Gln Arg His Trp Lys Gly Trp Glu Arg Thr Arg Asp
                 325   330   335

Asp Leu Asn Ser Glu Gln Ser Gln Ile Glu Arg Val Ala Arg Ser Leu
            340   345   350

Cys Trp Arg Lys Leu Val Gln Arg Glu Asp Leu Ala Val Trp Gln Lys
            355   360   365

Pro Thr Asn His Val His Cys Lys Arg Asn Arg Ile Ala Leu Gly Arg
    370   375   380

335

```
Pro Pro Phe Cys His Arg Thr Leu Pro Asn Gln Gly Trp Tyr Thr Lys
385             390             395             400


Leu Glu Thr Cys Leu Thr Pro Leu Pro Glu Val Thr Gly Ser Glu Ile
            405             410             415


Lys Glu Val Ala Gly Gly Gln Leu Ala Arg Trp Pro Glu Arg Leu Asn
            420             425             430


Ala Leu Pro Pro Arg Ile Lys Ser Gly Ser Leu Glu Gly Ile Thr Glu
            435             440             445


Asp Glu Phe Val Ser Asn Thr Glu Lys Trp Gln Arg Arg Val Ser Tyr
    450             455             460


Tyr Lys Lys Tyr Asp Gln Gln Leu Ala Glu Thr Gly Arg Tyr Arg Asn
465             470             - 475               480


Phe Leu Asp Met Asn Ala His Leu Gly Gly Phe Ala Ser Ala Leu Val
            485             490             495


Asp Asp Pro Val Trp Val Met Asn Val Val Pro Val Glu Ala Ser Val
            500             505             510


Asn Thr Leu Gly Val Ile Tyr Glu Arg Gly Leu Ile Gly Thr Tyr Gln
            515             520             525


Asn Trp Cys Glu Ala Met Ser Thr Tyr Pro Arg Thr Tyr Asp Phe Ile
            530             535             540


His Ala Asp Ser Val Phe Ser Leu Tyr Lys Asp Arg Cys Asp Met Glu
545             550             555             560


Asp Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Lys Gly Ser Val
            565             570             575


Ile Ile Arg Asp Asp Ile Asp Val Leu Thr Lys Val Lys Lys Ile Thr
            580             585             590


Asp Ala Met Gln Trp Glu Gly Arg Ile Gly Asp His Glu Asn Gly Pro
            595             600             605


Leu Glu Arg Glu Lys Ile Leu Phe Leu Val Lys Glu Tyr Trp Thr Ala
            610             615             620
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336

Pro Ala Pro Asp Gln Ser Ser Asp Pro
625   630

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<221> CDS <222> (123)..(1217) <223> G1229

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tttgggcggg tctttctttc cctaaatctt tcttttattt tgctgtttaa aaaaaaaatc
60

caaccataag acaaaacaac gaacgaggaa gagagagaga gaaggatata tctctaatca
120

cg atg cag gag ata ata ccg gat ttt ctt gaa gag tgt gaa ttt gtc
167
   Met Gln Glu Ile Ile Pro Asp Phe Leu Glu Glu Cys Glu Phe Val
    1   5   10   15

gac act tca cta gcc gga gat gat cta ttt gcc atc tta gag agt ctt
215
Asp Thr Ser Leu Ala Gly Asp Asp Leu Phe Ala Ile Leu Glu Ser Leu
            20   25   30

gaa ggt gcc gga gag ata tct ccg aca gct gca tct aca cct aaa gat
263
Glu Gly Ala Gly Glu Ile Ser Pro Thr Ala Ala Ser Thr Pro Lys Asp
            35   40   45

gga acc aca agt tcc aag gag tta gtt aag gat caa gat tat gaa aac
311
Gly Thr Thr Ser Ser Lys Glu Leu Val Lys Asp Gln Asp Tyr Glu Asn
         50   55   60

tca tct cct aag agg aaa aag caa aga cta gaa acc agg aaa gaa gag
359
Ser Ser Pro Lys Arg Lys Lys Gln Arg Leu Glu Thr Arg Lys Glu Glu
      65   70   75

gac gaa gaa gaa gaa gac gga gac gga gaa gca gaa gaa gat aat aag
407
Asp Glu Glu Glu Glu Asp Gly Asp Gly Glu Ala Glu Glu Asp Asn Lys
80   85   90   95

caa gat ggg caa caa aag atg tct cat gta acc gtg gaa cgt aac cgg
455
Gln Asp Gly Gln Gln Lys Met Ser His Val Thr Val Glu Arg Asn Arg
            100   105   110

aga aag caa atg aac gag cac tta acc gtt ttg cgt tct ctt atg cct
503
Arg Lys Gln Met Asn Glu His Leu Thr Val Leu Arg Ser Leu Met Pro
            115   120   125

tgt ttc tac gtc aaa cgg ggg gac caa gca tcg atc ata gga gga gtt
551
Cys Phe Tyr Val Lys Arg Gly Asp Gln Ala Ser Ile Ile Gly Gly Val
         130   135   140

337

```
gtg gag tac ata agc gag tta caa caa gtt ctc caa tct ttg gaa gcc
599
Val Glu Tyr Ile Ser Glu Leu Gln Gln Val Leu Gln Ser Leu Glu Ala
    145                 150                 155

aag aaa caa cgt aaa acc tac gcc gaa gtc cta agc ccg aga gtt gtc
647
Lys Lys Gln Arg Lys Thr Tyr Ala Glu Val Leu Ser Pro Arg Val Val
160                 165                 170                 175

ccg agc cct cgt cct tca ccg cct gtt cta agc cca aga aaa ccg cct
695
Pro Ser Pro Arg Pro Ser Pro Pro Val Leu Ser Pro Arg Lys Pro Pro
                180                 185                 190

ctt agc ccg cgc atc aac cac cac cag att cac cac cac cta ctt ctc
743
Leu Ser Pro Arg Ile Asn His His Gln Ile His His His Leu Leu Leu
                195                 200                 205

cct ccc ata agt cct cga aca cct cag cca aca agc cca tac cgg gcc
791
Pro Pro Ile Ser Pro Arg Thr Pro Gln Pro Thr Ser Pro Tyr Arg Ala
        210                 215                 220

att cca ccg caa cta cca ctc atc cca cag cct ccg ctt cgc tct tac
839
Ile Pro Pro Gln Leu Pro Leu Ile Pro Gln Pro Pro Leu Arg Ser Tyr
    225                 230                 235

agc tca ttg gcc agt tgc agc agc tta gga gat cca cct cca tac tct
887
Ser Ser Leu Ala Ser Cys Ser Ser Leu Gly Asp Pro Pro Pro Tyr Ser
240                 245                 250                 255

cct gct tca tct tct tca tct cct tca gtt agt agt aac cat gag agt
935
Pro Ala Ser Ser Ser Ser Ser Pro Ser Val Ser Ser Asn His Glu Ser
                260                 265                 270

agt gtg atc aat gag ctt gtt gct aac tca aaa tcg gct ttg gct gat
983
Ser Val Ile Asn Glu Leu Val Ala Asn Ser Lys Ser Ala Leu Ala Asp
            275                 280                 285

gtg gaa gtg aag ttt tca gga gct aac gtg ctg ctc aaa acg gtg tcg
1031
Val Glu Val Lys Phe Ser Gly Ala Asn Val Leu Leu Lys Thr Val Ser
            290                 295                 300

cat aag atc ccg gga caa gtt atg aag ata att gct gct ctt gaa gat
1079
His Lys Ile Pro Gly Gln Val Met Lys Ile Ile Ala Ala Leu Glu Asp
        305                 310                 315

ttg gct ctt gag att ctt cag gtt aat att aac acc gtc gac gaa acc
1127
Leu Ala Leu Glu Ile Leu Gln Val Asn Ile Asn Thr Val Asp Glu Thr
320                 325                 330                 335
```

338

```
atg ctt aat tct ttc acc atc aag att gga att gag tgc caa cta agt
1175
Met Leu Asn Ser Phe Thr Ile Lys Ile Gly Ile Glu Cys Gln Leu Ser
            340                 345                 350

gca gaa gaa ctg gct caa caa att cag caa aca ttc tgc tag
1217
Ala Glu Glu Leu Ala Gln Gln Ile Gln Gln Thr Phe Cys
        355                 360

taaagaagga tttaatatag cttcgtataa accttaacga gagagcagta cgtactcact
1277

ttctctcctt agtatccctt taattatctt ttcagttttc tgcaaagata tggagtttaa
1337

aaaaataaaa ttgttatcta agttttaat caaatattga ttaattataa ctaatatagg
1397

tataagtgag ttttaaagat tatcagcttc ataacagcca tcgtcatgtt tactttcttt
1457

taaattttag aatttagacg tactcctacc atgtaatttt atttctgtca ttacatcaag
1517

cattgtagct gtaattgcat atgaatgaac aatagtgtat gagtgatctc atgaataata
1577

ttcttcttgc aacacaaaaa aaaaaaa
1604
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<210> 188 <211> 364 <212> PRT <213> Arabidopsis thaliana <400>
188

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Met Gln Glu Ile Ile Pro Asp Phe Leu Glu Glu Cys Glu Phe Val Asp
1               5                   10                  15

Thr Ser Leu Ala Gly Asp Asp Leu Phe Ala Ile Leu Glu Ser Leu Glu
            20                  25                  30

Gly Ala Gly Glu Ile Ser Pro Thr Ala Ala Ser Thr Pro Lys Asp Gly
        35                  40                  45

Thr Thr Ser Ser Lys Glu Leu Val Lys Asp Gln Asp Tyr Glu Asn Ser
    50                  55                  60

Ser Pro Lys Arg Lys Lys Gln Arg Leu Glu Thr Arg Lys Glu Glu Asp
65                  70                  75                  80

Glu Glu Glu Glu Asp Gly Asp Gly Glu Ala Glu Glu Asp Asn Lys Gln
                85                  90                  95

Asp Gly Gln Gln Lys Met Ser His Val Thr Val Glu Arg Asn Arg Arg
            100                 105                 110
```

Lys Gln Met Asn Glu His Leu Thr Val Leu Arg Ser Leu Met Pro Cys
      115   120   125

Phe Tyr Val Lys Arg Gly Asp Gln Ala Ser Ile Ile Gly Gly Val Val
      130   135   140

Glu Tyr Ile Ser Glu Leu Gln Gln Val Leu Gln Ser Leu Glu Ala Lys
145   150   155   160

Lys Gln Arg Lys Thr Tyr Ala Glu Val Leu Ser Pro Arg Val Val Pro
              165   170   175

Ser Pro Arg Pro Ser Pro Pro Val Leu Ser Pro Arg Lys Pro Pro Leu
          180   185   190

Ser Pro Arg Ile Asn His His Gln Ile His His His Leu Leu Leu Pro
          195   200   205

Pro Ile Ser Pro Arg Thr Pro Gln Pro Thr Ser Pro Tyr Arg Ala Ile
      210   215   220

Pro Pro Gln Leu Pro Leu Ile Pro Gln Pro Pro Leu Arg Ser Tyr Ser
225   230   235   240

Ser Leu Ala Ser Cys Ser Ser Leu Gly Asp Pro Pro Pro Tyr Ser Pro
              245   250   255

Ala Ser Ser Ser Ser Ser Pro Ser Val Ser Ser Asn His Glu Ser Ser
          260   265   270

Val Ile Asn Glu Leu Val Ala Asn Ser Lys Ser Ala Leu Ala Asp Val
      275   280   285

Glu Val Lys Phe Ser Gly Ala Asn Val Leu Leu Lys Thr Val Ser His
      290   295   300

Lys Ile Pro Gly Gln Val Met Lys Ile Ile Ala Ala Leu Glu Asp Leu
305   310   315   320

Ala Leu Glu Ile Leu Gln Val Asn Ile Asn Thr Val Asp Glu Thr Met
              325   330   335

Leu Asn Ser Phe Thr Ile Lys Ile Gly Ile Glu Cys Gln Leu Ser Ala
              340   345   350

340

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Glu Glu Leu Ala Gln Gln Ile Gln Gln Thr Phe Cys
        355                 360
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<210> 189 <211> 2481 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (280)..(2202) <223> G1242

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gcgccgagac ttttcagcac caactatcgg cttcttatca cgggaacccc ccttcagaat
60

aatctccatg aattgtgggc ccttctcaat tttcttctcc ctgaggtttt tagttcagca
120

gaaactttg acgagtggtt tcaaatttct ggtgaaaacg accagcaaga agttgttcaa
180

caacttcaca aggttctgcg accatttctt cttcggaggt taaaatcaga tgtagagaaa
240

ggcttacctc caaaaaagga gacaatactc aaagttggc atg tct caa atg caa
294
                                          Met Ser Gln Met Gln
                                          1   5

aaa cag tac tac aag gct tta ctg cag aag gat ctt gaa gtg gtt aat
342
Lys Gln Tyr Tyr Lys Ala Leu Leu Gln Lys Asp Leu Glu Val Val Asn
               10   15   20

ggt ggt gga gaa cgc aaa cgt ctg ttg aac ata gca atg caa ttg cgg
390
Gly Gly Gly Glu Arg Lys Arg Leu Leu Asn Ile Ala Met Gln Leu Arg
           25   30   35

aaa tgc tgc aat cac cct tat ctc ttc cag ggt gcg gag cct ggt ccc
438
Lys Cys Cys Asn His Pro Tyr Leu Phe Gln Gly Ala Glu Pro Gly Pro
       40   45   50

cca tat act aca gga gat cac ctt gta aca aac gca ggt aag atg gtt
486
Pro Tyr Thr Thr Gly Asp His Leu Val Thr Asn Ala Gly Lys Met Val
       55   60   65

ctc tta gat aaa ttg cta cct aag ttg aag gat cga gat tca agg gtt
534
Leu Leu Asp Lys Leu Leu Pro Lys Leu Lys Asp Arg Asp Ser Arg Val
70   75   80   85

ctg ata ttt tct cag atg aca agg ctt ttg gat att ctc gag gat tac
582
Leu Ile Phe Ser Gln Met Thr Arg Leu Leu Asp Ile Leu Glu Asp Tyr
               90   95   100

cta atg tat cgt ggt tac cag tac tgc cgt att gat gga aat act ggt
630
Leu Met Tyr Arg Gly Tyr Gln Tyr Cys Arg Ile Asp Gly Asn Thr Gly
           105   110   115

341

```
ggt gac gaa cga gat gct tcc ata gaa gcc tat aac aag cca gga agt
678
Gly Asp Glu Arg Asp Ala Ser Ile Glu Ala Tyr Asn Lys Pro Gly Ser
        120                 125                 130

gag aaa ttc gtt ttc ttg tta tcc act aga gct gga gga ctt ggt atc
726
Glu Lys Phe Val Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile
    135                 140                 145

aat ctt gct act gca gat gtt gtg atc ctc tat gat agt gac tgg aac
774
Asn Leu Ala Thr Ala Asp Val Val Ile Leu Tyr Asp Ser Asp Trp Asn
150                 155                 160                 165

cct caa gtt gac ttg caa gct cag gat cgt gca cat agg att ggt caa
822
Pro Gln Val Asp Leu Gln Ala Gln Asp Arg Ala His Arg Ile Gly Gln
                170                 175                 180

aaa aaa gaa gtt caa gtg ttc cgg ttc tgc acc gag aat gct att gag
870
Lys Lys Glu Val Gln Val Phe Arg Phe Cys Thr Glu Asn Ala Ile Glu
                185                 190  –                195

gct aaa gtc att gag aga gct tac aag aag ttg gca ctt gat gct ctg
918
Ala Lys Val Ile Glu Arg Ala Tyr Lys Lys Leu Ala Leu Asp Ala Leu
        200                 205                 210

gtt att cag caa ggg aga ttg gca gaa cag aaa act gtt aat aag gat
966
Val Ile Gln Gln Gly Arg Leu Ala Glu Gln Lys Thr Val Asn Lys Asp
    215                 220                 225

gag ttg ctt caa atg gtg aga tat ggt gct gaa atg gtg ttt agt tct
1014
Glu Leu Leu Gln Met Val Arg Tyr Gly Ala Glu Met Val Phe Ser Ser
230                 235                 240                 245

aaa gat agc aca att acg gat gag gat att gac aga atc att gcc aaa
1062
Lys Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp Arg Ile Ile Ala Lys
                250                 255                 260

gga gaa gag gca acg gct gaa ctt gat gcc aag atg aag aaa ttt act
1110
Gly Glu Glu Ala Thr Ala Glu Leu Asp Ala Lys Met Lys Lys Phe Thr
        265                 270                 275

gaa gat gca ata cag ttt aaa atg gat gac agt gct gac ttt tat gat
1158
Glu Asp Ala Ile Gln Phe Lys Met Asp Asp Ser Ala Asp Phe Tyr Asp
        280                 285                 290

ttt gac gat gac aac aag gat gag agc aag gtg gat ttt aaa aag att
1206
Phe Asp Asp Asp Asn Lys Asp Glu Ser Lys Val Asp Phe Lys Lys Ile
    295                 300 ·               305
```

342

```
gtg agt gaa aat tgg aat gat cca cca aaa aga gag aga aag cgc aac
1254
Val Ser Glu Asn Trp Asn Asp Pro Pro Lys Arg Glu Arg Lys Arg Asn
310             315         320             325

tac tct gaa gtt gaa tac ttc aag caa acg ttg cga caa ggt gct cca
1302
Tyr Ser Glu Val Glu Tyr Phe Lys Gln Thr Leu Arg Gln Gly Ala Pro
            330         335             340

gct aaa cct aaa gag cct aga att cca cgc atg ccc caa ttg cat gat
1350
Ala Lys Pro Lys Glu Pro Arg Ile Pro Arg Met Pro Gln Leu His Asp
            345             350             355

ttt cag ttc ttt aac att cag agg ctg act gag ctg tat gaa aaa gaa
1398
Phe Gln Phe Phe Asn Ile Gln Arg Leu Thr Glu Leu Tyr Glu Lys Glu
        360             365             370

gtg cga tac ctt atg caa gca cat cag aaa act caa atg aaa gac aca
1446
Val Arg Tyr Leu Met Gln Ala His Gln Lys Thr Gln Met Lys Asp Thr
    375             380             385

att gag gtt gat gaa cct gaa gaa gtt gga gat ccc tta act gct gaa
1494
Ile Glu Val Asp Glu Pro Glu Glu Val Gly Asp Pro Leu Thr Ala Glu
390             395             400             405

gaa gtg gaa gaa aag gag cta ttg ctg gaa gag ggt ttc tca aca tgg
1542
Glu Val Glu Glu Lys Glu Leu Leu Leu Glu Glu Gly Phe Ser Thr Trp
            410         415             420

agc aga aga gac ttc aat gcc ttc att agg gct tgt gag aag tat ggc
1590
Ser Arg Arg Asp Phe Asn Ala Phe Ile Arg Ala Cys Glu Lys Tyr Gly
            425             430             435

cgg aac gac ata aag agt att gcc tct gag atg gaa ggg aaa act gag
1638
Arg Asn Asp Ile Lys Ser Ile Ala Ser Glu Met Glu Gly Lys Thr Glu
            440             445             450

gaa gag gtt gaa cga tat gct caa gtt ttc caa gtg cga tat aaa gag
1686
Glu Glu Val Glu Arg Tyr Ala Gln Val Phe Gln Val Arg Tyr Lys Glu
        455             460             465

ctg aat gat tac gac aga atc atc aag aat att gag aga ggg gaa gca
1734
Leu Asn Asp Tyr Asp Arg Ile Ile Lys Asn Ile Glu Arg Gly Glu Ala
470             475             480             485

aga atc tct agg aaa gat gaa atc atg aaa gct att ggg aag aaa ctg
1782
Arg Ile Ser Arg Lys Asp Glu Ile Met Lys Ala Ile Gly Lys Lys Leu
            490             495             500
```

343

gat cgc tac aga aac ccg tgg ctg gaa ctg aag att caa tat ggt cag
1830
Asp Arg Tyr Arg Asn Pro Trp Leu Glu Leu Lys Ile Gln Tyr Gly Gln
        505   510   515

aac aaa ggg aag ctg tac aat gaa gag tgc gac cgt ttc atg ata tgc
1878
Asn Lys Gly Lys Leu Tyr Asn Glu Glu Cys Asp Arg Phe Met Ile Cys
        520   525   530

atg gtc cat aaa ctt ggg tat gga aac tgg gat gag cta aag gca gcg
1926
Met Val His Lys Leu Gly Tyr Gly Asn Trp Asp Glu Leu Lys Ala Ala
        535   540   545

ttt cgg aca tcc ccc ttg ttt agg ttt gac tgg ttt gta aaa tcc cgc
1974
Phe Arg Thr Ser Pro Leu Phe Arg Phe Asp Trp Phe Val Lys Ser Arg
550   555   560   565

aca act cag gaa ctt gca agg aga tgt gac aca cta atc agg ttg att
2022
Thr Thr Gln Glu Leu Ala Arg Arg Cys Asp Thr Leu Ile Arg Leu Ile
            570   575   580

gag aaa gag aat caa gaa ttt gat gag aga gag agg caa gcc cga aaa
2070
Glu Lys Glu Asn Gln Glu Phe Asp Glu Arg Glu Arg Gln Ala Arg Lys
            585   590   595

gag aag aag ctt tca aag agt gca acg cca tca aaa cga cct tcg ggt
2118
Glu Lys Lys Leu Ser Lys Ser Ala Thr Pro Ser Lys Arg Pro Ser Gly
        600   605   610

agg caa gca aat gag agc cct tca tct ctt ctg aag aaa cga aag cag
2166
Arg Gln Ala Asn Glu Ser Pro Ser Ser Leu Leu Lys Lys Arg Lys Gln
        615   620   625

ctg tca atg gat gat tat gga aag cgt agg aaa taa gaaggcttgt
2212
Leu Ser Met Asp Asp Tyr Gly Lys Arg Arg Lys
630   635   640

gttgaatcca tcactaagta atcagaaaga tttatgatca cttctaggtt tgattccgaa
2272

tcggagaatt agttagaaga agctccttag agacaaggat ctaatatttt gtacccgcaa
2332

gcatcactgc attgtctccg acttctctta tttcttcaac gtgtatttta ctctattttg
2392

tttgtagaaa tattcaccac attcctagta gtgcgttttt agtaaatctc aaatgaactt
2452

ttgtggtcgg atttgaacaa aaaaaaaaa
2481

<210> 190 <211> 640 <212> PRT <213> Arabidopsis thaliana <400>
190

Met Ser Gln Met Gln Lys Gln Tyr Tyr Lys Ala Leu Leu Gln Lys Asp
1   5   10   15

Leu Glu Val Val Asn Gly Gly Glu Arg Lys Arg Leu Leu Asn Ile
            20   25   30

Ala Met Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Gln Gly
        35   40   45

Ala Glu Pro Gly Pro Pro Tyr Thr Thr Gly Asp His Leu Val Thr Asn
        50   55   60

Ala Gly Lys Met Val Leu Leu Asp Lys Leu Leu Pro Lys Leu Lys Asp
65   70   75   80

Arg Asp Ser Arg Val Leu Ile Phe Ser Gln Met Thr Arg Leu Leu Asp
                85   90   95

Ile Leu Glu Asp Tyr Leu Met Tyr Arg Gly Tyr Gln Tyr Cys Arg Ile
            100   105   110

Asp Gly Asn Thr Gly Gly Asp Glu Arg Asp Ala Ser Ile Glu Ala Tyr
            115   120   125

Asn Lys Pro Gly Ser Glu Lys Phe Val Phe Leu Leu Ser Thr Arg Ala
    130   135   140

Gly Gly Leu Gly Ile Asn Leu Ala Thr Ala Asp Val Val Ile Leu Tyr
145   150   155   160

Asp Ser Asp Trp Asn Pro Gln Val Asp Leu Gln Ala Gln Asp Arg Ala
                165   170   175

His Arg Ile Gly Gln Lys Lys Glu Val Gln Val Phe Arg Phe Cys Thr
            180   185   190

Glu Asn Ala Ile Glu Ala Lys Val Ile Glu Arg Ala Tyr Lys Lys Leu
            195   200   205

Ala Leu Asp Ala Leu Val Ile Gln Gln Gly Arg Leu Ala Glu Gln Lys
    210   215   220

Thr Val Asn Lys Asp Glu Leu Leu Gln Met Val Arg Tyr Gly Ala Glu
225   230   235   240

345

Met Val Phe Ser Ser Lys Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp
                 245   250   255

Arg Ile Ile Ala Lys Gly Glu Glu Ala Thr Ala Glu Leu Asp Ala Lys
             260   265   270

Met Lys Lys Phe Thr Glu Asp Ala Ile Gln Phe Lys Met Asp Asp Ser
     275   280   285

Ala Asp Phe Tyr Asp Phe Asp Asp Asn Lys Asp Glu Ser Lys Val
290   295   300

Asp Phe Lys Lys Ile Val Ser Glu Asn Trp Asn Asp Pro Pro Lys Arg
305   310   315   320

Glu Arg Lys Arg Asn Tyr Ser Glu Val Glu Tyr Phe Lys Gln Thr Leu
             325   330   335

Arg Gln Gly Ala Pro Ala Lys Pro Lys Glu Pro Arg Ile Pro Arg Met
             340   345   350

Pro Gln Leu His Asp Phe Gln Phe Phe Asn Ile Gln Arg Leu Thr Glu
         355   360   365

Leu Tyr Glu Lys Glu Val Arg Tyr Leu Met Gln Ala His Gln Lys Thr
     370   375   380

Gln Met Lys Asp Thr Ile Glu Val Asp Glu Pro Glu Glu Val Gly Asp
385   390   395   400

Pro Leu Thr Ala Glu Glu Val Glu Glu Lys Glu Leu Leu Leu Glu Glu
             405   410   415

Gly Phe Ser Thr Trp Ser Arg Arg Asp Phe Asn Ala Phe Ile Arg Ala
             420   425   430

Cys Glu Lys Tyr Gly Arg Asn Asp Ile Lys Ser Ile Ala Ser Glu Met
         435   440   445

Glu Gly Lys Thr Glu Glu Glu Val Glu Arg Tyr Ala Gln Val Phe Gln
     450   455   460

Val Arg Tyr Lys Glu Leu Asn Asp Tyr Asp Arg Ile Ile Lys Asn Ile
465   470   475   480

```
Glu Arg Gly Glu Ala Arg Ile Ser Arg Lys Asp Glu Ile Met Lys Ala
              485                   490                   495


Ile Gly Lys Lys Leu Asp Arg Tyr Arg Asn Pro Trp Leu Glu Leu Lys
              500                   505                   510


Ile Gln Tyr Gly Gln Asn Lys Gly Lys Leu Tyr Asn Glu Glu Cys Asp
          515                   520                   525


Arg Phe Met Ile Cys Met Val His Lys Leu Gly Tyr Gly Asn Trp Asp
      530                   535                   540


Glu Leu Lys Ala Ala Phe Arg Thr Ser Pro Leu Phe Arg Phe Asp Trp
545                   550                   555                   560


Phe Val Lys Ser Arg Thr Thr Gln Glu Leu Ala Arg Arg Cys Asp Thr
                  565                   570                   575


Leu Ile Arg Leu Ile Glu Lys Glu Asn Gln Glu Phe Asp Glu Arg Glu
              580                   585                   590


Arg Gln Ala Arg Lys Glu Lys Lys Leu Ser Lys Ser Ala Thr Pro Ser
          595                   600                   605


Lys Arg Pro Ser Gly Arg Gln Ala Asn Glu Ser Pro Ser Ser Leu Leu
    610                   615                   620


Lys Lys Arg Lys Gln Leu Ser Met Asp Asp Tyr Gly Lys Arg Arg Lys
625                   630                   635                   640
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<221> CDS <222> (62)..(718) <223> G1266

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60

c atg gat cca ttt tta att cag tcc cca ttc tcc ggc ttc tca ccg gaa
109
  Met Asp Pro Phe Leu Ile Gln Ser Pro Phe Ser Gly Phe Ser Pro Glu
  1               5                   10                  15

tat tct atc gga tct tct cca gat tct ttc tca tcc tct tct tct aac
157
Tyr Ser Ile Gly Ser Ser Pro Asp Ser Phe Ser Ser Ser Ser Ser Asn
              20                  25                  30

aat tac tct ctt ccc ttc aac gag aac gac tca gag gaa atg ttt ctc
205
Asn Tyr Ser Leu Pro Phe Asn Glu Asn Asp Ser Glu Glu Met Phe Leu
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347

```
          35                    40                    45

tac ggt cta atc gag cag tcc acg caa caa acc tat att gac tcg gat
253
Tyr Gly Leu Ile Glu Gln Ser Thr Gln Gln Thr Tyr Ile Asp Ser Asp
    50                    55                    60

agt caa gac ctt ccg atc aaa tcc gta agc tca aga aag tca gag aag
301
Ser Gln Asp Leu Pro Ile Lys Ser Val Ser Ser Arg Lys Ser Glu Lys
65                    70                    75                    80

tct tac aga ggc gta aga cga cgg cca tgg ggg aaa ttc gcg gcg gag
349
Ser Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu
                85                    90                    95

ata aga gat tcg act aga aac ggt att agg gtt tgg ctc ggg acg ttc
397
Ile Arg Asp Ser Thr Arg Asn Gly Ile Arg Val Trp Leu Gly Thr Phe
                100                   105                   110

gaa agc gcg gaa gag gcg gct tta gcc tac gat caa gct gct ttc tcg
445
Glu Ser Ala Glu Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala Phe Ser
            115                   120                   125

atg aga ggg tcc tcg gcg att ctc aat ttt tcg gcg gag aga gtt caa
493
Met Arg Gly Ser Ser Ala Ile Leu Asn Phe Ser Ala Glu Arg Val Gln
    130                   135                   140

gag tcg ctt tcg gag att aaa tat acc tac gag gat ggt tgt tct ccg
541
Glu Ser Leu Ser Glu Ile Lys Tyr Thr Tyr Glu Asp Gly Cys Ser Pro
145                   150                   155                   160

gtt gtg gcg ttg aag agg aaa cac tcg atg aga cgg aga atg acc aat
589
Val Val Ala Leu Lys Arg Lys His Ser Met Arg Arg Arg Met Thr Asn
                165                   170                   175

aag aag acg aaa gat agt gac ttt gat cac cgc tcc gtg aag tta gat
637
Lys Lys Thr Lys Asp Ser Asp Phe Asp His Arg Ser Val Lys Leu Asp
                180                   185                   190

aat gta gtt gtc ttt gag gat ttg gga gaa cag tac ctt gag gag ctt
685
Asn Val Val Val Phe Glu Asp Leu Gly Glu Gln Tyr Leu Glu Glu Leu
            195                   200                   205

ttg ggg tct tct gaa aat agt ggg act tgg tga aagattagga tttgtattag
738
Leu Gly Ser Ser Glu Asn Ser Gly Thr Trp
    210                   215

ggaccttaag tttgaagtgg ttgattaatt ttaaccctaa tatgtttttt gtttgcttaa
798
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348

atatttgatt ctattgagaa acatcgaaaa cagtttgtat gtacttttgt gatacttggc
858

g
859

<210> 192 <211> 218 <212> PRT <213> Arabidopsis thaliana <400>
192

Met Asp Pro Phe Leu Ile Gln Ser Pro Phe Ser Gly Phe Ser Pro Glu
1   5   10   15

Tyr Ser Ile Gly Ser Ser Pro Asp Ser Phe Ser Ser Ser Ser Ser Asn
            20   25   30

Asn Tyr Ser Leu Pro Phe Asn Glu Asn Asp Ser Glu Glu Met Phe Leu
            35   40   45

Tyr Gly Leu Ile Glu Gln Ser Thr Gln Gln Thr Tyr Ile Asp Ser Asp
        50   55   60

Ser Gln Asp Leu Pro Ile Lys Ser Val Ser Ser Arg Lys Ser Glu Lys
65   70   75   80

Ser Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu
            85   90   95

Ile Arg Asp Ser Thr Arg Asn Gly Ile Arg Val Trp Leu Gly Thr Phe
            100   105   110

Glu Ser Ala Glu Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala Phe Ser
        115   120   125

Met Arg Gly Ser Ser Ala Ile Leu Asn Phe Ser Ala Glu Arg Val Gln
        130   135   140

Glu Ser Leu Ser Glu Ile Lys Tyr Thr Tyr Glu Asp Gly Cys Ser Pro
145   150   155   160

Val Val Ala Leu Lys Arg Lys His Ser Met Arg Arg Arg Met Thr Asn
            165   170   175

Lys Lys Thr Lys Asp Ser Asp Phe Asp His Arg Ser Val Lys Leu Asp
            180   185   190

Asn Val Val Val Phe Glu Asp Leu Gly Glu Gln Tyr Leu Glu Glu Leu
        195   200   205

349

Leu Gly Ser Ser Glu Asn Ser Gly Thr Trp
    210   215

<210> 193 <211> 1072 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (152)..(967) <223> G1267

<400> 193
aagtagagaa taataatcac atcaagattg attataaccc tctcactaat caccttctta
60

atcaccaccc tctccggctc tcaacagaac aacaacaaaa aaacagcttc cgttgtcctg
120

ttccggcgaa atcggacggt cgagatcaat c atg cat cgt aga gca gca att
172
                                   Met His Arg Arg Ala Ala Ile
                                   1   5

caa gaa tcg gat gac gaa gaa gat gag act tac aac gac gtc gtt cct
220
Gln Glu Ser Asp Asp Glu Glu Asp Glu Thr Tyr Asn Asp Val Val Pro
        10   15   20

gaa tct cct tct tct tgt gaa gac tca aag atc tca aaa cca act cca
268
Glu Ser Pro Ser Ser Cys Glu Asp Ser Lys Ile Ser Lys Pro Thr Pro
    25   30   35

aag aaa agg agg aac gta gag aag aga gtt gtc tca gtt ccg ata gct
316
Lys Lys Arg Arg Asn Val Glu Lys Arg Val Val Ser Val Pro Ile Ala
40   45   50   55

gac gtg gaa gga tct aag agc aga ggc gaa gta tat cca ccg tcc gat
364
Asp Val Glu Gly Ser Lys Ser Arg Gly Glu Val Tyr Pro Pro Ser Asp
                60   65   70

tca tgg gcc tgg aga aag tac gga caa aaa ccg atc aaa ggc tcg cct
412
Ser Trp Ala Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro
                75   80   85

tat ccc agg gga tat tac aga tgt agt agc tca aaa gga tgt ccg gcg
460
Tyr Pro Arg Gly Tyr Tyr Arg Cys Ser Ser Ser Lys Gly Cys Pro Ala
            90   95   100

agg aag cag gtg gag aga agc cgt gtg gac cct tct aag ctt atg att
508
Arg Lys Gln Val Glu Arg Ser Arg Val Asp Pro Ser Lys Leu Met Ile
    105   110   115

act tac gcc tgc gac cac aat cac cct ttc cct tcc tcc tcc gct aac
556
Thr Tyr Ala Cys Asp His Asn His Pro Phe Pro Ser Ser Ser Ala Asn
120   125   130   135

350

```
acc aaa tcc cac cac cgc tcc tcc gtc gtc ctc aaa acc gca aag aaa
604
Thr Lys Ser His His Arg Ser Ser Val Val Leu Lys Thr Ala Lys Lys
            140              145              150

gag gaa gaa tac gaa gag gag gaa gaa gaa cta acc gtc acc gcc gca
652
Glu Glu Glu Tyr Glu Glu Glu Glu Glu Glu Leu Thr Val Thr Ala Ala
            155              160              165

gag gaa cca ccg gcg gga ctt gat cta agc cac gta gac tca ccg ttg
700
Glu Glu Pro Pro Ala Gly Leu Asp Leu Ser His Val Asp Ser Pro Leu
            170              175              180

cta tta ggc ggc tgc tac agc gaa atc gga gag ttc ggg tgg ttc tac
748
Leu Leu Gly Gly Cys Tyr Ser Glu Ile Gly Glu Phe Gly Trp Phe Tyr
        185              190              195

gac gcg tcg atc tca tca tca tct ggt tct tcg aat ttc ctc gac gta
796
Asp Ala Ser Ile Ser Ser Ser Ser Gly Ser Ser Asn Phe Leu Asp Val
200              205              210              215

act cta gag aga ggt ttt tca gta ggc caa gag gaa gat gag tct ttg
844
Thr Leu Glu Arg Gly Phe Ser Val Gly Gln Glu Glu Asp Glu Ser Leu
            220              225              230

ttc ggt gat ctc ggt gat tta cct gat tgc gcc tcc gtg ttc cgc cgt
892
Phe Gly Asp Leu Gly Asp Leu Pro Asp Cys Ala Ser Val Phe Arg Arg
            235              240              245

ggg act gtt gcg acg gag gag caa cat cga aga tgt gat ttt ggc gcc
940
Gly Thr Val Ala Thr Glu Glu Gln His Arg Arg Cys Asp Phe Gly Ala
            250              255              260

att cct ttc tgt gat agt tct aga tga gtttgtgtgt gtagccaaaa
987
Ile Pro Phe Cys Asp Ser Ser Arg
        265              270

ccaaaagaaa aaaacacaat tttttatttt tccactgtaa aggtgtatca atggtggatt
1047

cattttttta aaaaaaaaaa aaaaa
1072


<210> 194 <211> 271 <212> PRT <213> Arabidopsis thaliana <400>
194

Met His Arg Arg Ala Ala Ile Gln Glu Ser Asp Asp Glu Glu Asp Glu
1           5               10              15


Thr Tyr Asn Asp Val Val Pro Glu Ser Pro Ser Ser Cys Glu Asp Ser
            20              25              30
```

351

```
Lys Ile Ser Lys Pro Thr Pro Lys Lys Arg Arg Asn Val Glu Lys Arg
        35                  40                  45

Val Val Ser Val Pro Ile Ala Asp Val Glu Gly Ser Lys Ser Arg Gly
    50                  55                  60

Glu Val Tyr Pro Pro Ser Asp Ser Trp Ala Trp Arg Lys Tyr Gly Gln
65                  70                  75                  80

Lys Pro Ile Lys Gly Ser Pro Tyr Pro Arg Gly Tyr Tyr Arg Cys Ser
            85                  90                  95

Ser Ser Lys Gly Cys Pro Ala Arg Lys Gln Val Glu Arg Ser Arg Val
            100                 105                 110

Asp Pro Ser Lys Leu Met Ile Thr Tyr Ala Cys Asp His Asn His Pro
        115                 120                 125

Phe Pro Ser Ser Ser Ala Asn Thr Lys Ser His His Arg Ser Ser Val
    130                 135                 140

Val Leu Lys Thr Ala Lys Lys Glu Glu Glu Tyr Glu Glu Glu Glu Glu
145                 150                 155                 160

Glu Leu Thr Val Thr Ala Ala Glu Glu Pro Pro Ala Gly Leu Asp Leu
            165                 170                 175

Ser His Val Asp Ser Pro Leu Leu Leu Gly Gly Cys Tyr Ser Glu Ile
            180                 185                 190

Gly Glu Phe Gly Trp Phe Tyr Asp Ala Ser Ile Ser Ser Ser Ser Gly
        195                 200                 205

Ser Ser Asn Phe Leu Asp Val Thr Leu Glu Arg Gly Phe Ser Val Gly
    210                 215                 220

Gln Glu Glu Asp Glu Ser Leu Phe Gly Asp Leu Gly Asp Leu Pro Asp
225                 230                 235                 240

Cys Ala Ser Val Phe Arg Arg Gly Thr Val Ala Thr Glu Glu Gln His
            245                 250                 255

Arg Arg Cys Asp Phe Gly Ala Ile Pro Phe Cys Asp Ser Ser Arg
        260                 265                 270
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352

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<221> CDS <222> (58)..(579) <223> G1275

<400> 195
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57

atg aat gat gca gac aca aac ttg ggg agt agt ttc agc gat gat act
105
Met Asn Asp Ala Asp Thr Asn Leu Gly Ser Ser Phe Ser Asp Asp Thr
1   5   10   15

cac tct gtg ttc gag ttt ccg gag cta gac ttg tca gat gaa tgg atg
153
His Ser Val Phe Glu Phe Pro Glu Leu Asp Leu Ser Asp Glu Trp Met
            20   25   30

gat gat gat ctt gtg tct gcg gtt tcc ggg atg aat cag tct tat ggt
201
Asp Asp Asp Leu Val Ser Ala Val Ser Gly Met Asn Gln Ser Tyr Gly
        35   40   45

tat cag act agt gat gtt gct ggt gct tta ttc tca ggt tct tct agc
249
Tyr Gln Thr Ser Asp Val Ala Gly Ala Leu Phe Ser Gly Ser Ser Ser
    50   55   60

tgt ttc agt cat cct gaa tct cca agt acc aaa act tat gtt gct gct
297
Cys Phe Ser His Pro Glu Ser Pro Ser Thr Lys Thr Tyr Val Ala Ala
65   70   75   80

aca gcc act gct tct gcc gac aac caa aac aag aaa gaa aag aaa aaa
345
Thr Ala Thr Ala Ser Ala Asp Asn Gln Asn Lys Lys Glu Lys Lys Lys
                85   90   95

att aaa ggg aga gtt gcg ttc aag aca cgg tcc gag gtg gaa gtg ctt
393
Ile Lys Gly Arg Val Ala Phe Lys Thr Arg Ser Glu Val Glu Val Leu
            100   105   110

gac gac ggg ttc aag tgg aga aag tat ggg aag aag atg gtg aag aac
441
Asp Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys Lys Met Val Lys Asn
            115   120   125

agc cca cat cca aga aac tac tac aaa tgt tca gtt gat ggc tgt ccc
489
Ser Pro His Pro Arg Asn Tyr Tyr Lys Cys Ser Val Asp Gly Cys Pro
    130   135   140

gtg aag aaa agg gtt gaa cga gac aga gat gat ccg agc ttt gtg ata
537
Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Pro Ser Phe Val Ile
145   150   155   160

aca act tac gag ggt tcc cac aat cac tca agc atg aac taa
579
Thr Thr Tyr Glu Gly Ser His Asn His Ser Ser Met Asn

```
                  165              .       170

gactcgaact aaggctcaag gcgaccatgc tatattcagc acatcttatt ttctatggtt
639

acgaacgata cttaaaactg cttctagttc tttatatcca ttgtaaactg gttgcaggtt
699

cacaaatttt gagaggttta tgacattcta aatctgtagt acttatata
748
```

<210> 196 <211> 173 <212> PRT <213> Arabidopsis thaliana <400>
196

```
Met Asn Asp Ala Asp Thr Asn Leu Gly Ser Ser Phe Ser Asp Asp Thr
1               5               10              15


His Ser Val Phe Glu Phe Pro Glu Leu Asp Leu Ser Asp Glu Trp Met
            20              25          .       30


Asp Asp Asp Leu Val Ser Ala Val Ser Gly Met Asn Gln Ser Tyr Gly
        35              40              45


Tyr Gln Thr Ser Asp Val Ala Gly Ala Leu Phe Ser Gly Ser Ser Ser
    50              55          '       60


Cys Phe Ser His Pro Glu Ser Pro Ser Thr Lys Thr Tyr Val Ala Ala
65              70              75              80


Thr Ala Thr Ala Ser Ala Asp Asn Gln Asn Lys Lys Glu Lys Lys Lys
            85              90              95


Ile Lys Gly Arg Val Ala Phe Lys Thr Arg Ser Glu Val Glu Val Leu
            100             105             110


Asp Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys Lys Met Val Lys Asn
        115             120.            125


Ser Pro His Pro Arg Asn Tyr Tyr Lys Cys Ser Val Asp Gly Cys Pro
    130             135             140


Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Pro Ser Phe Val Ile
145             150             155             160


Thr Thr Tyr Glu Gly Ser His Asn His Ser Ser Met Asn
            165             170
```

<210> 197 <211> 800 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (41)..(757) <223> G1311

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<400>  197
aagtataata acacaaagaa acagagtaaa agaaagaaaa atg gat ttt aag aag
55
                                                  Met Asp Phe Lys Lys
                                                  1               5

gaa gaa aca ctt cgt aga ggg cca tgg ctc gaa gaa gaa gac gaa cgg
103
Glu Glu Thr Leu Arg Arg Gly Pro Trp Leu Glu Glu Glu Asp Glu Arg
                10              15                  20

cta gtg aag gtc att agt ctt ttg gga gaa cgt cgt tgg gat tct tta
151
Leu Val Lys Val Ile Ser Leu Leu Gly Glu Arg Arg Trp Asp Ser Leu
            25              30                  35

gca ata gtt tcc ggt ttg aag agg agt ggt aag agt tgc agg cta agg
199
Ala Ile Val Ser Gly Leu Lys Arg Ser Gly Lys Ser Cys Arg Leu Arg
            40              45                  50

tgg atg aac tat ctg aat ccg act ctg aag cgt gga ccg atg agt caa
247
Trp Met Asn Tyr Leu Asn Pro Thr Leu Lys Arg Gly Pro Met Ser Gln
        55              60                  65

gaa gaa gag aga atc atc ttt cag ctc cat gct cta tgg ggt aac aag
295
Glu Glu Glu Arg Ile Ile Phe Gln Leu His Ala Leu Trp Gly Asn Lys
70              75                  80                  85

tgg tcg aag att gcg aga aga tta ccc ggt agg act gat aac gag ata
343
Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile
                90              95                  100

aag aac tat tgg aga act cat tat aga aag aaa cag gaa gct caa aac
391
Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys Gln Glu Ala Gln Asn
                105             110                 115

tat gga aag ctc ttt gag tgg aga gga aat aca gga gaa gaa ttg ttg
439
Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr Gly Glu Glu Leu Leu
        120             125                 130

cac aag tat aag gaa aca gag atc act agg aca aag acg acg tct caa
487
His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr Lys Thr Thr Ser Gln
    135                 140                 145

gaa cat ggt ttt gtt gaa gtt gtg agc atg gaa agt ggt aaa gaa gcc
535
Glu His Gly Phe Val Glu Val Val Ser Met Glu Ser Gly Lys Glu Ala
150                 155                 160                 165

aac ggt ggt gtt ggt gga aga gaa agc ttc ggt gtt atg aaa tca ccg
583
Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly Val Met Lys Ser Pro
                170                 175                 180
```

```
tat gaa aat cgg att tcg gat tgg ata tca gag att tct act gac cag
631
Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu Ile Ser Thr Asp Gln
            185                 190                 195

agt gaa gca aat ctt tca gaa gat cac agc agc aat agc tgc agt gag
679
Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser Asn Ser Cys Ser Glu
            200                 205                 210

aac aat att aac att ggt act tgg tgg ttt caa gag act agg gac ttt
727
Asn Asn Ile Asn Ile Gly Thr Trp Trp Phe Gln Glu Thr Arg Asp Phe
            215                 220                 225

gag gag ttt tca tgt tct cta tgg tca taa ttctaaagtt ggtttattta
777
Glu Glu Phe Ser Cys Ser Leu Trp Ser
230                 235

cttttaaaa aaaaaaaaaa aaa
800


<210>  198 <211>  238 <212>  PRT <213>  Arabidopsis thaliana  <400>
198

Met Asp Phe Lys Lys Glu Glu Thr Leu Arg Arg Gly Pro Trp Leu Glu
1               5                   10                  15


Glu Glu Asp Glu Arg Leu Val Lys Val Ile Ser Leu Leu Gly Glu Arg
            20                  25                  30


Arg Trp Asp Ser Leu Ala Ile Val Ser Gly Leu Lys Arg Ser Gly Lys
            35                  40                  45


Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Asn Pro Thr Leu Lys Arg
            50                  55                  60


Gly Pro Met Ser Gln Glu Glu Glu Arg Ile Ile Phe Gln Leu His Ala
65                  70                  75                  80


Leu Trp Gly Asn Lys Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg
                85                  90                  95


Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys
            100                 105                 110


Gln Glu Ala Gln Asn Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr
            115                 120                 125


Gly Glu Glu Leu Leu His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr
```

```
     130                    135                    140


Lys Thr Thr Ser Gln Glu His Gly Phe Val Glu Val Val Ser Met Glu
145                 150                 155                 160


Ser Gly Lys Glu Ala Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly
                165                 170                 175


Val Met Lys Ser Pro Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu
            180                 185                 190


Ile Ser Thr Asp Gln Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser
        195                 200                 205


Asn Ser Cys Ser Glu Asn Asn Ile Asn Ile Gly Thr Trp Trp Phe Gln
    210                 215                 220


Glu Thr Arg Asp Phe Glu Glu Phe Ser Cys Ser Leu Trp Ser
225                 230                 235
```

<210> 199 <211> 1081 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (7)..(849) <223> G1318

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 <400> 199
aaaaat atg agg aag cca gag gta gcc att gca gct agt act cac caa       48
       Met Arg Lys Pro Glu Val Ala Ile Ala Ala Ser Thr His Gln
       1               5                   10


gta aag aag atg aag aag gga ctt tgg tct cct gag gaa gac tca aag       96
Val Lys Lys Met Lys Lys Gly Leu Trp Ser Pro Glu Glu Asp Ser Lys
15                  20                  25                  30


ctg atg caa tac atg tta agc aat gga caa gga tgt tgg agt gat gtt      144
Leu Met Gln Tyr Met Leu Ser Asn Gly Gln Gly Cys Trp Ser Asp Val
                35                  40                  45


gcg aaa aac gca gga ctt caa aga tgt ggc aaa agc tgc cgt ctt cgt      192
Ala Lys Asn Ala Gly Leu Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg
                50                  55                  60


tgg atc aac tat ctt cgt cct gac ctc aag cgt ggc gct ttc tct cct      240
Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Ala Phe Ser Pro
            65                  70                  75


caa gaa gag gat ctc atc att cgc ttt cat tcc atc ctc ggc aac agg      288
Gln Glu Glu Asp Leu Ile Ile Arg Phe His Ser Ile Leu Gly Asn Arg
        80                  85                  90
```

```
tgg tct cag att gca gca cga ttg cct ggt cgg acc gat aac gag atc
336
Trp Ser Gln Ile Ala Ala Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile
95              100             105             110

aag aat ttc tgg aac tca aca ata aag aaa agg cta aag aag atg tcc
384
Lys Asn Phe Trp Asn Ser Thr Ile Lys Lys Arg Leu Lys Lys Met Ser
            115             120             125

gat acc tcc aac tta atc aac aac tca tcc tca tca ccc aac aca gca
432
Asp Thr Ser Asn Leu Ile Asn Asn Ser Ser Ser Ser Pro Asn Thr Ala
            130             135             140

agc gat tcc tct tct aat tcc gca tct tct ttg gat att aaa gac att
480
Ser Asp Ser Ser Ser Asn Ser Ala Ser Ser Leu Asp Ile Lys Asp Ile
            145             150             155

ata gga agc ttc atg tcc tta caa gaa caa ggc ttc gtc aac cct tcc
528
Ile Gly Ser Phe Met Ser Leu Gln Glu Gln Gly Phe Val Asn Pro Ser
    160             165             170

ttg acc cac ata caa acc aac aat cca ttt cca acg gga aac atg atc
576
Leu Thr His Ile Gln Thr Asn Asn Pro Phe Pro Thr Gly Asn Met Ile
175             180             185             190

agc cac ccg tgc aat gac gat ttt acc cct tat gta gat ggt atc tat
624
Ser His Pro Cys Asn Asp Asp Phe Thr Pro Tyr Val Asp Gly Ile Tyr
            195             200             205

gga gta aac gca ggg gta caa ggg gaa ctc tac ttc cca cct ttg gaa
672
Gly Val Asn Ala Gly Val Gln Gly Glu Leu Tyr Phe Pro Pro Leu Glu
            210             215             220

tgt gaa gaa ggt gat tgg tac aat gca aat ata aac aac cac tta gac
720
Cys Glu Glu Gly Asp Trp Tyr Asn Ala Asn Ile Asn Asn His Leu Asp
            225             230             235

gag ttg aac act aat gga tcc gga aac gca cct gag ggt atg aga cca
768
Glu Leu Asn Thr Asn Gly Ser Gly Asn Ala Pro Glu Gly Met Arg Pro
        240             245             250

gtg gaa gaa ttt tgg gac ctt gac cag ttg atg aac act gag gtt cct
816
Val Glu Glu Phe Trp Asp Leu Asp Gln Leu Met Asn Thr Glu Val Pro
255             260             265             270

tcg ttt tac ttc aac ttc aaa caa agc ata tga atatttttac gtcatcttat
869
Ser Phe Tyr Phe Asn Phe Lys Gln Ser Ile
                275             280
```

358

tctttttct attgcggttt atactcaaga ttcttagcca cacacacata aatgcaaata
929

tatatacatt gttagagagt attttgtatt tcgtataatc ttttcgtact agggcttgag
989

ccttgaggtc ccatgtaacg attagtcaat gtaaaacata tatcctataa taaataaata
1049

aaagaaataa taagcacata aaaaaaaaaa aa
1081

<210> 200 <211> 280 <212> PRT <213> Arabidopsis thaliana <400>
200

Met Arg Lys Pro Glu Val Ala Ile Ala Ala Ser Thr His Gln Val Lys
1   5   10   15

Lys Met Lys Lys Gly Leu Trp Ser Pro Glu Glu Asp Ser Lys Leu Met
            20   25   30

Gln Tyr Met Leu Ser Asn Gly Gln Gly Cys Trp Ser Asp Val Ala Lys
        35   40   45

Asn Ala Gly Leu Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile
    50   55   60

Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Ala Phe Ser Pro Gln Glu
65   70   75   80

Glu Asp Leu Ile Ile Arg Phe His Ser Ile Leu Gly Asn Arg Trp Ser
                85   90   95

Gln Ile Ala Ala Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn
            100   105   110

Phe Trp Asn Ser Thr Ile Lys Lys Arg Leu Lys Lys Met Ser Asp Thr
            115   120   125

Ser Asn Leu Ile Asn Asn Ser Ser Ser Ser Pro Asn Thr Ala Ser Asp
    130   135   140

Ser Ser Ser Asn Ser Ala Ser Ser Leu Asp Ile Lys Asp Ile Ile Gly
145   150   155   160

Ser Phe Met Ser Leu Gln Glu Gln Gly Phe Val Asn Pro Ser Leu Thr
                165   170   175

His Ile Gln Thr Asn Asn Pro Phe Pro Thr Gly Asn Met Ile Ser His

                              359

```
              180                   185                   190
```

Pro Cys Asn Asp Asp Phe Thr Pro Tyr Val Asp Gly Ile Tyr Gly Val
        195   200   205

Asn Ala Gly Val Gln Gly Glu Leu Tyr Phe Pro Pro Leu Glu Cys Glu
    210   215   220

Glu Gly Asp Trp Tyr Asn Ala Asn Ile Asn Asn His Leu Asp Glu Leu
225   230   235   240

Asn Thr Asn Gly Ser Gly Asn Ala Pro Glu Gly Met Arg Pro Val Glu
            245   250   255

Glu Phe Trp Asp Leu Asp Gln Leu Met Asn Thr Glu Val Pro Ser Phe
        260   265   270

Tyr Phe Asn Phe Lys Gln Ser Ile   -
    275   280

<210> 201 <211> 1041 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (72)..(803) <223> G1321

 <400> 201
gttcttgtat tggtttggat cggtatactt agttgattac gtaattaaat agatcggcgt
60

gaagaagaaa a atg atc atg tgc agc cga ggc cat tgg aga cca gct gaa
110
            Met Ile Met Cys Ser Arg Gly His Trp Arg Pro Ala Glu
            1   5   10

gac gag aag ctc aag gat ctt gtc gaa caa tac ggt cct cac aat tgg
158
Asp Glu Lys Leu Lys Asp Leu Val Glu Gln Tyr Gly Pro His Asn Trp
    15   20   25

aac gcc att gct ctc aag ctt cct ggt cgc tct ggt aag agt tgt aga
206
Asn Ala Ile Ala Leu Lys Leu Pro Gly Arg Ser Gly Lys Ser Cys Arg
30   35   40   45

ttg aga tgg ttt aat caa ttg gat cca agg atc aac cga aac cct ttc
254
Leu Arg Trp Phe Asn Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe
                50   55   60

acg gaa gaa gaa gaa gaa aga ctt tta gcg gct cat cgg atc cat ggg
302
Thr Glu Glu Glu Glu Glu Arg Leu Leu Ala Ala His Arg Ile His Gly
                65   70   75

aac aga tgg tcc atc atc gca agg ctt ttc cct gga aga act gat aac
350
```

```
Asn Arg Trp Ser Ile Ile Ala Arg Leu Phe Pro Gly Arg Thr Asp Asn
        80                      85              90

gcc gtc aag aac cat tgg cac gtc atc atg gct cgt cgc aca cgc caa
398
Ala Val Lys Asn His Trp His Val Ile Met Ala Arg Arg Thr Arg Gln
    95                  100                 105

acc tct aag cct cgt ctt ctt ccc tcg acg act tcg tct tct tct tta
446
Thr Ser Lys Pro Arg Leu Leu Pro Ser Thr Thr Ser Ser Ser Ser Leu
110             115                 120                     125

atg gcg agt gaa caa atc atg atg agt tct ggt ggt tat aat cat aat
494
Met Ala Ser Glu Gln Ile Met Met Ser Ser Gly Gly Tyr Asn His Asn
                130                 135                 140

tat agt tcc gat gat cgg aag aaa ata ttt cca gca gac ttt ata aat
542
Tyr Ser Ser Asp Asp Arg Lys Lys Ile Phe Pro Ala Asp Phe Ile Asn
            145                 150                 155

ttc cct tac aaa ttc tct cat atc aat cat ctt cac ttc cta aag gag
590
Phe Pro Tyr Lys Phe Ser His Ile Asn His Leu His Phe Leu Lys Glu
        160                 165                 170

ttt ttc ccc gga aag atc gct tta agt cac aaa gca aat cag agt aag
638
Phe Phe Pro Gly Lys Ile Ala Leu Ser His Lys Ala Asn Gln Ser Lys
    175                 180                 185

aag cct atg gag ttc tac aat ttt cta caa gta aac aca gat tca aac
686
Lys Pro Met Glu Phe Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Asn
190             195                 200                     205

aag agc gag att ata gat caa gat tca ggt caa agc aaa cgc agt gac
734
Lys Ser Glu Ile Ile Asp Gln Asp Ser Gly Gln Ser Lys Arg Ser Asp
                210                 215                 220

tcg gac acc aaa cat gaa agt cat gtt cca ttc ttc gac ttt tta tcc
782
Ser Asp Thr Lys His Glu Ser His Val Pro Phe Phe Asp Phe Leu Ser
            225                 230                 235

gtt gga aac tct gcc tcc tag gattagtttt tttgcagtaa ctcctaaatt
833
Val Gly Asn Ser Ala Ser
            240

tctagattaa ctatttagtc cgtatacgta cgagattatc taggtcgtta gcatgtatgc
893

ttgatgtgta taatcactaa ctagtgagct attacctgcg aaaattgtaa gaaaaataca
953

taatgttgat gtatcacaca ttctcaatgt ctgtaaaatt tccatcgagt tgttaactat
1013
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361

caaagttatc cgtttgaaaa aaaaaaaa
1041

<210> 202 <211> 243 <212> PRT <213> Arabidopsis thaliana <400>
202

Met Ile Met Cys Ser Arg Gly His Trp Arg Pro Ala Glu Asp Glu Lys
1   5   10   15

Leu Lys Asp Leu Val Glu Gln Tyr Gly Pro His Asn Trp Asn Ala Ile
        20   25   30

Ala Leu Lys Leu Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp
        35   40   45

Phe Asn Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe Thr Glu Glu
    50   55   60

Glu Glu Glu Arg Leu Leu Ala Ala His Arg Ile His Gly Asn Arg Trp
65   70   75   80

Ser Ile Ile Ala Arg Leu Phe Pro Gly Arg Thr Asp Asn Ala Val Lys
            85   90   95

Asn His Trp His Val Ile Met Ala Arg Arg Thr Arg Gln Thr Ser Lys
        100   105   110

Pro Arg Leu Leu Pro Ser Thr Thr Ser Ser Ser Ser Leu Met Ala Ser
        115   120   125

Glu Gln Ile Met Met Ser Ser Gly Gly Tyr Asn His Asn Tyr Ser Ser
    130   135   140

Asp Asp Arg Lys Lys Ile Phe Pro Ala Asp Phe Ile Asn Phe Pro Tyr
145   150   155   160

Lys Phe Ser His Ile Asn His Leu His Phe Leu Lys Glu Phe Phe Pro
            165   170   175

Gly Lys Ile Ala Leu Ser His Lys Ala Asn Gln Ser Lys Lys Pro Met
        180   185   190

Glu Phe Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Asn Lys Ser Glu
        195   200   205

Ile Ile Asp Gln Asp Ser Gly Gln Ser Lys Arg Ser Asp Ser Asp Thr

362

```
           210                    215                    220
```

```
Lys His Glu Ser His Val Pro Phe Phe Asp Phe Leu Ser Val Gly Asn
225                 230                 235                 240
```

```
Ser Ala Ser
```

<210> 203 <211> 1088 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (49)..(870) <223> G1323

 <400> 203
aagagggaat ctcaaaagtg tgtgtctgtg agagaggaga gagagaat atg ggc aaa
57
                                                         Met Gly Lys
                                                         1

```
gga aga gca cca tgt tgt gac aaa acc aaa gtg aag aga gga cca tgg
105
Gly Arg Ala Pro Cys Cys Asp Lys Thr Lys Val Lys Arg Gly Pro Trp
    5                   10                  15
```

```
agc cat gat gaa gac ttg aaa ctc atc tct ttc att cac aag aat ggt
153
Ser His Asp Glu Asp Leu Lys Leu Ile Ser Phe Ile His Lys Asn Gly
20                  25                  30                  35
```

```
cat gag aat tgg aga tct ctc cca aag caa gct gga ttg ttg agg tgt
201
His Glu Asn Trp Arg Ser Leu Pro Lys Gln Ala Gly Leu Leu Arg Cys
                40                  45                  50
```

```
ggc aag agt tgt cgt ctg cga tgg att aat tac ctc aga cct gat gtg
249
Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Val
            55                  60                  65
```

```
aaa cgt ggc aat ttc agt gca gag gaa gaa gac acc atc atc aaa ctt
297
Lys Arg Gly Asn Phe Ser Ala Glu Glu Glu Asp Thr Ile Ile Lys Leu
        70                  75                  80
```

```
cac cag agc ttt ggt aac aag tgg tcg aag att gct tct aag ctg cct
345
His Gln Ser Phe Gly Asn Lys Trp Ser Lys Ile Ala Ser Lys Leu Pro
        85                  90                  95
```

```
gga aga aca gac aat gag atc aag aat gtg tgg cat aca cat ctc aag
393
Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu Lys
100                 105                 110                 115
```

```
aaa aga ttg agc tcg gaa act aac ctt aat gcc gat gaa gcg ggt tca
441
Lys Arg Leu Ser Ser Glu Thr Asn Leu Asn Ala Asp Glu Ala Gly Ser
                120                 125                 130
```

aaa ggt tct ttg aat gaa gaa gag aac tct caa gag tca tct cca aat
489
Lys Gly Ser Leu Asn Glu Glu Glu Asn Ser Gln Glu Ser Ser Pro Asn
            135   140   145

gct tca atg tct ttt gct ggt tcc aac att tca agc aaa gac gat gat
537
Ala Ser Met Ser Phe Ala Gly Ser Asn Ile Ser Ser Lys Asp Asp Asp
            150   155   160

gca cag ata agt caa atg ttt gag cac att cta act tat agc gag ttt
585
Ala Gln Ile Ser Gln Met Phe Glu His Ile Leu Thr Tyr Ser Glu Phe
    165   170   175

acg ggg atg tta caa gag gta gac aaa cca gag ctg ctg gag atg cct
633
Thr Gly Met Leu Gln Glu Val Asp Lys Pro Glu Leu Leu Glu Met Pro
180   185   190   195

ttt gat tta gat cct gac att tgg agt ttc ata gat ggt tca gac tca
681
Phe Asp Leu Asp Pro Asp Ile Trp Ser Phe Ile Asp Gly Ser Asp Ser
                200   205   210

ttc caa caa cca gag aac aga gct ctt caa gag tct gaa gaa gat gaa
729
Phe Gln Gln Pro Glu Asn Arg Ala Leu Gln Glu Ser Glu Glu Asp Glu
            215   220   225

gtt gat aaa tgg ttt aag cac ctg gaa agc gaa ctc ggg tta gaa gaa
777
Val Asp Lys Trp Phe Lys His Leu Glu Ser Glu Leu Gly Leu Glu Glu
            230   235   240

aac gat aac caa caa caa caa cag cat aaa cag gga aca gaa gat gaa
825
Asn Asp Asn Gln Gln Gln Gln Gln His Lys Gln Gly Thr Glu Asp Glu
            245   250   255

cat tca tca tca ctc ttg gag agt tac gag ctc ctc ata cat taa
870
His Ser Ser Ser Leu Leu Glu Ser Tyr Glu Leu Leu Ile His
260   265   270

tgaagccata aagcaagtca ttttcacctt gaaaatggaa ttattagcta acttattggc
930

attattagta tataagcaag atcagatagg cgcatgtagt agcaacaacg aagaaacgtc
990

gaattgtaga caaaatgtag atattacaga gttgaaagat tgtattttgc aaatgattgc
1050

tttgtagtga aatcaagtta tcacaaaaaa aaaaaaaa
1088

<210> 204 <211> 273 <212> PRT <213> Arabidopsis thaliana <400>
204

364

```
Met Gly Lys Gly Arg Ala Pro Cys Cys Asp Lys Thr Lys Val Lys Arg
1               5                   10                  15


Gly Pro Trp Ser His Asp Glu Asp Leu Lys Leu Ile Ser Phe Ile His
            20                  25                  30


Lys Asn Gly His Glu Asn Trp Arg Ser Leu Pro Lys Gln Ala Gly Leu
        35                  40                  45


Leu Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg
    50                  55              .       60


Pro Asp Val Lys Arg Gly Asn Phe Ser Ala Glu Glu Glu Asp Thr Ile
65                  70                  75                  80


Ile Lys Leu His Gln Ser Phe Gly Asn Lys Trp Ser Lys Ile Ala Ser
            85                  90                  95


Lys Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr
            100                 105                 110


His Leu Lys Lys Arg Leu Ser Ser Glu Thr Asn Leu Asn Ala Asp Glu
        115                 120                 125


Ala Gly Ser Lys Gly Ser Leu Asn Glu Glu Glu Asn Ser Gln Glu Ser
    130                 135                 140


Ser Pro Asn Ala Ser Met Ser Phe Ala Gly Ser Asn Ile Ser Ser Lys
145                 150                 155                 160


Asp Asp Asp Ala Gln Ile Ser Gln Met Phe Glu His Ile Leu Thr Tyr
                165                 170                 175


Ser Glu Phe Thr Gly Met Leu Gln Glu Val Asp Lys Pro Glu Leu Leu
            180                 185                 190


Glu Met Pro Phe Asp Leu Asp Pro Asp Ile Trp Ser Phe Ile Asp Gly
        195                 200                 205


Ser Asp Ser Phe Gln Gln Pro Glu Asn Arg Ala Leu Gln Glu Ser Glu
    210                 215                 220


Glu Asp Glu Val Asp Lys Trp Phe Lys His Leu Glu Ser Glu Leu Gly
225                 230                 235                 240


Leu Glu Glu Asn Asp Asn Gln Gln Gln Gln Gln His Lys Gln Gly Thr
```

365

```
              245              250              255
                                ·

Glu Asp Glu His Ser Ser Ser Leu Leu Glu Ser Tyr Glu Leu Leu Ile
        260           ·   265           270


His


<210> 205 <211> 880 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (32)..(784) <223> G1326

 <400> 205
cgacggtacg gtggagatag agatagcatc c atg gag atg tct aga gga agc
                                                                52
                                 Met Glu Met Ser Arg Gly Ser
                                  1               5

aac agt ttt gac aat aag aag cct agt tgc caa aga ggt cac tgg aga
100
Asn Ser Phe Asp Asn Lys Lys Pro Ser Cys Gln Arg Gly His Trp Arg
        10              15      --        20

cct gtt gaa gat gac aat ctc cgg caa ctc gtt gaa caa tac ggt ccc
148
Pro Val Glu Asp Asp Asn Leu Arg Gln Leu Val Glu Gln Tyr Gly Pro
    25              30              35

aag aac tgg aat ttt att gct caa cat ctc tat gga aga tca ggg aaa
196
Lys Asn Trp Asn Phe Ile Ala Gln His Leu Tyr Gly Arg Ser Gly Lys
40              45              50              55

agc tgt aga tta aga tgg tac aac caa ctt gat cca aac atc acc aag
244
Ser Cys Arg Leu Arg Trp Tyr Asn Gln Leu Asp Pro Asn Ile Thr Lys
            60              65              70

aaa ccc ttc acc gag gag gaa gaa gag aga ctg ctt aaa gct cat cgg
292
Lys Pro Phe Thr Glu Glu Glu Glu Glu Arg Leu Leu Lys Ala His Arg
            75              80              85

atc caa ggg aat cgt tgg gcc tcc ata gcc cga ctg ttc ccc ggg agg
340
Ile Gln Gly Asn Arg Trp Ala Ser Ile Ala Arg Leu Phe Pro Gly Arg
            90              95              100

acc gac aac gct gtc aaa aac cat ttt cat gtc atc atg gct aga cgc
388
Thr Asp Asn Ala Val Lys Asn His Phe His Val Ile Met Ala Arg Arg
        105             110            · 115

aaa cgg gaa aac ttc tct tcc aca gct act tct acg ttc aac caa act
436
Lys Arg Glu Asn Phe Ser Ser Thr Ala Thr Ser Thr Phe Asn Gln Thr
120             125             130             135
```

```
tgg cat act gtt ttg agc cct agt tct agt ctt aca agg cta aat aga
484
Trp His Thr Val Leu Ser Pro Ser Ser Ser Leu Thr Arg Leu Asn Arg
            140               145               150

tcc cat ttc ggg cta tgg agg tat cga aag gat aag agt tgc ggt ctc
532
Ser His Phe Gly Leu Trp Arg Tyr Arg Lys Asp Lys Ser Cys Gly Leu
            155               160               165

tgg cct tac tct ttt gtt tca cca cct acg aat ggt caa ttt gga tct
580
Trp Pro Tyr Ser Phe Val Ser Pro Pro Thr Asn Gly Gln Phe Gly Ser
            170               175               180

tca tct gtc tct aac gta cac cac gaa att tat ctt gag agg aga aag
628
Ser Ser Val Ser Asn Val His His Glu Ile Tyr Leu Glu Arg Arg Lys
        185               190               195

tcg aaa gag ttg gtg gat cct cag aat tac aca ttt cat gca gcc aca
676
Ser Lys Glu Leu Val Asp Pro Gln Asn Tyr Thr Phe His Ala Ala Thr
200               205               210               215

cca gat cat aag atg act tca aat gaa gat gga cca tcc atg gga gat
724
Pro Asp His Lys Met Thr Ser Asn Glu Asp Gly Pro Ser Met Gly Asp
            220               225               230

gat ggt gag aag aac gat gtt act ttc att gat ttt ctt ggt gtt gga
772
Asp Gly Glu Lys Asn Asp Val Thr Phe Ile Asp Phe Leu Gly Val Gly
            235               240               245

tta gct tct tag gttataacat cacaagtcaa agcttttaag ggtttctatc
824
Leu Ala Ser
        250

attagggtta ggcatcattt tcagcctttt gcttccttaa actctcatat ggatct
880


<210>  206 <211>  250 <212>  PRT <213>  Arabidopsis thaliana  <400>
206

Met Glu Met Ser Arg Gly Ser Asn Ser Phe Asp Asn Lys Lys Pro Ser
1               5               10               15


Cys Gln Arg Gly His Trp Arg Pro Val Glu Asp Asp Asn Leu Arg Gln
            20               25               30


Leu Val Glu Gln Tyr Gly Pro Lys Asn Trp Asn Phe Ile Ala Gln His
        35               40               45


Leu Tyr Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Tyr Asn Gln
        50               55               60
```

367

Leu Asp Pro Asn Ile Thr Lys Lys Pro Phe Thr Glu Glu Glu Glu Glu
65   70   75   80

Arg Leu Leu Lys Ala His Arg Ile Gln Gly Asn Arg Trp Ala Ser Ile
            85   90   95

Ala Arg Leu Phe Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His Phe
            100   105   110

His Val Ile Met Ala Arg Arg Lys Arg Glu Asn Phe Ser Ser Thr Ala
        115   120   125

Thr Ser Thr Phe Asn Gln Thr Trp His Thr Val Leu Ser Pro Ser Ser
    130   135   140

Ser Leu Thr Arg Leu Asn Arg Ser His Phe Gly Leu Trp Arg Tyr Arg
145   150   155   160

Lys Asp Lys Ser Cys Gly Leu Trp Pro Tyr Ser Phe Val Ser Pro Pro
            165   170   175

Thr Asn Gly Gln Phe Gly Ser Ser Ser Val Ser Asn Val His His Glu
            180   185   190

Ile Tyr Leu Glu Arg Arg Lys Ser Lys Glu Leu Val Asp Pro Gln Asn
        195   200   205

Tyr Thr Phe His Ala Ala Thr Pro Asp His Lys Met Thr Ser Asn Glu
    210   215   220

Asp Gly Pro Ser Met Gly Asp Asp Gly Glu Lys Asn Asp Val Thr Phe
225   230   235   240

Ile Asp Phe Leu Gly Val Gly Leu Ala Ser
            245   250

<210> 207 <211> 981 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (36)..(959) <223> G1330

 <400> 207
gtaccggcga cctctttgtg ggtcactctt catca atg ggt gac aaa gga agg
53
                                       Met Gly Asp Lys Gly Arg
                                       1   5

agc tta aag atc aac aag aac atg gag gaa ttc acg aaa gtg gaa gaa
101

368

```
Ser Leu Lys Ile Asn Lys Asn Met Glu Glu Phe Thr Lys Val Glu Glu
            10              15              20

gaa atg gac gta agg aga ggt cca tgg aca gtt gag gaa gat tta gag
149
Glu Met Asp Val Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Glu
            25              30              35

ctc atc aat tac att gct agt cat ggt gaa ggt cga tgg aac tct ctc
197
Leu Ile Asn Tyr Ile Ala Ser His Gly Glu Gly Arg Trp Asn Ser Leu
        40              45              50

gct cgt tgc gcc gaa ctc aaa agg acc gga aaa agc tgc aga ctt cgg
245
Ala Arg Cys Ala Glu Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg
55              60              65              70

tgg ctg aac tat ctc cga cca gat gtg cgc cgt gga aac ata acc ctc
293
Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu
            75              80              85

gaa gaa caa ctc ttg att ctt gaa ctt cac aca cgt tgg ggc aat aga
341
Glu Glu Gln Leu Leu Ile Leu Glu Leu His Thr Arg Trp Gly Asn Arg
            90              95              100

tgg tct aag att gca caa tat tta cca gga aga acg gat aac gag atc
389
Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile
        105             110             115

aaa aac tat tgg aga aca cgt gtt caa aag cat gca aaa cag ctt aaa
437
Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Lys
        120             125             130

tgc gac gtg aac agt caa caa ttt aaa gac acc atg aag tat ctt tgg
485
Cys Asp Val Asn Ser Gln Gln Phe Lys Asp Thr Met Lys Tyr Leu Trp
135             140             145             150

atg cct cgg ctc gta gaa agg atc caa gcc gcg tcc atc ggg tct gtt
533
Met Pro Arg Leu Val Glu Arg Ile Gln Ala Ala Ser Ile Gly Ser Val
            155             160             165

tcc atg tca tct tgc gtc acc acc tcc tca gat cag ttc gtg atc aac
581
Ser Met Ser Ser Cys Val Thr Thr Ser Ser Asp Gln Phe Val Ile Asn
            170             175             180

aac aac aac acc aac aac gtg gat aat ttg gct tta atg agt aac cct
629
Asn Asn Asn Thr Asn Asn Val Asp Asn Leu Ala Leu Met Ser Asn Pro
            185             190             195

aat ggt tac atc acg ccg gat aat tcc agc gtg gca gta tct cct gta
677
Asn Gly Tyr Ile Thr Pro Asp Asn Ser Ser Val Ala Val Ser Pro Val
```

369

        200   205   210

```
tca gat ttg acg gag tgt caa gtg agt agt gaa gtg tgg aag att ggt
725
Ser Asp Leu Thr Glu Cys Gln Val Ser Ser Glu Val Trp Lys Ile Gly
215             220             225                 230


cag gat gag aat ttg gtg gat cca aaa atg aca tcg ccg aat tat atg
773
Gln Asp Glu Asn Leu Val Asp Pro Lys Met Thr Ser Pro Asn Tyr Met
            235             240             245


gat aat agc agt gga cta tta aac gga gat ttt acg aag atg caa gat
821
Asp Asn Ser Ser Gly Leu Leu Asn Gly Asp Phe Thr Lys Met Gln Asp
            250             255             260


caa agt gac ctt aat tgg ttt gaa aat att aat ggg atg gta cca aat
869
Gln Ser Asp Leu Asn Trp Phe Glu Asn Ile Asn Gly Met Val Pro Asn
        265             270             275


tat tcg gac agt ttt tgg aac att gga aat gat gaa gac ttc tgg ctc
917
Tyr Ser Asp Ser Phe Trp Asn Ile Gly Asn Asp Glu Asp Phe Trp Leu
    280             285             290


tta caa caa cat caa caa gtc cac gac aat gga agc ttc tga
959
Leu Gln Gln His Gln Gln Val His Asp Asn Gly Ser Phe
295             300             305


atagacaaga agctatgcgg cc
981
```

<210> 208 <211> 307 <212> PRT <213> Arabidopsis thaliana <400>
208

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Met Gly Asp Lys Gly Arg Ser Leu Lys Ile Asn Lys Asn Met Glu Glu
1           5               10              15


Phe Thr Lys Val Glu Glu Glu Met Asp Val Arg Arg Gly Pro Trp Thr
            20              25              30


Val Glu Glu Asp Leu Glu Leu Ile Asn Tyr Ile Ala Ser His Gly Glu
            35              40              45


Gly Arg Trp Asn Ser Leu Ala Arg Cys Ala Glu Leu Lys Arg Thr Gly
    50              55              60


Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg
65              70              75              80


Arg Gly Asn Ile Thr Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His
            85              90              95
```

370

Thr Arg Trp Gly Asn Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly
          100   105   110

Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys
          115   120   125

His Ala Lys Gln Leu Lys Cys Asp Val Asn Ser Gln Gln Phe Lys Asp
    130   135   140

Thr Met Lys Tyr Leu Trp Met Pro Arg Leu Val Glu Arg Ile Gln Ala
145   150   155   160

Ala Ser Ile Gly Ser Val Ser Met Ser Ser Cys Val Thr Thr Ser Ser
              165   170   175

Asp Gln Phe Val Ile Asn Asn Asn Asn Thr Asn Asn Val Asp Asn Leu
          180   185   190

Ala Leu Met Ser Asn Pro Asn Gly Tyr Ile Thr Pro Asp Asn Ser Ser
          195   200   205

Val Ala Val Ser Pro Val Ser Asp Leu Thr Glu Cys Gln Val Ser Ser
    210   215   220

Glu Val Trp Lys Ile Gly Gln Asp Glu Asn Leu Val Asp Pro Lys Met
225   230   235   240

Thr Ser Pro Asn Tyr Met Asp Asn Ser Ser Gly Leu Leu Asn Gly Asp
              245   250   255

Phe Thr Lys Met Gln Asp Gln Ser Asp Leu Asn Trp Phe Glu Asn Ile
          260   265   270

Asn Gly Met Val Pro Asn Tyr Ser Asp Ser Phe Trp Asn Ile Gly Asn
          275   280   285

Asp Glu Asp Phe Trp Leu Leu Gln Gln His Gln Gln Val His Asp Asn
    290   295   300

Gly Ser Phe
305

<210> 209 <211> 1964 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (128)..(1567) <223> G1367

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<400> 209
tccttccaca aaacttttt aattttatct gaaaaattaa aacaaccgaa acaaaaaaaa
60

aaaactaaaa atcaaaaatc tcatcacctt ccttgctctg tattttttct ctctcactaa
120

atcctcc atg gat cct tct ctc tct gca acc aat gat cct cat cat cct
169
        Met Asp Pro Ser Leu Ser Ala Thr Asn Asp Pro His His Pro
        1               5                   10

cct cct cct cag ttc aca tct ttc cct cct ttc acc aac acc aac ccc
217
Pro Pro Pro Gln Phe Thr Ser Phe Pro Pro Phe Thr Asn Thr Asn Pro
15                  20                  25                  30

ttc gcc tct cca aac cac ccc ttc ttc acc gga ccc acc gcc gtc gcg
265
Phe Ala Ser Pro Asn His Pro Phe Phe Thr Gly Pro Thr Ala Val Ala
                35                  40                  45

ccg cca aac aac atc cat ctc tat caa gca gct cct ccg cag cag cca
313
Pro Pro Asn Asn Ile His Leu Tyr Gln Ala Ala Pro Pro Gln Gln Pro
                50                  55                  60

caa aca tct cca gtt cct cct cat cca tct att tcc cac cct cct tac
361
Gln Thr Ser Pro Val Pro Pro His Pro Ser Ile Ser His Pro Pro Tyr
            65                  70                  75

tct gac atg att tgc acg gcg att gca gcg tta aac gaa cca gat ggg
409
Ser Asp Met Ile Cys Thr Ala Ile Ala Ala Leu Asn Glu Pro Asp Gly
        80                  85                  90

tca agc aag caa gct att tcg agg tac ata gag aga att tac act ggg
457
Ser Ser Lys Gln Ala Ile Ser Arg Tyr Ile Glu Arg Ile Tyr Thr Gly
95                  100                 105                 110

att cct act gct cat gga gct ttg ttg aca cac cat ctc aag act ttg
505
Ile Pro Thr Ala His Gly Ala Leu Leu Thr His His Leu Lys Thr Leu
                115                 120                 125

aag acc agt ggg att ctt gtc atg gtt aag aaa tct tac aag ctt gct
553
Lys Thr Ser Gly Ile Leu Val Met Val Lys Lys Ser Tyr Lys Leu Ala
                130                 135                 140

tct act cct cct cct cct cct cct act agt gta gct cct agt ctt gaa
601
Ser Thr Pro Pro Pro Pro Pro Pro Thr Ser Val Ala Pro Ser Leu Glu
                145                 150                 155

cct ccc aga tct gat ttc ata gtc aac gag aac caa cct tta cct gat
649
Pro Pro Arg Ser Asp Phe Ile Val Asn Glu Asn Gln Pro Leu Pro Asp
        160                 165                 170
```

```
ccg gtt ttg gct tct tct act cct cag act att aaa cgt ggt cgt ggt
697
Pro Val Leu Ala Ser Ser Thr Pro Gln Thr Ile Lys Arg Gly Arg Gly
175                 180             185                 190

cga cct cca aaa gct aaa cca gat gtt gtt caa cct caa cct ctg act
745
Arg Pro Pro Lys Ala Lys Pro Asp Val Val Gln Pro Gln Pro Leu Thr
                195             200             205

aat gga aaa ctc acc tgg gaa cag agt gaa tta cct gtc tct cga cca
793
Asn Gly Lys Leu Thr Trp Glu Gln Ser Glu Leu Pro Val Ser Arg Pro
            210             215             220

gag gag ata cag ata cag ccg cca cag tta ccg tta cag cca cag cag
841
Glu Glu Ile Gln Ile Gln Pro Pro Gln Leu Pro Leu Gln Pro Gln Gln
        225             230             235

ccg gtt aag aga ccg ccg ggt cgt cct aga aaa gat gga act tcg ccg
889
Pro Val Lys Arg Pro Pro Gly Arg Pro Arg Lys Asp Gly Thr Ser Pro
    240             245             250

acg gtg aag cca gct gct tct gtt tcc ggt ggt gtg gag act gtg aaa
937
Thr Val Lys Pro Ala Ala Ser Val Ser Gly Gly Val Glu Thr Val Lys
255             260             265             270

cga aga ggt aga cct ccg agt gga aga gct gct ggg agg gag aga aag
985
Arg Arg Gly Arg Pro Pro Ser Gly Arg Ala Ala Gly Arg Glu Arg Lys
            275             280             285

cct ata gta gtc tca gct cca gct tca gtg ttc ccg tat gtt gct aat
1033
Pro Ile Val Val Ser Ala Pro Ala Ser Val Phe Pro Tyr Val Ala Asn
            290             295             300

ggt ggt gtt aga cgc cga ggg aga cca aag aga gtt gac gct ggt ggt
1081
Gly Gly Val Arg Arg Arg Gly Arg Pro Lys Arg Val Asp Ala Gly Gly
        305             310             315

gct tcc tct gtt gct cca cca cca cca cca cca act aac gta gag agt
1129
Ala Ser Ser Val Ala Pro Pro Pro Pro Pro Pro Thr Asn Val Glu Ser
    320             325             330

gga gga gag gag gtt gca gtc aag aaa cga gga aga gga cgg cct cct
1177
Gly Gly Glu Glu Val Ala Val Lys Lys Arg Gly Arg Gly Arg Pro Pro
335             340             345             350

aag att gga ggt gtt atc agg aag cct atg aag ccg atg aga agc ttt
1225
Lys Ile Gly Gly Val Ile Arg Lys Pro Met Lys Pro Met Arg Ser Phe
            355             360             365
```

gct cgt act gga aaa ccc gta gga aga ccc aga aag aat gcg gtg tca
1273
Ala Arg Thr Gly Lys Pro Val Gly Arg Pro Arg Lys Asn Ala Val Ser
          370   375   380

gtg gga gct tct gga cga caa gat ggt gac tat gga gaa ctg aag aag
1321
Val Gly Ala Ser Gly Arg Gln Asp Gly Asp Tyr Gly Glu Leu Lys Lys
          385   390   395

aag ttt gag ttg ttt caa gcg aga gct aag gat att gta att gtg ttg
1369
Lys Phe Glu Leu Phe Gln Ala Arg Ala Lys Asp Ile Val Ile Val Leu
      400   405   410

aaa tcc gag ata gga gga agt gga aat caa gca gtg gtt caa gcc ata
1417
Lys Ser Glu Ile Gly Gly Ser Gly Asn Gln Ala Val Val Gln Ala Ile
415   420   425   430

cag gac ctg gaa ggg ata gca gag aca aca aac gag cca aag cac atg
1465
Gln Asp Leu Glu Gly Ile Ala Glu Thr Thr Asn Glu Pro Lys His Met
          435   440   445

gaa gaa gtg cag ctg cca gac gag gaa cac ctt gaa acc gaa cca gaa
1513
Glu Glu Val Gln Leu Pro Asp Glu Glu His Leu Glu Thr Glu Pro Glu
          450   455   460

gca gag ggt caa gga cag aca gaa gca gag gca atg caa gaa gct ctg
1561
Ala Glu Gly Gln Gly Gln Thr Glu Ala Glu Ala Met Gln Glu Ala Leu
          465   470   475

ttc taa agataaagcc ttgacataaa aagctagcaa gtggtgggtt tacttgttgt
1617
Phe

gtgttacatg aaatttttaa tcttataagg gtgtttgcag gagaaaaaca aaaagaacaa
1677

tgtgatgaac tgatgatgat gattgtgtct ctaaccaaac aacaaggaga ggtagggtaa
1737

tgtctgtaaa gtgaattagg atgttaccat tgttcatgct tcccatctct ctccatcgtc
1797

catatctgtg taggcagctt tgttctttgt tccctcgtgt tttttttaga ctgttgtgtc
1857

tcttattcta ttttgtctcc ttaggctttt taggagttgt tgttgatgtt tatcaaaaac
1917

gcttatgtaa tttttatgac cacttctact ttttatgatg gtttctt
1964

<210> 210 <211> 479 <212> PRT <213> Arabidopsis thaliana <400>
210

374

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Met Asp Pro Ser Leu Ser Ala Thr Asn Asp Pro His His Pro Pro Pro
1               5                   10                  15

Pro Gln Phe Thr Ser Phe Pro Pro Phe Thr Asn Thr Asn Pro Phe Ala
            20              25                  30

Ser Pro Asn His Pro Phe Phe Thr Gly Pro Thr Ala Val Ala Pro Pro
        35                  40                  45

Asn Asn Ile His Leu Tyr Gln Ala Ala Pro Pro Gln Gln Pro Gln Thr
    50                  55                  60

Ser Pro Val Pro Pro His Pro Ser Ile Ser His Pro Pro Tyr Ser Asp
65              70                  75                  80

Met Ile Cys Thr Ala Ile Ala Ala Leu Asn Glu Pro Asp Gly Ser Ser
            85                  90                  95

Lys Gln Ala Ile Ser Arg Tyr Ile Glu Arg Ile Tyr Thr Gly Ile Pro
            100             105                 110

Thr Ala His Gly Ala Leu Leu Thr His His Leu Lys Thr Leu Lys Thr
        115                 120                 125

Ser Gly Ile Leu Val Met Val Lys Lys Ser Tyr Lys Leu Ala Ser Thr
    130             135                 140

Pro Pro Pro Pro Pro Pro Thr Ser Val Ala Pro Ser Leu Glu Pro Pro
145             150                 155                 160

Arg Ser Asp Phe Ile Val Asn Glu Asn Gln Pro Leu Pro Asp Pro Val
            165                 170                 175

Leu Ala Ser Ser Thr Pro Gln Thr Ile Lys Arg Gly Arg Gly Arg Pro
            180                 185                 190

Pro Lys Ala Lys Pro Asp Val Val Gln Pro Gln Pro Leu Thr Asn Gly
        195                 200                 205

Lys Leu Thr Trp Glu Gln Ser Glu Leu Pro Val Ser Arg Pro Glu Glu
    210                 215                 220

Ile Gln Ile Gln Pro Pro Gln Leu Pro Leu Gln Pro Gln Gln Pro Val
225                 230                 235                 240
```

375

Lys Arg Pro Pro Gly Arg Pro Arg Lys Asp Gly Thr Ser Pro Thr Val
            245   250   255

Lys Pro Ala Ala Ser Val Ser Gly Gly Val Glu Thr Val Lys Arg Arg
            260   265   270

Gly Arg Pro Pro Ser Gly Arg Ala Ala Gly Arg Glu Arg Lys Pro Ile
        275   280   285

Val Val Ser Ala Pro Ala Ser Val Phe Pro Tyr Val Ala Asn Gly Gly
    290   295   300

Val Arg Arg Arg Gly Arg Pro Lys Arg Val Asp Ala Gly Gly Ala Ser
305   310   315   320

Ser Val Ala Pro Pro Pro Pro Pro Thr Asn Val Glu Ser Gly Gly
            325   330   335

Glu Glu Val Ala Val Lys Lys Arg Gly Arg Gly Arg Pro Pro Lys Ile
            340   345   350

Gly Gly Val Ile Arg Lys Pro Met Lys Pro Met Arg Ser Phe Ala Arg
        355   360   365

Thr Gly Lys Pro Val Gly Arg Pro Arg Lys Asn Ala Val Ser Val Gly
    370   375   380

Ala Ser Gly Arg Gln Asp Gly Asp Tyr Gly Glu Leu Lys Lys Lys Phe
385   390   395   400

Glu Leu Phe Gln Ala Arg Ala Lys Asp Ile Val Ile Val Leu Lys Ser
            405   410   415

Glu Ile Gly Gly Ser Gly Asn Gln Ala Val Val Gln Ala Ile Gln Asp
        420   425   430

Leu Glu Gly Ile Ala Glu Thr Thr Asn Glu Pro Lys His Met Glu Glu
        435   440   445

Val Gln Leu Pro Asp Glu Glu His Leu Glu Thr Glu Pro Glu Ala Glu
    450   455   460

Gly Gln Gly Gln Thr Glu Ala Glu Ala Met Gln Glu Ala Leu Phe
465   470   475

<210> 211 <211> 1674 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (261)..(1475) <223> G1399

<400> 211
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60

ctttagctta gcttagcttc tactgatctg tttttgctac aaaatcccat ctttttcttt
120

aaaactcttt atctctgaat cttgagtttc ttgtagaaga agaagcaatt ttgaatcttt
180

cgtaatcata aagattcgtg gaggatctct actgatttgt cggaatctct cactacagaa
240

tcacttgatc ttatgtccgg atg gag gag aga gaa gga acc aac atc aac aac
293
            Met Glu Glu Arg Glu Gly Thr Asn Ile Asn Asn
            1   5   10

aac atc act agc agt ttc ggc ttg aag cag caa cat gaa gct gct gct
341
Asn Ile Thr Ser Ser Phe Gly Leu Lys Gln Gln His Glu Ala Ala Ala
        15   20   25

tct gat ggt ggt tac tca atg gac cca cca cca aga ccc gaa aac cct
389
Ser Asp Gly Gly Tyr Ser Met Asp Pro Pro Pro Arg Pro Glu Asn Pro
        30   35   40

aac ccg ttt tta gtc cca ccc act act gtc ccc gcg gcc gcc acc gta
437
Asn Pro Phe Leu Val Pro Pro Thr Thr Val Pro Ala Ala Ala Thr Val
    45   50   55

gca gca gct gtt act gag aat gcg gct act ccg ttt agc tta aca atg
485
Ala Ala Ala Val Thr Glu Asn Ala Ala Thr Pro Phe Ser Leu Thr Met
60   65   70   75

ccg acg gag aac act tca gct gag cag ctg aaa aag aag aga ggt agg
533
Pro Thr Glu Asn Thr Ser Ala Glu Gln Leu Lys Lys Lys Arg Gly Arg
                80   85   90

ccg aga aag tat aat ccc gat ggg act ctt gtc gtg act tta tcg ccg
581
Pro Arg Lys Tyr Asn Pro Asp Gly Thr Leu Val Val Thr Leu Ser Pro
            95   100   105

atg cca atc tcg tcc tct gtt ccg ttg acg tcg gag ttt cct cca agg
629
Met Pro Ile Ser Ser Ser Val Pro Leu Thr Ser Glu Phe Pro Pro Arg
            110   115   120

aaa cga gga aga gga cgt ggc aag tct aat cga tgg ctc aag aag tct
677
Lys Arg Gly Arg Gly Arg Gly Lys Ser Asn Arg Trp Leu Lys Lys Ser
    125   130   135

caa atg ttc caa ttc gat aga agt cct gtt gat acc aat ttg gca ggt
725
Gln Met Phe Gln Phe Asp Arg Ser Pro Val Asp Thr Asn Leu Ala Gly
140   145   150   155

gta gga act gct gat ttt gtt ggt gcc aac ttt aca cct cat gta ctg
773
Val Gly Thr Ala Asp Phe Val Gly Ala Asn Phe Thr Pro His Val Leu
                 160   165   170

atc gtc aac gcc gga gag gat gtg acg atg aag ata atg aca ttc tct
821
Ile Val Asn Ala Gly Glu Asp Val Thr Met Lys Ile Met Thr Phe Ser
                 175   180   185

caa caa gga tct cgt gct atc tgc atc ctt tca gct aat ggt ccc atc
869
Gln Gln Gly Ser Arg Ala Ile Cys Ile Leu Ser Ala Asn Gly Pro Ile
             190   195   200

tcc aat gtt acg ctt cgt caa tct atg aca tcc ggt ggt act cta act
917
Ser Asn Val Thr Leu Arg Gln Ser Met Thr Ser Gly Gly Thr Leu Thr
         205   210   —   215

tat gag ggt cgt ttt gag att ctc tct ttg acg ggt tcg ttt atg caa
965
Tyr Glu Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Ser Phe Met Gln
220   225   230   235

aat gac tct gga gga act cga agt aga gct ggt ggt atg agt gtt tgc
1013
Asn Asp Ser Gly Gly Thr Arg Ser Arg Ala Gly Gly Met Ser Val Cys
             240   245   250

ctt gca gga cca gat ggt cgt gtc ttt ggt gga gga ctc gct ggt ctc
1061
Leu Ala Gly Pro Asp Gly Arg Val Phe Gly Gly Gly Leu Ala Gly Leu
             255   260   265

ttt ctt gct gct ggt cct gtc cag gta atg gta ggg act ttt ata gct
1109
Phe Leu Ala Ala Gly Pro Val Gln Val Met Val Gly Thr Phe Ile Ala
             270   275   280

ggt caa gag cag tca cag ctg gag cta gca aaa gaa aga cgg cta aga
1157
Gly Gln Glu Gln Ser Gln Leu Glu Leu Ala Lys Glu Arg Arg Leu Arg
         285   290   295

ttt ggg gct caa cca tct tct atc tcc ttt aac ata tcc gca gaa gaa
1205
Phe Gly Ala Gln Pro Ser Ser Ile Ser Phe Asn Ile Ser Ala Glu Glu
300   305   310   315

cgg aag gcg aga ttc gag agg ctt aac aag tct gtt gct att cct gca
1253
Arg Lys Ala Arg Phe Glu Arg Leu Asn Lys Ser Val Ala Ile Pro Ala
             320   325   330

378

```
cca acc act tca tac acg cat gta aac aca aca aat gcg gtt cac agt
1301
Pro Thr Thr Ser Tyr Thr His Val Asn Thr Thr Asn Ala Val His Ser
            335            340            345


tac tat aca aac tcg gtt aac cat gtc aag gat ccc ttc tcg tct atc
1349
Tyr Tyr Thr Asn Ser Val Asn His Val Lys Asp Pro Phe Ser Ser Ile
         .350            355            360


cca gta gga gga gga gga ggt gga gag gta gga gaa gaa gag ggt gaa
1397
Pro Val Gly Gly Gly Gly Gly Gly Glu Val Gly Glu Glu Glu Gly Glu
    365            370            375


gaa gat gat gat gaa tta gaa ggt gaa gac gaa gaa ttc gga ggc gat
1445
Glu Asp Asp Asp Glu Leu Glu Gly Glu Asp Glu Glu Phe Gly Gly Asp
380            385            390            395


agc caa tct gac aac gag att ccg agc tga tgatgatcat acggtttctt
1495
Ser Gln Ser Asp Asn Glu Ile Pro Ser
            400


ttcgcggatt tgttaggttt gatggatttc agattttggt tgattgtttt tattaacaca
1555


gaatgtttag aagctgctat ctttaggttc ccatcctctt gtgattgttg agtatccttg
1615


ttagaaacaa acttactgtt gcaaaactct cttcaaaaaa gtttcacttt gctttccca
1674



<210> 212 <211> 404 <212> PRT <213> Arabidopsis thaliana <400>
212


Met Glu Glu Arg Glu Gly Thr Asn Ile Asn Asn Asn Ile Thr Ser Ser
1           5              10             15


Phe Gly Leu Lys Gln Gln His Glu Ala Ala Ala Ser Asp Gly Gly Tyr
         20             25             30


Ser Met Asp Pro Pro Pro Arg Pro Glu Asn Pro Asn Pro Phe Leu Val
  .      35             40             45


Pro Pro Thr Thr Val Pro Ala Ala Ala Thr Val Ala Ala Ala Val Thr
   50             55             60


Glu Asn Ala Ala Thr Pro Phe Ser Leu Thr Met Pro Thr Glu Asn Thr
65             70  '         75             80


Ser Ala Glu Gln Leu Lys Lys Lys Arg Gly Arg Pro Arg Lys Tyr Asn
            85             90             95
```

Pro Asp Gly Thr Leu Val Val Thr Leu Ser Pro Met Pro Ile Ser Ser
            100   105   110

Ser Val Pro Leu Thr Ser Glu Phe Pro Pro Arg Lys Arg Gly Arg Gly
            115   120   125

Arg Gly Lys Ser Asn Arg Trp Leu Lys Lys Ser Gln Met Phe Gln Phe
            130   135   140

Asp Arg Ser Pro Val Asp Thr Asn Leu Ala Gly Val Gly Thr Ala Asp
145   150   155   160

Phe Val Gly Ala Asn Phe Thr Pro His Val Leu Ile Val Asn Ala Gly
                165   170   175

Glu Asp Val Thr Met Lys Ile Met Thr Phe Ser Gln Gln Gly Ser Arg
            180   185   190

Ala Ile Cys Ile Leu Ser Ala Asn Gly Pro Ile Ser Asn Val Thr Leu
            195   200   205

Arg Gln Ser Met Thr Ser Gly Gly Thr Leu Thr Tyr Glu Gly Arg Phe
210   215   220

Glu Ile Leu Ser Leu Thr Gly Ser Phe Met Gln Asn Asp Ser Gly Gly
225   230   235   240

Thr Arg Ser Arg Ala Gly Gly Met Ser Val Cys Leu Ala Gly Pro Asp
                245   250   255

Gly Arg Val Phe Gly Gly Gly Leu Ala Gly Leu Phe Leu Ala Ala Gly
            260   265   270

Pro Val Gln Val Met Val Gly Thr Phe Ile Ala Gly Gln Glu Gln Ser
            275   280   285

Gln Leu Glu Leu Ala Lys Glu Arg Arg Leu Arg Phe Gly Ala Gln Pro
            290   295   300

Ser Ser Ile Ser Phe Asn Ile Ser Ala Glu Glu Arg Lys Ala Arg Phe
305   310   315   320

Glu Arg Leu Asn Lys Ser Val Ala Ile Pro Ala Pro Thr Thr Ser Tyr
                325   330   335

380

```
Thr His Val Asn Thr Thr Asn Ala Val His Ser Tyr Tyr Thr Asn Ser
            340             345             350
```

```
Val Asn His Val Lys Asp Pro Phe Ser Ser Ile Pro Val Gly Gly Gly
            355             360             365
```

```
Gly Gly Gly Glu Val Gly Glu Glu Glu Gly Glu Glu Asp Asp Asp Glu
    370             375             380
```

```
Leu Glu Gly Glu Asp Glu Glu Phe Gly Gly Asp Ser Gln Ser Asp Asn
385             390             395             400
```

```
Glu Ile Pro Ser
```

<210> 213 <211> 1034 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (110)..(856) <223> G1411

<400> 213
taaagaaaaa ctgaacaacc ctaaagtact gtataaatcc tatatcaaat tttttttttg
60

```
gaagaaaagg ctatatttaa aagaaaatca agcaaaagta gatcctcgg atg tat ggg
118
                                                       Met Tyr Gly
                                                         1
```

```
aag agg cct ttt gga ggt gat gaa tct gaa gaa agg gaa gaa gat gag
166
Lys Arg Pro Phe Gly Gly Asp Glu Ser Glu Glu Arg Glu Glu Asp Glu
      5               10              15
```

```
aac ttg ttc ccg gtc ttc tcg gcc cga tct caa cac gac atg cgt gtt
214
Asn Leu Phe Pro Val Phe Ser Ala Arg Ser Gln His Asp Met Arg Val
20              25              30              35
```

```
atg gtc tcg gcc ttg act caa gta atc gga aac caa caa agc aaa tct
262
Met Val Ser Ala Leu Thr Gln Val Ile Gly Asn Gln Gln Ser Lys Ser
              40              45              50
```

```
cat gat aac atc agc tct att gat gat aac tat cct tct gtg tat aat
310
His Asp Asn Ile Ser Ser Ile Asp Asp Asn Tyr Pro Ser Val Tyr Asn
              55              60              65
```

```
cca caa gac cct aat caa caa gtt gcg cct act cat caa gac caa ggg
358
Pro Gln Asp Pro Asn Gln Gln Val Ala Pro Thr His Gln Asp Gln Gly
          70              75              80
```

```
gac ttg agg agg aga cat tat aga ggt gta agg caa agg cca tgg gga
406
Asp Leu Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly
      85              90              95
```

```
aag tgg gca gct gaa atc cga gac cca aaa aag gcg gca cgt gtg tgg
454
Lys Trp Ala Ala Glu Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp
100               105              110                  115

ctc ggg aca ttt gaa acc gct gaa tct gcg gcc tta gct tat gat gaa
502
Leu Gly Thr Phe Glu Thr Ala Glu Ser Ala Ala Leu Ala Tyr Asp Glu
              120              125                  130

gca gcc cta aag ttc aaa gga agc aaa gca aaa ctc aat ttc ccg gag
550
Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys Leu Asn Phe Pro Glu
              135              140                  145

agg gtt cag ctt gga agt aac tct aca tat tac tcc tcc aac caa att
598
Arg Val Gln Leu Gly Ser Asn Ser Thr Tyr Tyr Ser Ser Asn Gln Ile
          150              155              160

cca caa atg gaa cca caa agt ata ccg aac tat aat caa tac tat cat
646
Pro Gln Met Glu Pro Gln Ser Ile Pro Asn Tyr Asn Gln Tyr Tyr His
      165              170              175

gat gcg agt agt ggt gat atg cta agt ttt aat ttg ggc ggt ggg tat
694
Asp Ala Ser Ser Gly Asp Met Leu Ser Phe Asn Leu Gly Gly Gly Tyr
180              185              190                  195

ggg agt ggt acc gga tat tca atg tct cat gat aat agt act acg act
742
Gly Ser Gly Thr Gly Tyr Ser Met Ser His Asp Asn Ser Thr Thr Thr
              200              205                  210

gct gct aca act tct tcg tct tct ggt ggc tct tct agg caa caa gaa
790
Ala Ala Thr Thr Ser Ser Ser Ser Gly Gly Ser Ser Arg Gln Gln Glu
              215              220                  225

gag caa gat tat gcc aga ttc tgg cgc ttt ggg gat tct tct tcc tct
838
Glu Gln Asp Tyr Ala Arg Phe Trp Arg Phe Gly Asp Ser Ser Ser Ser
          230              235              240

cct cat tcg gga tat taa ttaggagatt tgatcagtta cttgtgatga
886
Pro His Ser Gly Tyr
      245

agtaatgata catttcccgt caaaattgag atgatcatat gcttcctgaa tgtttttgag
946

tgtcattttt gtcttccgcg ttaagattta ttgaacgtgt tttcttgttt ttttggttaa
1006

aaaaaaaaaa aaaaaaaaaa aaaaaaaa
1034
```

382

<210> 214 <211> 248 <212> PRT <213> Arabidopsis thaliana <400> 214

```
Met Tyr Gly Lys Arg Pro Phe Gly Gly Asp Glu Ser Glu Glu Arg Glu
1               5                   10                  15

Glu Asp Glu Asn Leu Phe Pro Val Phe Ser Ala Arg Ser Gln His Asp
                20                  25                  30

Met Arg Val Met Val Ser Ala Leu Thr Gln Val Ile Gly Asn Gln Gln
        35                  40                  45

Ser Lys Ser His Asp Asn Ile Ser Ser Ile Asp Asp Asn Tyr Pro Ser
    50                  55                  60

Val Tyr Asn Pro Gln Asp Pro Asn Gln Gln Val Ala Pro Thr His Gln
65                  70                  75                  80

Asp Gln Gly Asp Leu Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg
                85                  90                  95

Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Lys Lys Ala Ala
                100                 105                 110

Arg Val Trp Leu Gly Thr Phe Glu Thr Ala Glu Ser Ala Ala Leu Ala
        115                 120                 125

Tyr Asp Glu Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys Leu Asn
    130                 135                 140

Phe Pro Glu Arg Val Gln Leu Gly Ser Asn Ser Thr Tyr Tyr Ser Ser
145                 150                 155                 160

Asn Gln Ile Pro Gln Met Glu Pro Gln Ser Ile Pro Asn Tyr Asn Gln
                165                 170                 175

Tyr Tyr His Asp Ala Ser Ser Gly Asp Met Leu Ser Phe Asn Leu Gly
                180                 185                 190

Gly Gly Tyr Gly Ser Gly Thr Gly Tyr Ser Met Ser His Asp Asn Ser
        195                 200                 205

Thr Thr Thr Ala Ala Thr Thr Ser Ser Ser Ser Gly Gly Ser Ser Arg
    210                 215                 220

Gln Gln Glu Glu Gln Asp Tyr Ala Arg Phe Trp Arg Phe Gly Asp Ser
225                 230                 235                 240
```

383

Ser Ser Ser Pro His Ser Gly Tyr
                245

<210> 215 <211> 820 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (27)..(692) <223> G1419

 <400> 215
gaagactcca acataattca tcatct atg gct tct tca cat caa caa cag caa
53
                           Met Ala Ser Ser His Gln Gln Gln Gln
                           1   5

gaa caa gac cag tca gct tta gat ctc ata acc caa cac ctt ctt act
101
Glu Gln Asp Gln Ser Ala Leu Asp Leu Ile Thr Gln His Leu Leu Thr
10   15   20   25

gat ttc cct tcc tta gac acc ttt gcc tcc acc atc cac cac tgc acc
149
Asp Phe Pro Ser Leu Asp Thr Phe Ala Ser Thr Ile His His Cys Thr
            30   35   40

acc tca act cta agc caa cgc aaa cca cct ctt gcc act ata gca gtt
197
Thr Ser Thr Leu Ser Gln Arg Lys Pro Pro Leu Ala Thr Ile Ala Val
            45   50   55

cct act act gca ccg gtg gtt caa gag aat gat caa agg cat tac aga
245
Pro Thr Thr Ala Pro Val Val Gln Glu Asn Asp Gln Arg His Tyr Arg
        60   65   70

ggc gtc agg aga aga cca tgg ggt aag tat gcg gct gag atc aga gac
293
Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile Arg Asp
    75   80   85

cca aac aag aaa ggt gtt cgt gtc tgg tta ggc act ttt gac aca gcc
341
Pro Asn Lys Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asp Thr Ala
90   95   100   105

atg gaa gct gca aga ggt tat gac aag gca gct ttt aaa cta cga gga
389
Met Glu Ala Ala Arg Gly Tyr Asp Lys Ala Ala Phe Lys Leu Arg Gly
            110   115   120

agc aaa gct att ctt aac ttc cca ctt gaa gca gga aag cat gag gac
437
Ser Lys Ala Ile Leu Asn Phe Pro Leu Glu Ala Gly Lys His Glu Asp
            125   130   135

ttg gga gac aac aag aag act att tct tta aaa gca aag agg aag aga
485
Leu Gly Asp Asn Lys Lys Thr Ile Ser Leu Lys Ala Lys Arg Lys Arg
        140   145   150

384

```
cag gtg acg gag gat gaa agc cag ctg atc agc cgt aaa gct gtt aag
533
Gln Val Thr Glu Asp Glu Ser Gln Leu Ile Ser Arg Lys Ala Val Lys
    155             160             165

agg gaa gaa gct cag gtt cag gct gat gct tgt cca tta acg cca tca
581
Arg Glu Glu Ala Gln Val Gln Ala Asp Ala Cys Pro Leu Thr Pro Ser
170             175             180             185

agt tgg aag ggg ttt tgg gac gga gca gac agt aaa gac atg gga ata
629
Ser Trp Lys Gly Phe Trp Asp Gly Ala Asp Ser Lys Asp Met Gly Ile
            190             195             200

ttt tcc gtg cct ctg tta tct cct tgt cca tct ctt gga cac tct caa
677
Phe Ser Val Pro Leu Leu Ser Pro Cys Pro Ser Leu Gly His Ser Gln
            205             210             215

ctc gta gtt act taa gcttcagagg gtcaaactgg aaaaaatcaa cattggattg
732
Leu Val Val Thr
            220

ttttcaaagc ttctagatta gctgattgta aaaaaatgtt ttactatatt cattcattct
792

tcttaaatgc aattctttct acccttcc
820
```

<210> 216 <211> 221 <212> PRT <213> Arabidopsis thaliana <400>
216 ·

```
Met Ala Ser Ser His Gln Gln Gln Gln Glu Gln Asp Gln Ser Ala Leu
1               5               10              15

Asp Leu Ile Thr Gln His Leu Leu Thr Asp Phe Pro Ser Leu Asp Thr
            20              25              30

Phe Ala Ser Thr Ile His His Cys Thr Thr Ser Thr Leu Ser Gln Arg
        35              40              45

Lys Pro Pro Leu Ala Thr Ile Ala Val Pro Thr Thr Ala Pro Val Val
    50              55              60

Gln Glu Asn Asp Gln Arg His Tyr Arg Gly Val Arg Arg Arg Pro Trp
65              70              75              80

Gly Lys Tyr Ala Ala Glu Ile Arg Asp Pro Asn Lys Lys Gly Val Arg
                85              90              95

Val Trp Leu Gly Thr Phe Asp Thr Ala Met Glu Ala Ala Arg Gly Tyr
            100             105             110
```

Asp Lys Ala Ala Phe Lys Leu Arg Gly Ser Lys Ala Ile Leu Asn Phe
        115   120   125

Pro Leu Glu Ala Gly Lys His Glu Asp Leu Gly Asp Asn Lys Lys Thr
    130   135   140

Ile Ser Leu Lys Ala Lys Arg Lys Arg Gln Val Thr Glu Asp Glu Ser
145   150   155   160

Gln Leu Ile Ser Arg Lys Ala Val Lys Arg Glu Glu Ala Gln Val Gln
                165   170   175

Ala Asp Ala Cys Pro Leu Thr Pro Ser Ser Trp Lys Gly Phe Trp Asp
            180   185   190

Gly Ala Asp Ser Lys Asp Met Gly Ile Phe Ser Val Pro Leu Leu Ser
        195   200   205

Pro Cys Pro Ser Leu Gly His Ser Gln Leu Val Val Thr
    210   215   220

<210> 217 <211> 1260 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (292)..(1155) <223> G1421

<400> 217
gaaatttcat ccctaaataa gaaaaaagca tctccttctt tagtgtcctc cttcaccaaa
60

ctcttgattc cataagcata tattaaaaaa gctctctgct ttcttcaact ttcccgggaa
120

aatcttcttg ttacaaagca tcaatctctt gttttaccaa ttttctctct ttattccttt
180

tttgcccttt acttttccta actttggtct ttatatataa acacacgaca caaagaagaa
240

cacacataag ttaaaactat tacaacagtt ttaaagagag agatttaaaa a atg gag
297
                                                        Met Glu
                                                        1

aca gag aag aaa gtt tct ctc cca aga atc tta cga atc tct gtt act
345
Thr Glu Lys Lys Val Ser Leu Pro Arg Ile Leu Arg Ile Ser Val Thr
        5   10   15

gat cct tac gca aca gat tcg tca agc gac gaa gaa gaa gaa gtt gat
393
Asp Pro Tyr Ala Thr Asp Ser Ser Ser Asp Glu Glu Glu Glu Val Asp
    20   25   30

386

```
ttt gat gca tta tct aca aaa cga cgt cgt gtt aag aag tac gtg aag
441
Phe Asp Ala Leu Ser Thr Lys Arg Arg Arg Val Lys Lys Tyr Val Lys
35              40              45                      50

gaa gtg gtg ctt gat tcg gtg gtt tct gat aaa gag aag ccg atg aag
489
Glu Val Val Leu Asp Ser Val Val Ser Asp Lys Glu Lys Pro Met Lys
                55              60                      65

aag aag aga aag aag cgc gtt gtt act gtt cca gtg gtt gtt acg acg
537
Lys Lys Arg Lys Lys Arg Val Val Thr Val Pro Val Val Val Thr Thr
            70              75                      80

gcg acg agg aag ttt cgt gga gtg agg caa aga ccg tgg gga aaa tgg
585
Ala Thr Arg Lys Phe Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp
            85              90                      95

gcg gcg gag att aga gat ccg agt aga cgt gtt agg gtt tgg tta ggt
633
Ala Ala Glu Ile Arg Asp Pro Ser Arg Arg Val Arg Val Trp Leu Gly
    100             105             110

act ttt gac acg gcg gag gaa gct gcc att gtt tac gat aac gca gct
681
Thr Phe Asp Thr Ala Glu Glu Ala Ala Ile Val Tyr Asp Asn Ala Ala
115             120             125                     130

att cag cta cgt ggt cct aac gca gag ctt aac ttc cct cct cct ccg
729
Ile Gln Leu Arg Gly Pro Asn Ala Glu Leu Asn Phe Pro Pro Pro Pro
            135                 140             145

gtg acg gag aat gtt gaa gaa gct tcg acg gag gtg aaa gga gtt tcg
777
Val Thr Glu Asn Val Glu Glu Ala Ser Thr Glu Val Lys Gly Val Ser
            150             155             160

gat ttt atc att ggc ggt gga gaa tgt ctt cgt tcg ccg gtt tct gtt
825
Asp Phe Ile Ile Gly Gly Gly Glu Cys Leu Arg Ser Pro Val Ser Val
            165             170             175

ctc gaa tct ccg ttc tcc ggc gag tct act gcg gtt aaa gag gag ttt
873
Leu Glu Ser Pro Phe Ser Gly Glu Ser Thr Ala Val Lys Glu Glu Phe
    180             185             190

gtc ggt gta tcg acg gcg gag att gtg gtt aaa aag gag ccg tct ttt
921
Val Gly Val Ser Thr Ala Glu Ile Val Val Lys Lys Glu Pro Ser Phe
195                 200             205                     210

aac ggt tca gat ttc tcg gcg ccg ttg ttc tcg gac gac gac gtt ttt
969
Asn Gly Ser Asp Phe Ser Ala Pro Leu Phe Ser Asp Asp Asp Val Phe
            215                 220             225
```

387

```
ggt ttc tcg acg tcg atg agt gaa agt ttc ggc ggc gat tta ttt gga
1017
Gly Phe Ser Thr Ser Met Ser Glu Ser Phe Gly Gly Asp Leu Phe Gly
            230             235             240

gat aat ctt ttt gcg gat atg agt ttt gga tcc ggg ttt gga ttc ggg
1065
Asp Asn Leu Phe Ala Asp Met Ser Phe Gly Ser Gly Phe Gly Phe Gly
            245             250             255

tct ggg tct gga ttc tcc agc tgg cac gtt gag gac cat ttt caa gat
1113
Ser Gly Ser Gly Phe Ser Ser Trp His Val Glu Asp His Phe Gln Asp
        260             265             270

att ggg gat tta ttc ggg tcg gat cct gtc tta act gtt taa
1155
Ile Gly Asp Leu Phe Gly Ser Asp Pro Val Leu Thr Val
275             280             285

gaaataactg gccgtttaac ggcgtttagt gaagttttgt taccggcgac ggcgaggatt
1215

aaaaaaaaac ggcgatttat tttttgaatg aagatttgtt aaata
1260


<210> 218 <211> 287 <212> PRT <213> Arabidopsis thaliana <400>
218

Met Glu Thr Glu Lys Lys Val Ser Leu Pro Arg Ile Leu Arg Ile Ser
1               5               10              15

Val Thr Asp Pro Tyr Ala Thr Asp Ser Ser Ser Asp Glu Glu Glu Glu
            20              25              30

Val Asp Phe Asp Ala Leu Ser Thr Lys Arg Arg Arg Val Lys Lys Tyr
            35              40              45

Val Lys Glu Val Val Leu Asp Ser Val Val Ser Asp Lys Glu Lys Pro
        50              55              60

Met Lys Lys Lys Arg Lys Lys Arg Val Val Thr Val Pro Val Val Val
65              70              75              80

Thr Thr Ala Thr Arg Lys Phe Arg Gly Val Arg Gln Arg Pro Trp Gly
                85              90              95

Lys Trp Ala Ala Glu Ile Arg Asp Pro Ser Arg Arg Val Arg Val Trp
            100             105             110

Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Ile Val Tyr Asp Asn
        115             120             125
```

Ala Ala Ile Gln Leu Arg Gly Pro Asn Ala Glu Leu Asn Phe Pro Pro
    130   135   140

Pro Pro Val Thr Glu Asn Val Glu Glu Ala Ser Thr Glu Val Lys Gly
145   150   155   160

Val Ser Asp Phe Ile Ile Gly Gly Gly Glu Cys Leu Arg Ser Pro Val
            165   170   175

Ser Val Leu Glu Ser Pro Phe Ser Gly Glu Ser Thr Ala Val Lys Glu
            180   185   190

Glu Phe Val Gly Val Ser Thr Ala Glu Ile Val Val Lys Lys Glu Pro
        195   200   205

Ser Phe Asn Gly Ser Asp Phe Ser Ala Pro Leu Phe Ser Asp Asp Asp
    210   215   220

Val Phe Gly Phe Ser Thr Ser Met Ser Glu Ser Phe Gly Gly Asp Leu
225   230   235   240

Phe Gly Asp Asn Leu Phe Ala Asp Met Ser Phe Gly Ser Gly Phe Gly
            245   250   255

Phe Gly Ser Gly Ser Gly Phe Ser Ser Trp His Val Glu Asp His Phe
            260   265   270

Gln Asp Ile Gly Asp Leu Phe Gly Ser Asp Pro Val Leu Thr Val
        275   280   285

<210> 219 <211> 1281 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (8)..(904) <223> G1435

 <400> 219
gtgaaac atg ggg aag gaa gtt atg gtg agc gat tac ggt gac gac gac
49
        Met Gly Lys Glu Val Met Val Ser Asp Tyr Gly Asp Asp Asp
        1   5   10

gga gaa gac gcc ggc ggc ggc gat gaa tat agg att ccg gaa tgg gaa
97
Gly Glu Asp Ala Gly Gly Gly Asp Glu Tyr Arg Ile Pro Glu Trp Glu
15   20   25   30

att ggt tta ccc aac gga gat gat ttg act ccg tta tct caa tat cta
145
Ile Gly Leu Pro Asn Gly Asp Asp Leu Thr Pro Leu Ser Gln Tyr Leu
                35   40   45

389

```
gtc ccg tcg att ctc gcg tta gct ttc agc atg atc cca gaa cga agc
193
Val Pro Ser Ile Leu Ala Leu Ala Phe Ser Met Ile Pro Glu Arg Ser
            50              55              60

cgt aca att cac gac gtc aat cgc gcg tcg caa atc acg ctc tct tcg
241
Arg Thr Ile His Asp Val Asn Arg Ala Ser Gln Ile Thr Leu Ser Ser
        65              70              75

ttg aga agc agt acc aat gct tcg tct gtg atg gag gag gtc gtg gat
289
Leu Arg Ser Ser Thr Asn Ala Ser Ser Val Met Glu Glu Val Val Asp
        80              85              90

cga gtt gaa tcg agt gtt cca gga tca gat ccg aag aaa cag aag aaa
337
Arg Val Glu Ser Ser Val Pro Gly Ser Asp Pro Lys Lys Gln Lys Lys
95              100             105                     110

tcg gat ggt ggt gaa gca gcg gcg gtg gag gat tcc acg gcg gag gaa
385
Ser Asp Gly Gly Glu Ala Ala Ala Val Glu Asp Ser Thr Ala Glu Glu
                115             120             125

gga gac tcc ggg cct gaa gac gcg tct ggg aag aca tcg aaa cga ccg
433
Gly Asp Ser Gly Pro Glu Asp Ala Ser Gly Lys Thr Ser Lys Arg Pro
                130             135             140

cgt tta gtg tgg aca ccg cag cta cac aag aga ttt gtg gac gtt gtg
481
Arg Leu Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val Val
        145             150             155

gct cat cta ggg att aaa aac gca gtg ccg aag acg att atg cag ctg
529
Ala His Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln Leu
    160             165             170

atg aac gtg gaa gga ctt act cgt gag aac gtt gcg tct cat ttg cag
577
Met Asn Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu Gln
175             180             185                     190

aaa tat agg ctt tac ctt aaa cgg att caa gga ttg acg acg gaa gaa
625
Lys Tyr Arg Leu Tyr Leu Lys Arg Ile Gln Gly Leu Thr Thr Glu Glu
                195             200             205

gat cct tat tcg tcg tcg gat cag ctc ttc tct tca acg ccg gtt cct
673
Asp Pro Tyr Ser Ser Ser Asp Gln Leu Phe Ser Ser Thr Pro Val Pro
            210             215             220

cca cag agc ttt caa gac ggc gga gga agt aac gga aag ttg ggg gtt
721
Pro Gln Ser Phe Gln Asp Gly Gly Gly Ser Asn Gly Lys Leu Gly Val
            225             230             235
```

```
ccg gtt ccg gtt ccg tcg atg gtg cct att cca ggc tat ggg aat caa
769
Pro Val Pro Val Pro Ser Met Val Pro Ile Pro Gly Tyr Gly Asn Gln
    240             245             250

atg ggt atg caa gga tat tat caa cag tat agt aac cat ggc aat gaa
817
Met Gly Met Gln Gly Tyr Tyr Gln Gln Tyr Ser Asn His Gly Asn Glu
255             260             265             270

tca aac caa tat atg atg cag cag aat aag ttt gga aca atg gtg aca
865
Ser Asn Gln Tyr Met Met Gln Gln Asn Lys Phe Gly Thr Met Val Thr
            275             280             285

tat cct tct gtt ggt ggt ggt gac gtg aat gac aag taa atggatctta
914
Tyr Pro Ser Val Gly Gly Gly Asp Val Asn Asp Lys
            290             295

aaggtctata atttgctcta cagagagata ctggttcttg gcttatggtt tattttccca
974

cttcatgagg ttgttgtgac ttttaattct ccatgttttc cacacaagtc tttattgcct
1034

ttgtatagaa aatgatttcg agaaaatcac tgggaagctt ggtattgttg gaggatgaag
1094

ccttctatga atgatttagt ttcctactgt ctccattctt tatgaggtaa taaagccttc
1154

ttttgctcat cgcttgtagt cttcttaaat tcaagacagc gtcacatgtt tgttcggtta
1214

tgttaattgt ttctttcttt ggataatgaa gatagcatca ggtctcatgt ctcctcactt
1274

tgataaa
1281


<210> 220 <211> 298 <212> PRT <213> Arabidopsis thaliana <400>
220

Met Gly Lys Glu Val Met Val Ser Asp Tyr Gly Asp Asp Asp Gly Glu
1           5               10.             15


Asp Ala Gly Gly Gly Asp Glu Tyr Arg Ile Pro Glu Trp Glu Ile Gly
        20              25              30


Leu Pro Asn Gly Asp Asp Leu Thr Pro Leu Ser Gln Tyr Leu Val Pro
        35              40              45


Ser Ile Leu Ala Leu Ala Phe Ser Met Ile Pro Glu Arg Ser Arg Thr
    50              55              60
```

Ile His Asp Val Asn Arg Ala Ser Gln Ile Thr Leu Ser Ser Leu Arg
65   70   75   80

Ser Ser Thr Asn Ala Ser Ser Val Met Glu Glu Val Val Asp Arg Val
                85   90   95

Glu Ser Ser Val Pro Gly Ser Asp Pro Lys Lys Gln Lys Lys Ser Asp
            100   105   110

Gly Gly Glu Ala Ala Ala Val Glu Asp Ser Thr Ala Glu Glu Gly Asp
            115   120   125

Ser Gly Pro Glu Asp Ala Ser Gly Lys Thr Ser Lys Arg Pro Arg Leu
    130   135   140

Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val Val Ala His
145   150   155   160

Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln Leu Met Asn
            165   170   175

Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu Gln Lys Tyr
            180   185   190

Arg Leu Tyr Leu Lys Arg Ile Gln Gly Leu Thr Thr Glu Glu Asp Pro
    195   200   205

Tyr Ser Ser Ser Asp Gln Leu Phe Ser Ser Thr Pro Val Pro Pro Gln
    210   215   220

Ser Phe Gln Asp Gly Gly Gly Ser Asn Gly Lys Leu Gly Val Pro Val
225   230   235   240

Pro Val Pro Ser Met Val Pro Ile Pro Gly Tyr Gly Asn Gln Met Gly
            245   250   255

Met Gln Gly Tyr Tyr Gln Gln Tyr Ser Asn His Gly Asn Glu Ser Asn
            260   265   270

Gln Tyr Met Met Gln Gln Asn Lys Phe Gly Thr Met Val Thr Tyr Pro
    275   280   285

Ser Val Gly Gly Gly Asp Val Asn Asp Lys
290   295

392

<210> 221 <211> 799 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (105)..(581) <223> G1449

<400> 221
tagacagaga gaaatagaaa tagagagaga gagacatgaa gagcactctc aatagagaag
60

agaaggaagc atgaagctag ctctgcagct tcaaggtctc atta atg gag gtc tct
116
                                                      Met Glu Val Ser
                                                      1

aac tct tgt tct tca ttt tct tca tcc tct gtc gac agt act aaa cct
164
Asn Ser Cys Ser Ser Phe Ser Ser Ser Ser Val Asp Ser Thr Lys Pro
5   10   15   20

tct cct tct gaa tct tct gtt aat ctc tcc ctt agt ctc aca ttt cct
212
Ser Pro Ser Glu Ser Ser Val Asn Leu Ser Leu Ser Leu Thr Phe Pro
            25   30   35

tct act tct cca caa aga gaa gca aga caa gat tgg cca ccg ata aag
260
Ser Thr Ser Pro Gln Arg Glu Ala Arg Gln Asp Trp Pro Pro Ile Lys
            40   45   50

tct aga tta aga gat aca cta aag ggt cgt cgt ctt ctt cgt cgt ggt
308
Ser Arg Leu Arg Asp Thr Leu Lys Gly Arg Arg Leu Leu Arg Arg Gly
        55   60   65

gat gac act tct ctc ttt gtt aag gtt tat atg gaa ggt gtt ccc att
356
Asp Asp Thr Ser Leu Phe Val Lys Val Tyr Met Glu Gly Val Pro Ile
    70   75   80

gga aga aaa ctc gac ctt tgc gta ttc tca ggc tac gag agt cta tta
404
Gly Arg Lys Leu Asp Leu Cys Val Phe Ser Gly Tyr Glu Ser Leu Leu
85   90   95   100

gaa aat ctc tct cac atg ttc gat act tca atc atc tgc ggt aat cga
452
Glu Asn Leu Ser His Met Phe Asp Thr Ser Ile Ile Cys Gly Asn Arg
                105   110   115

gat cga aaa cat cat gtt ttg aca tat gaa gac aag gat gga gat tgg
500
Asp Arg Lys His His Val Leu Thr Tyr Glu Asp Lys Asp Gly Asp Trp
            120   125   130

atg atg gtc gga gat att cca tgg gat atg ttt ctt gaa acc gtg aga
548
Met Met Val Gly Asp Ile Pro Trp Asp Met Phe Leu Glu Thr Val Arg
            135   140   145

aga cta aag atc acg aga ccg gag agg tat taa aacttggatc ggtcaaggct
601
Arg Leu Lys Ile Thr Arg Pro Glu Arg Tyr
        150   155

393

```
gtgattgcgc agttacgaga cgtgtaagat ttaggcattg atgaagagac ttgaggcggg
661

acggagctat tgctgcatat tgcaacaaag gccttgaaga agttggagaa ttgattgatg
721

catatattta tttatatgac acctttgagt gtgttttttc ttataaataa atcacaatat
781

ccaagacttc tctttaaa
799
```

<210> 222 <211> 158 <212> PRT <213> Arabidopsis thaliana <400>
222

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Met Glu Val Ser Asn Ser Cys Ser Ser Phe Ser Ser Ser Ser Val Asp
1               5               10              15


Ser Thr Lys Pro Ser Pro Ser Glu Ser Ser Val Asn Leu Ser Leu Ser
            20              25              30


Leu Thr Phe Pro Ser Thr Ser Pro Gln Arg Glu Ala Arg Gln Asp Trp
        35              40              45


Pro Pro Ile Lys Ser Arg Leu Arg Asp Thr Leu Lys Gly Arg Arg Leu
    50              55              60


Leu Arg Arg Gly Asp Asp Thr Ser Leu Phe Val Lys Val Tyr Met Glu
65              70              75              80


Gly Val Pro Ile Gly Arg Lys Leu Asp Leu Cys Val Phe Ser Gly Tyr
                85              90              95


Glu Ser Leu Leu Glu Asn Leu Ser His Met Phe Asp Thr Ser Ile Ile
            100             105             110


Cys Gly Asn Arg Asp Arg Lys His His Val Leu Thr Tyr Glu Asp Lys
        115             120             125


Asp Gly Asp Trp Met Met Val Gly Asp Ile Pro Trp Asp Met Phe Leu
    130             135             140


Glu Thr Val Arg Arg Leu Lys Ile Thr Arg Pro Glu Arg Tyr
145             150             155
```

<210> 223 <211> 1424 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (114)..(1406) <223> G1494

<400> 223

tcgacagagt tgtgttgggc gtggaacttg gactagttcc acatatcagg ttatatagat
60

cttctctttc aacttctgat tcgtccagaa gctttcctaa tctgagatct gac atg
116
                                                                Met
                                                                1

gaa cac caa ggt tgg agt ttt gag gag aat tat agt ttg tcc act aat
164
Glu His Gln Gly Trp Ser Phe Glu Glu Asn Tyr Ser Leu Ser Thr Asn
              5   10   15

aga aga tct atc agg cca caa gat gaa cta gtg gag tta tta tgg cga
212
Arg Arg Ser Ile Arg Pro Gln Asp Glu Leu Val Glu Leu Leu Trp Arg
            20   25   30

gat gga caa gtg gtt ctg cag agc caa act cat aga gaa caa acc caa
260
Asp Gly Gln Val Val Leu Gln Ser Gln Thr His Arg Glu Gln Thr Gln
        35   40   45

acc cag aaa caa gat cat cat gaa gaa gcc cta aga tcc agc acc ttt
308
Thr Gln Lys Gln Asp His His Glu Glu Ala Leu Arg Ser Ser Thr Phe
50   55   60   65

ctt gaa gat caa gaa act gtc tct tgg atc caa tac cct cca gat gaa
356
Leu Glu Asp Gln Glu Thr Val Ser Trp Ile Gln Tyr Pro Pro Asp Glu
                70   75   80

gac cca ttc gaa ccc gac gac ttc tcc tcc cac ttc ttc tca acc atg
404
Asp Pro Phe Glu Pro Asp Asp Phe Ser Ser His Phe Phe Ser Thr Met
            85   90   95

gat ccc ctc cag aga cca acc tca gag acg gtt aag cct aag tcc agt
452
Asp Pro Leu Gln Arg Pro Thr Ser Glu Thr Val Lys Pro Lys Ser Ser
            100   105   110

cct gaa cct cct caa gtc atg gtt aag cct aag gcc tgt cct gac cct
500
Pro Glu Pro Pro Gln Val Met Val Lys Pro Lys Ala Cys Pro Asp Pro
        115   120   125

cct cct caa gtc atg cct cct cca aaa ttt agg tta aca aat tca tca
548
Pro Pro Gln Val Met Pro Pro Pro Lys Phe Arg Leu Thr Asn Ser Ser
130   135   140   145

tcg ggg att agg gaa aca gaa atg gaa cag tac tcg gta acg acc gtt
596
Ser Gly Ile Arg Glu Thr Glu Met Glu Gln Tyr Ser Val Thr Thr Val
                150   155   160

gga cct agc cat tgc gga agc aac cca tca cag aac gat ctc gat gtc
644
Gly Pro Ser His Cys Gly Ser Asn Pro Ser Gln Asn Asp Leu Asp Val

395

```
              165                    170                    175
```

tca atg agt cat gat cga agc aaa aac ata gaa gaa aag ctt aat ccg
692
Ser Met Ser His Asp Arg Ser Lys Asn Ile Glu Glu Lys Leu Asn Pro
        180   185   190

aac gca agt tcc tca tca ggt ggc tcc tct ggt tgc agc ttt ggc aaa
740
Asn Ala Ser Ser Ser Ser Gly Gly Ser Ser Gly Cys Ser Phe Gly Lys
        195   200   205

gat atc aaa gaa atg gct agt gga aga tgc atc aca acc gac cgt aag
788
Asp Ile Lys Glu Met Ala Ser Gly Arg Cys Ile Thr Thr Asp Arg Lys
210   215   220   225

aga aaa cgt ata aat cac act gac gaa tct gta tct cta tca gat gca
836
Arg Lys Arg Ile Asn His Thr Asp Glu Ser Val Ser Leu Ser Asp Ala
                230   235   240

atc ggt aac aag tcg aac caa cga tca gga tca aac cga agg agt cga
884
Ile Gly Asn Lys Ser Asn Gln Arg Ser Gly Ser Asn Arg Arg Ser Arg
            245   250   255

gca gct gaa gtt cat aat ctc tcc gaa agg agg agg aga gat agg atc
932
Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg Arg Arg Asp Arg Ile
            260   265   270

aat gag aga atg aag gct ttg caa gaa cta ata cct cac tgc agt aaa
980
Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile Pro His Cys Ser Lys
            275   280   285

act gat aaa gct tcg att tta gac gaa gcc ata gat tat ttg aaa tca
1028
Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile Asp Tyr Leu Lys Ser
290   295   300   305

ctt cag tta cag ctt caa gtg atg tgg atg ggg agt gga atg gcg gcg
1076
Leu Gln Leu Gln Leu Gln Val Met Trp Met Gly Ser Gly Met Ala Ala
                310   315   320

gcg gcg gct tcg gct ccg atg atg ttc ccc gga gtt caa cct cag cag
1124
Ala Ala Ala Ser Ala Pro Met Met Phe Pro Gly Val Gln Pro Gln Gln
            325   330   335

ttc ata cgt cag ata cag agc ccg gta cag tta cct cga ttt ccg gtt
1172
Phe Ile Arg Gln Ile Gln Ser Pro Val Gln Leu Pro Arg Phe Pro Val
            340   345   350

atg gat cag tct gca att cag aac aat ccc ggt tta gtt tgc caa aac
1220
Met Asp Gln Ser Ala Ile Gln Asn Asn Pro Gly Leu Val Cys Gln Asn
            355   360   365

396

```
ccg gta caa aac cag atc atc tcc gac cgg ttt gct aga tac atc ggt
1268
Pro Val Gln Asn Gln Ile Ile Ser Asp Arg Phe Ala Arg Tyr Ile Gly
370             375             380             385

ggg ttc cca cac atg cag gcc gcg act cag atg cag ccg atg gag atg
1316
Gly Phe Pro His Met Gln Ala Ala Thr Gln Met Gln Pro Met Glu Met
            390             395.            400

ttg aga ttt agt tca ccg gcg gga cag caa agt caa caa ccg tcg tct
1364
Leu Arg Phe Ser Ser Pro Ala Gly Gln Gln Ser Gln Gln Pro Ser Ser
            405             410             415

gtg ccg acg aag acc acc gac ggt tct cgt ttg gac cac tag
1406
Val Pro Thr Lys Thr Thr Asp Gly Ser Arg Leu Asp His
        420             425             430

gttggtgagc cactttgc
1424


<210>  224 <211>  430 <212>  PRT <213>  Arabidopsis thaliana  <400>
224

Met Glu His Gln Gly Trp Ser Phe Glu Glu Asn Tyr Ser Leu Ser Thr
1               5               10              15

Asn Arg Arg Ser Ile Arg Pro Gln Asp Glu Leu Val Glu Leu Leu Trp
            20              25              30

Arg Asp Gly Gln Val Val Leu Gln Ser Gln Thr His Arg Glu Gln Thr
            35              40              45

Gln Thr Gln Lys Gln Asp His His Glu Glu Ala Leu Arg Ser Ser Thr
    50              55              60

Phe Leu Glu Asp Gln Glu Thr Val Ser Trp Ile Gln Tyr Pro Pro Asp
65              70              75              80

Glu Asp Pro Phe Glu Pro Asp Asp Phe Ser Ser His Phe Phe Ser Thr
            85              90              95

Met Asp Pro Leu Gln Arg Pro Thr Ser Glu Thr Val Lys Pro Lys Ser
            100             105             110

Ser Pro Glu Pro Pro Gln Val Met Val Lys Pro Lys Ala Cys Pro Asp
        115             120             125

Pro Pro Pro Gln Val Met Pro Pro Pro Lys Phe Arg Leu Thr Asn Ser
```

```
        130                    135                    140          .


Ser Ser Gly Ile Arg Glu Thr Glu Met Glu Gln Tyr Ser Val Thr Thr
145                 150                 155                 160


Val Gly Pro Ser His Cys Gly Ser Asn Pro Ser Gln Asn Asp Leu Asp
                165                 170                 175


Val Ser Met Ser His Asp Arg Ser Lys Asn Ile Glu Glu Lys Leu Asn
                180                 185                 190


Pro Asn Ala Ser Ser Ser Ser Gly Gly Ser Ser Gly Cys Ser Phe Gly
            195                 200                 205


Lys Asp Ile Lys Glu Met Ala Ser Gly Arg Cys Ile Thr Thr Asp Arg
        210                 215                 220


Lys Arg Lys Arg Ile Asn His Thr Asp Glu Ser Val Ser Leu Ser Asp
225                 230                 235                 240


Ala Ile Gly Asn Lys Ser Asn Gln Arg Ser Gly Ser Asn Arg Arg Ser
                245                 250                 255


Arg Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg Arg Arg Asp Arg
            260                 265                 270


Ile Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile Pro His Cys Ser
        275                 280                 285


Lys Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile Asp Tyr Leu Lys
    290                 295                 300


Ser Leu Gln Leu Gln Leu Gln Val Met Trp Met Gly Ser Gly Met Ala
305                 310                 315                 320


Ala Ala Ala Ala Ser Ala Pro Met Met Phe Pro Gly Val Gln Pro Gln
                325                 330                 335


Gln Phe Ile Arg Gln Ile Gln Ser Pro Val Gln Leu Pro Arg Phe Pro
            340                 345                 350


Val Met Asp Gln Ser Ala Ile Gln Asn Asn Pro Gly Leu Val Cys Gln
        355                 360                 365


Asn Pro Val Gln Asn Gln Ile Ile Ser Asp Arg Phe Ala Arg Tyr Ile
    370                 375                 380
```

398

```
Gly Gly Phe Pro His Met Gln Ala Ala Thr Gln Met Gln Pro Met Glu
385                 390             395                 400


Met Leu Arg Phe Ser Ser Pro Ala Gly Gln Gln Ser Gln Gln Pro Ser
                405             410                 415


Ser Val Pro Thr Lys Thr Thr Asp Gly Ser Arg Leu Asp His
            420             425             430
```

<210> 225 <211> 1306 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (116)..(1123) <223> G1496

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60

acttttggtc tcactttaaa agatcataag ttgaaagatt tctgcagaga acaat atg
118

```
                                                                    Met
                                                                    1

ttg gaa ggt ctt gtc tct caa gaa agc ttg tcc tta aac tct atg gac
166
Leu Glu Gly Leu Val Ser Gln Glu Ser Leu Ser Leu Asn Ser Met Asp
            5               10                  15

atg tct gta ctt gaa agg ctt aaa tgg gta caa cag caa caa cag caa
214
Met Ser Val Leu Glu Arg Leu Lys Trp Val Gln Gln Gln Gln Gln Gln
        20              25                  30

ctg caa caa gtt gtg tcc cat agc agt aat aat tca cct gaa ctt ctt
262
Leu Gln Gln Val Val Ser His Ser Ser Asn Asn Ser Pro Glu Leu Leu
    35              40                  45

cag ata ctt cag ttc cat gga agc aac aat gat gag ttg ttg gag agt
310
Gln Ile Leu Gln Phe His Gly Ser Asn Asn Asp Glu Leu Leu Glu Ser
50              55                  60                  65

agt ttc agc caa ttt caa atg ctt gga tct ggt ttt gga cca aac tat
358
Ser Phe Ser Gln Phe Gln Met Leu Gly Ser Gly Phe Gly Pro Asn Tyr
                70                  75                  80

aac atg ggt ttt ggt cct cca cat gaa tcc att tca aga aca agt agc
406
Asn Met Gly Phe Gly Pro Pro His Glu Ser Ile Ser Arg Thr Ser Ser
                85                  90                  95

tgc cat atg gaa cct gtg gat aca atg gag gtt ttg ttg aag acc ggt
454
Cys His Met Glu Pro Val Asp Thr Met Glu Val Leu Leu Lys Thr Gly
            100                 105                 110
```

gaa gaa acc aga gcc gtt gcc ttg aag aac aag aga aaa cca gag gtt
502
Glu Glu Thr Arg Ala Val Ala Leu Lys Asn Lys Arg Lys Pro Glu Val
    115   120   125

aag aca agg gaa gag caa aag aca gag aag aag atc aaa gta gag gct
550
Lys Thr Arg Glu Glu Gln Lys Thr Glu Lys Lys Ile Lys Val Glu Ala
130   135   140   145

gag aca gag tca agc atg aaa gga aaa tca aac atg gga aac act gaa
598
Glu Thr Glu Ser Ser Met Lys Gly Lys Ser Asn Met Gly Asn Thr Glu
                150   155   160

gca tct tca gac act tca aag gag aca tcg aaa gga gct tca gag aat
646
Ala Ser Ser Asp Thr Ser Lys Glu Thr Ser Lys Gly Ala Ser Glu Asn
            165   170   175

cag aaa tta gat tat atc cac gtg aga gct cgt cga ggc caa gcc act
694
Gln Lys Leu Asp Tyr Ile His Val Arg Ala Arg Arg Gly Gln Ala Thr
        180   185   190

gac aga cac agc tta gca gaa agg gcg aga aga gaa aag atc agc aag
742
Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser Lys
    195   200   205

aaa atg aaa tat ctg caa gat att gtg cct gga tgc aat aag gtc aca
790
Lys Met Lys Tyr Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val Thr
210   215   220   225

gga aaa gct ggt atg ctt gat gag atc atc aat tat gtt caa tgt ctc
838
Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Cys Leu
                230   235   240

caa aga caa gtc gag ttc ctg tcg atg aaa ctt gct gtc ttg aac ccg
886
Gln Arg Gln Val Glu Phe Leu Ser Met Lys Leu Ala Val Leu Asn Pro
        245   250   255

gaa cta gag ctt gcc gtg gaa gat gta tcc gta aaa cag gct tac ttt
934
Glu Leu Glu Leu Ala Val Glu Asp Val Ser Val Lys Gln Ala Tyr Phe
        260   265   270

aca aat gta gtt gct tca aag caa tca ata atg gtt gat gtg cca ttg
982
Thr Asn Val Val Ala Ser Lys Gln Ser Ile Met Val Asp Val Pro Leu
    275   280   285

ttt ccg tta gac cag caa gga tct cta gat ttg tct gcg ata aac ccg
1030
Phe Pro Leu Asp Gln Gln Gly Ser Leu Asp Leu Ser Ala Ile Asn Pro
290   295   300   305

400

```
aac caa acg aca tct atc gaa gct cca tct gga agc tgg gaa act caa
1078
Asn Gln Thr Thr Ser Ile Glu Ala Pro Ser Gly Ser Trp Glu Thr Gln
                310                 315                 320
```

```
tca cag agt ctc tac aac aca tct agc ctc ggt ttt cat tac taa
1123
Ser Gln Ser Leu Tyr Asn Thr Ser Ser Leu Gly Phe His Tyr
            325                 330                 335
```

```
gcaagattca ttgaaacaac atggttgaca tcaatcaatc atcaaaatca gaagcaaatt
1183
```

```
ctattacatt tgctcatcaa agtagtaatt tcgaaatttg gttaatgcat tatcctttga
1243
```

```
tccttgtttt ctgatattta aaccagaaga actggagata gcaatccaat gatcttgtca
1303
```

```
cca
1306
```

<210> 226 <211> 335 <212> PRT <213> Arabidopsis thaliana <400>
226

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Met Leu Glu Gly Leu Val Ser Gln Glu Ser Leu Ser Leu Asn Ser Met
1               5                   10                  15
```

```
Asp Met Ser Val Leu Glu Arg Leu Lys Trp Val Gln Gln Gln Gln Gln
            20                  25                  30
```

```
Gln Leu Gln Gln Val Val Ser His Ser Ser Asn Asn Ser Pro Glu Leu
        35                  40                  45
```

```
Leu Gln Ile Leu Gln Phe His Gly Ser Asn Asn Asp Glu Leu Leu Glu
    50                  55                  60
```

```
Ser Ser Phe Ser Gln Phe Gln Met Leu Gly Ser Gly Phe Gly Pro Asn
65                  70                  75                  80
```

```
Tyr Asn Met Gly Phe Gly Pro Pro His Glu Ser Ile Ser Arg Thr Ser
                85                  90                  95
```

```
Ser Cys His Met Glu Pro Val Asp Thr Met Glu Val Leu Leu Lys Thr
            100                 105                 110
```

```
Gly Glu Glu Thr Arg Ala Val Ala Leu Lys Asn Lys Arg Lys Pro Glu
            115                 120                 125
```

```
Val Lys Thr Arg Glu Glu Gln Lys Thr Glu Lys Lys Ile Lys Val Glu
        130                 135                 140
```

```
Ala Glu Thr Glu Ser Ser Met Lys Gly Lys Ser Asn Met Gly Asn Thr
145                 150                 155                 160


Glu Ala Ser Ser Asp Thr Ser Lys Glu Thr Ser Lys Gly Ala Ser Glu
                165                 170                 175


Asn Gln Lys Leu Asp Tyr Ile His Val Arg Ala Arg Arg Gly Gln Ala
            180                 185                 190


Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser
            195                 200                 205


Lys Lys Met Lys Tyr Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val
    210                 215                 220


Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Cys
225                 230                 235                 240


Leu Gln Arg Gln Val Glu Phe Leu Ser Met Lys Leu Ala Val Leu Asn
                245                 250                 255


Pro Glu Leu Glu Leu Ala Val Glu Asp Val Ser Val Lys Gln Ala Tyr
            260                 265                 270


Phe Thr Asn Val Val Ala Ser Lys Gln Ser Ile Met Val Asp Val Pro
            275                 280                 285


Leu Phe Pro Leu Asp Gln Gln Gly Ser Leu Asp Leu Ser Ala Ile Asn
    290                 295                 300


Pro Asn Gln Thr Thr Ser Ile Glu Ala Pro Ser Gly Ser Trp Glu Thr
305                 310                 315                 320


Gln Ser Gln Ser Leu Tyr Asn Thr Ser Ser Leu Gly Phe His Tyr
                325                 330                 335


<210>  227 <211>  902 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (159)..(833) <223>  G1499

 <400>  227
tcgactcctt aattgcatca ccaacctaac ccctcatcat atgatcacct ttcttttttt
60

cctttaatat atatatatgc tcacacacac acatatatat atacatataa gcatcgcctc
120

aagcattaaa atttttacga accaaacaaa caaaaatt atg aat aat tat aat atg
176
```

```
                                              Met Asn Asn Tyr Asn Met         |
                                              1                 5

aac cca tct ctc ttc caa aat tac act tgg aac aac atc atc aac agc
224
Asn Pro Ser Leu Phe Gln Asn Tyr Thr Trp Asn Asn Ile Ile Asn Ser
            10              15                  20

agc aac aac aac aac aag aat gat gat cat cat cat caa cat aat aat
272
Ser Asn Asn Asn Asn Lys Asn Asp Asp His His His Gln His Asn Asn
        25                  30                  35

gat cca atc ggt atg gcc atg gac cag tac aca cag ctc cat atc ttc
320
Asp Pro Ile Gly Met Ala Met Asp Gln Tyr Thr Gln Leu His Ile Phe
        40                  45                  50

aat cct ttc tct tct tct cat ttc cct cct ctc tct tct tcc ctc aca
368
Asn Pro Phe Ser Ser Ser His Phe Pro Pro Leu Ser Ser Ser Leu Thr
55                  60                  65                  70

acc acc act ctt ctc tcc gga gat caa gaa gac gac gaa gac gaa gaa
416
Thr Thr Thr Leu Leu Ser Gly Asp Gln Glu Asp Asp Glu Asp Glu Glu
            75                  80                  85

gaa cct cta gag gaa ctc ggt gct atg aag gaa atg atg tac aag atc
464
Glu Pro Leu Glu Glu Leu Gly Ala Met Lys Glu Met Met Tyr Lys Ile
            90                  95                  100

gca gcc atg caa tcg gtt gac atc gac cca gca acc gtc aag aaa ccc
512
Ala Ala Met Gln Ser Val Asp Ile Asp Pro Ala Thr Val Lys Lys Pro
        105                 110                 115

aaa cgc cgt aac gtg agg atc tcc gac gac cct cag agt gtg gcg gct
560
Lys Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Ser Val Ala Ala
        120                 125                 130

aga cat cgc cgt gag aga atc agt gag agg atc aga att ctt cag aga
608
Arg His Arg Arg Glu Arg Ile Ser Glu Arg Ile Arg Ile Leu Gln Arg
135                 140                 145                 150

ctc gtg cca ggt ggc act aaa atg gat acg gct tca atg ctc gat gaa
656
Leu Val Pro Gly Gly Thr Lys Met Asp Thr Ala Ser Met Leu Asp Glu
                155                 160                 165

gct ata cgc tat gtc aag ttc ttg aaa cgg cag atc cgg cta ctc aat
704
Ala Ile Arg Tyr Val Lys Phe Leu Lys Arg Gln Ile Arg Leu Leu Asn
            170                 175                 180

aat aat acc gga tat act cct ccg ccg ccg caa gat caa gct tct cag
752
Asn Asn Thr Gly Tyr Thr Pro Pro Pro Pro Gln Asp Gln Ala Ser Gln
```

```
        185                    190                    195

gcg gtg acg acg tca tgg gtt tca ccg cca cca ccg cca agt ttc ggc
800
Ala Val Thr Thr Ser Trp Val Ser Pro Pro Pro Pro Pro Ser Phe Gly
    200                    205                    210


cgt ggg gga aga gga gta gga gaa tta atc tag acaagatgac atttccatta
853
Arg Gly Gly Arg Gly Val Gly Glu Leu Ile
215                    220


gtagtaacta aattatgcta taatgtgtga gtaatggtgc aattatgga
902


<210>  228 <211>  224 <212>  PRT <213>  Arabidopsis thaliana  <400>
228

Met Asn Asn Tyr Asn Met Asn Pro Ser Leu Phe Gln Asn Tyr Thr Trp
1               5                   10                  15


Asn Asn Ile Ile Asn Ser Ser Asn Asn Asn Asn Lys Asn Asp Asp His
            20                  25                  30


His His Gln His Asn Asn Asp Pro Ile Gly Met Ala Met Asp Gln Tyr
        35                  40                  45


Thr Gln Leu His Ile Phe Asn Pro Phe Ser Ser Ser His Phe Pro Pro
    50                  55                  60


Leu Ser Ser Ser Leu Thr Thr Thr Thr Leu Leu Ser Gly Asp Gln Glu
65                  70                  75                  80


Asp Asp Glu Asp Glu Glu Glu Pro Leu Glu Glu Leu Gly Ala Met Lys
            85                  90                  95


Glu Met Met Tyr Lys Ile Ala Ala Met Gln Ser Val Asp Ile Asp Pro
        100                 105                 110


Ala Thr Val Lys Lys Pro Lys Arg Arg Asn Val Arg Ile Ser Asp Asp
        115                 120                 125


Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile Ser Glu Arg
    130                 135                 140


Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys Met Asp Thr
145                 150                 155                 160


Ala Ser Met Leu Asp Glu Ala Ile Arg Tyr Val Lys Phe Leu Lys Arg
                165                 170                 175
```

404

```
Gln Ile Arg Leu Leu Asn Asn Asn Thr Gly Tyr Thr Pro Pro Pro Pro
        180             185             190
```

```
Gln Asp Gln Ala Ser Gln Ala Val Thr Thr Ser Trp Val Ser Pro Pro
        195             200             205
```

```
Pro Pro Pro Ser Phe Gly Arg Gly Gly Arg Gly Val Gly Glu Leu Ile
    210             215             220
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<210> 229 <211> 1233 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1233) <223> G1514

<400> 229

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atg gcc gaa act atg aaa gat att acg atg aag aac gat gaa tca cag
48
Met Ala Glu Thr Met Lys Asp Ile Thr Met Lys Asn Asp Glu Ser Gln
1               5               10              15
```

```
gaa gaa gaa atc ccc gat caa ttt ctc tgc tgc gtt tgc ctg gaa ctt
96
Glu Glu Glu Ile Pro Asp Gln Phe Leu Cys Cys Val Cys Leu Glu Leu
            20              25              30
```

```
ctt tac aag cca att gtg tta tct tgt ggt cat cta tca tgt ttt tgg
144
Leu Tyr Lys Pro Ile Val Leu Ser Cys Gly His Leu Ser Cys Phe Trp
        35              40              45
```

```
tgc gta cat aag tcc atg aat ggc ttt cgt gag tct cat tgt ccg ata
192
Cys Val His Lys Ser Met Asn Gly Phe Arg Glu Ser His Cys Pro Ile
        50              55              60
```

```
tgt aga gac ccg tat gtt cac ttt ccc tct gtg tgc cag aag ctt tat
240
Cys Arg Asp Pro Tyr Val His Phe Pro Ser Val Cys Gln Lys Leu Tyr
65              70              75              80
```

```
ttt ctg tta aag aag atg tac cca ctt gct cat aag aag aga gaa gaa
288
Phe Leu Leu Lys Lys Met Tyr Pro Leu Ala His Lys Lys Arg Glu Glu
            85              90              95
```

```
caa gtt tta aag gaa gag caa gaa cga gaa tgt ttt tct cct cag att
336
Gln Val Leu Lys Glu Glu Gln Glu Arg Glu Cys Phe Ser Pro Gln Ile
            100             105             110
```

```
gat ctt gtt ttg gat ttg tct gtg tgt agt gga gat tct ctc aat gtc
384
Asp Leu Val Leu Asp Leu Ser Val Cys Ser Gly Asp Ser Leu Asn Val
        115             120             125
```

```
tct gat aaa cag aag gtg gaa gag tgt tcg aat gca gcg aac tta tta
432
Ser Asp Lys Gln Lys Val Glu Glu Cys Ser Asn Ala Ala Asn Leu Leu
```

          130   135   140

tct agt tca tca agt aga ggt gac att cca tgt atc ccc aaa aat caa
480
Ser Ser Ser Ser Ser Arg Gly Asp Ile Pro Cys Ile Pro Lys Asn Gln
145 ·   150   155   160

gaa ccc aca gat gca aaa gct ctt aat gtt cat gaa aat gaa tta ctt
528
Glu Pro Thr Asp Ala Lys Ala Leu Asn Val His Glu Asn Glu Leu Leu
                    165   170   175

aag gat aac aaa gtc agt aag cag att tcg aaa gat gat ttg ctc tgt
576
Lys Asp Asn Lys Val Ser Lys Gln Ile Ser Lys Asp Asp Leu Leu Cys
                    180   185   190

tca gca tgt aag gag ctg ctt gta cga ccc gta gtt ctc aat tgc gga
624
Ser Ala Cys Lys Glu Leu Leu Val Arg Pro Val Val Leu Asn Cys Gly
                195   200   205

cat gtg tat tgt gaa gga tgt gta gta gat atg gct gaa gaa agc gaa
672
His Val Tyr Cys Glu Gly Cys Val Val Asp Met Ala Glu Glu Ser Glu
        210   215   220

aag atc aaa tgt caa gag tgt aat gtt tgt gac cca aga gga ttt cca
720
Lys Ile Lys Cys Gln Glu Cys Asn Val Cys Asp Pro Arg Gly Phe Pro
225   230   235   240

aaa gtt tgt ttg att ctt gaa cag ctt ttg gag gaa aac ttt cct gaa
768
Lys Val Cys Leu Ile Leu Glu Gln Leu Leu Glu Glu Asn Phe Pro Glu
                    245   250   255

gaa tac aat tca aga agc agt aag gtt cag aaa acg ctc gcc cat aat
816
Glu Tyr Asn Ser Arg Ser Ser Lys Val Gln Lys Thr Leu Ala His Asn
                260   265   270

agc aaa gga aat att caa agc tat ctc aaa gaa ggc ccg tcc tta tca
864
Ser Lys Gly Asn Ile Gln Ser Tyr Leu Lys Glu Gly Pro Ser Leu Ser
            275   280   285

aac gac aat aac aat gat gat ccc tgg ttg gca aac cct gga tca aat
912
Asn Asp Asn Asn Asn Asp Asp Pro Trp Leu Ala Asn Pro Gly Ser Asn
        290   295   300

gtt cac ttt gga gct ggt tgt gat tct tgt ggg gtg tat cca atc ata
960
Val His Phe Gly Ala Gly Cys Asp Ser Cys Gly Val Tyr Pro Ile Ile
305   310   315   320

ggg gat cga tac aga tgc aaa gac tgc aag gag gaa att ggg tat gac
1008
Gly Asp Arg Tyr Arg Cys Lys Asp Cys Lys Glu Glu Ile Gly Tyr Asp
                325   330 .   335

406

ctt tgc aaa gac tgt tac gag act cct tcg aaa gtt cca ggg aga ttc
1056
Leu Cys Lys Asp Cys Tyr Glu Thr Pro Ser Lys Val Pro Gly Arg Phe
        340   345   350

aac cag caa cac act cct gac cac agg ctt gag ctt gca cgg tct cct
1104
Asn Gln Gln His Thr Pro Asp His Arg Leu Glu Leu Ala Arg Ser Pro
        355   360   365

cag gtt ctg atc aat ttc aat tct atc ggt atc ctt ctc gga ccc gtt
1152
Gln Val Leu Ile Asn Phe Asn Ser Ile Gly Ile Leu Leu Gly Pro Val
    370   375   380   .

atc tca aat gaa ggc atg gat aca gat gaa ggc gag gaa ggg cct cct
1200
Ile Ser Asn Glu Gly Met Asp Thr Asp Glu Gly Glu Glu Gly Pro Pro
385   390   395   400

ggt tct tct aat gag tca tca agc aca gaa tga
1233
Gly Ser Ser Asn Glu Ser Ser Ser Thr Glu
                405   410

<210> 230 <211> 410 <212> PRT <213> Arabidopsis thaliana <400>
230

Met Ala Glu Thr Met Lys Asp Ile Thr Met Lys Asn Asp Glu Ser Gln
1   5   10   15

Glu Glu Glu Ile Pro Asp Gln Phe Leu Cys Cys Val Cys Leu Glu Leu
            20   25   30   .

Leu Tyr Lys Pro Ile Val Leu Ser Cys Gly His Leu Ser Cys Phe Trp
        35   40   . 45

Cys Val His Lys Ser Met Asn Gly Phe Arg Glu Ser His Cys Pro Ile
    50   55   60

Cys Arg Asp Pro Tyr Val His Phe Pro Ser Val Cys Gln Lys Leu Tyr
65   70   75   80

Phe Leu Leu Lys Lys Met Tyr Pro Leu Ala His Lys Lys Arg Glu Glu
                85   90   95

Gln Val Leu Lys Glu Glu Gln Glu Arg Glu Cys Phe Ser Pro Gln Ile
                100   105   110

Asp Leu Val Leu Asp Leu Ser Val Cys Ser Gly Asp Ser Leu Asn Val
            115   120   125

407

Ser Asp Lys Gln Lys Val Glu Glu Cys Ser Asn Ala Ala Asn Leu Leu
    130   135   140

Ser Ser Ser Ser Ser Arg Gly Asp Ile Pro Cys Ile Pro Lys Asn Gln
145   150   155   160

Glu Pro Thr Asp Ala Lys Ala Leu Asn Val His Glu Asn Glu Leu Leu
                165   170   175

Lys Asp Asn Lys Val Ser Lys Gln Ile Ser Lys Asp Asp Leu Leu Cys
            180   185   190

Ser Ala Cys Lys Glu Leu Leu Val Arg Pro Val Val Leu Asn Cys Gly
        195   200   205

His Val Tyr Cys Glu Gly Cys Val Val Asp Met Ala Glu Glu Ser Glu
    210   215   220

Lys Ile Lys Cys Gln Glu Cys Asn Val Cys Asp Pro Arg Gly Phe Pro
225   230   235   240

Lys Val Cys Leu Ile Leu Glu Gln Leu Leu Glu Glu Asn Phe Pro Glu
            245   250   255

Glu Tyr Asn Ser Arg Ser Ser Lys Val Gln Lys Thr Leu Ala His Asn
            260   265   270

Ser Lys Gly Asn Ile Gln Ser Tyr Leu Lys Glu Gly Pro Ser Leu Ser
        275   280   285

Asn Asp Asn Asn Asn Asp Asp Pro Trp Leu Ala Asn Pro Gly Ser Asn
    290   295   300

Val His Phe Gly Ala Gly Cys Asp Ser Cys Gly Val Tyr Pro Ile Ile
305   310   315   320

Gly Asp Arg Tyr Arg Cys Lys Asp Cys Lys Glu Glu Ile Gly Tyr Asp
            325   330   335

Leu Cys Lys Asp Cys Tyr Glu Thr Pro Ser Lys Val Pro Gly Arg Phe
        340   345   350

Asn Gln Gln His Thr Pro Asp His Arg Leu Glu Leu Ala Arg Ser Pro
    355   360   365

```
Gln Val Leu Ile Asn Phe Asn Ser Ile Gly Ile Leu Leu Gly Pro Val
    370                 375                 380


Ile Ser Asn Glu Gly Met Asp Thr Asp Glu Gly Glu Glu Gly Pro Pro
385                 390                 395                 400


Gly Ser Ser Asn Glu Ser Ser Ser Thr Glu
                405                 410
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<210> 231 <211> 1146 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1146) <223> G1519

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 <400>  231
atg agg ctt aat ggg gat tcg ggt ccg ggt cag gat gaa ccc ggt tcg
48
Met Arg Leu Asn Gly Asp Ser Gly Pro Gly Gln Asp Glu Pro Gly Ser
1               5                   10                  15

agc ggg ttt cac ggc gga atc aga cga ttc ccg tta gca gct cag ccg
96
Ser Gly Phe His Gly Gly Ile Arg Arg Phe Pro Leu Ala Ala Gln Pro
            20                  25                  30

gag att atg aga gct gct gag aaa gac gat caa tac gct tct ttc atc
144
Glu Ile Met Arg Ala Ala Glu Lys Asp Asp Gln Tyr Ala Ser Phe Ile
        35                  40                  45

cac gaa gct tgc cgc gat gcc ttc cga cac ctt ttc ggt aca aga atc
192
His Glu Ala Cys Arg Asp Ala Phe Arg His Leu Phe Gly Thr Arg Ile
    50                  55                  60

gct ctt gct tac cag aag gag atg aag cta ctt gga cag atg ctt tac
240
Ala Leu Ala Tyr Gln Lys Glu Met Lys Leu Leu Gly Gln Met Leu Tyr
65                  70                  75                  80

tat gtt ctt acg aca ggt tca ggg caa caa act tta gga gag gaa tat
288
Tyr Val Leu Thr Thr Gly Ser Gly Gln Gln Thr Leu Gly Glu Glu Tyr
                85                  90                  95

tgt gac att ata cag gtt gca ggg cct tat gga ctc tct cct aca cca
336
Cys Asp Ile Ile Gln Val Ala Gly Pro Tyr Gly Leu Ser Pro Thr Pro
                100                 105                 110

gct aga cgt gct ttg ttc ata ttg tac cag acc gca gtt cca tat atc
384
Ala Arg Arg Ala Leu Phe Ile Leu Tyr Gln Thr Ala Val Pro Tyr Ile
            115                 120                 125

gca gag aga att agc act cga gct gct acg caa gca gtc acc ttt gat
432
Ala Glu Arg Ile Ser Thr Arg Ala Ala Thr Gln Ala Val Thr Phe Asp
        130                 135                 140
```

409

gag tct gat gag ttt ttt ggt gat agt cat atc cac tca cca aga atg
480
Glu Ser Asp Glu Phe Phe Gly Asp Ser His Ile His Ser Pro Arg Met
145   150   155   160

ata gat ctt cca tct tca tct caa gtt gaa act tca act tct gta gta
528
Ile Asp Leu Pro Ser Ser Ser Gln Val Glu Thr Ser Thr Ser Val Val
                    165   170   175

tct agg tta aac gat aga ctt atg aga tcg tgg cac cga gct att cag
576
Ser Arg Leu Asn Asp Arg Leu Met Arg Ser Trp His Arg Ala Ile Gln
                180   185   190

cga tgg cct gtg gtt ctt cct gtt gcc cgc gaa gtc tta caa ctg gtt
624
Arg Trp Pro Val Val Leu Pro Val Ala Arg Glu Val Leu Gln Leu Val
                195   200   205

ttg cgt gcc aat ctg atg ctc ttc tac ttt gaa ggt ttt tat tat cat
672
Leu Arg Ala Asn Leu Met Leu Phe Tyr Phe Glu Gly Phe Tyr Tyr His
        210   215   220

ata tcg aaa cgt gca tcc ggg gtt cgt tat gtt ttc ata gga aag caa
720
Ile Ser Lys Arg Ala Ser Gly Val Arg Tyr Val Phe Ile Gly Lys Gln
225   230   235   240

ctg aat cag aga cct aga tac caa att ctt ggg gtt ttc ctt cta atc
768
Leu Asn Gln Arg Pro Arg Tyr Gln Ile Leu Gly Val Phe Leu Leu Ile
                245   250   255

caa ttg tgc atc ctt gct gct gag ggc ttg cgt cgg agt aat ttg tca
816
Gln Leu Cys Ile Leu Ala Ala Glu Gly Leu Arg Arg Ser Asn Leu Ser
                260   265   270

tct atc act agc tcc att cag cag gct tct ata gga tct tat caa act
864
Ser Ile Thr Ser Ser Ile Gln Gln Ala Ser Ile Gly Ser Tyr Gln Thr
        275   280   285

tca gga ggg aga ggt tta cct gtt tta aat gaa gag ggg aat ttg ata
912
Ser Gly Gly Arg Gly Leu Pro Val Leu Asn Glu Glu Gly Asn Leu Ile
    290   295   300

act tcg gaa gct gaa aag gga aac tgg tct acc tcc gat tca act tca
960
Thr Ser Glu Ala Glu Lys Gly Asn Trp Ser Thr Ser Asp Ser Thr Ser
305   310   315   320

acg gag gca gta ggg aaa tgc act ctc tgc tta agc acc cgt cag cac
1008
Thr Glu Ala Val Gly Lys Cys Thr Leu Cys Leu Ser Thr Arg Gln His
                325   330   335

cca acg gcc act cct tgt ggt cat gtg ttt tgt tgg agc tgc att atg
1056
Pro Thr Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met
        340   345   350

gaa tgg tgc aac gag aag caa gaa tgc cct ctt tgt cga acg ccc aat
1104
Glu Trp Cys Asn Glu Lys Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn
        355   360   365

acc cat tca agt ttg gtt tgt ttg tat cat tct gat ttt tag
1146
Thr His Ser Ser Leu Val Cys Leu Tyr His Ser Asp Phe
    370   375   380

<210> 232 <211> 381 <212> PRT <213> Arabidopsis thaliana <400>
232

Met Arg Leu Asn Gly Asp Ser Gly Pro Gly Gln Asp Glu Pro Gly Ser
1   5   10   15

Ser Gly Phe His Gly Gly Ile Arg Arg Phe Pro Leu Ala Ala Gln Pro
            20   25   30

Glu Ile Met Arg Ala Ala Glu Lys Asp Asp Gln Tyr Ala Ser Phe Ile
        35   40   45

His Glu Ala Cys Arg Asp Ala Phe Arg His Leu Phe Gly Thr Arg Ile
    50   55   60

Ala Leu Ala Tyr Gln Lys Glu Met Lys Leu Leu Gly Gln Met Leu Tyr
65   70   75   80

Tyr Val Leu Thr Thr Gly Ser Gly Gln Gln Thr Leu Gly Glu Glu Tyr
            85   90   95

Cys Asp Ile Ile Gln Val Ala Gly Pro Tyr Gly Leu Ser Pro Thr Pro
            100   105   110

Ala Arg Arg Ala Leu Phe Ile Leu Tyr Gln Thr Ala Val Pro Tyr Ile
        115   120   125

Ala Glu Arg Ile Ser Thr Arg Ala Ala Thr Gln Ala Val Thr Phe Asp
    130   135   140

Glu Ser Asp Glu Phe Phe Gly Asp Ser His Ile His Ser Pro Arg Met
145   150   155   160

Ile Asp Leu Pro Ser Ser Ser Gln Val Glu Thr Ser Thr Ser Val Val
            165   170   175

411

```
Ser Arg Leu Asn Asp Arg Leu Met Arg Ser Trp His Arg Ala Ile Gln
            180                 185                 190


Arg Trp Pro Val Val Leu Pro Val Ala Arg Glu Val Leu Gln Leu Val
            195             200                 205


Leu Arg Ala Asn Leu Met Leu Phe Tyr Phe Glu Gly Phe Tyr Tyr His
    210                 215                 220


Ile Ser Lys Arg Ala Ser Gly Val Arg Tyr Val Phe Ile Gly Lys Gln
225             230                 235                 240


Leu Asn Gln Arg Pro Arg Tyr Gln Ile Leu Gly Val Phe Leu Leu Ile
                245                 250                 255


Gln Leu Cys Ile Leu Ala Ala Glu Gly Leu Arg Arg Ser Asn Leu Ser
            260                 265                 270


Ser Ile Thr Ser Ser Ile Gln Gln Ala Ser Ile Gly Ser Tyr Gln Thr
            275                 280                 285


Ser Gly Gly Arg Gly Leu Pro Val Leu Asn Glu Glu Gly Asn Leu Ile
    290                 295                 300


Thr Ser Glu Ala Glu Lys Gly Asn Trp Ser Thr Ser Asp Ser Thr Ser
305                 310                 315                 320


Thr Glu Ala Val Gly Lys Cys Thr Leu Cys Leu Ser Thr Arg Gln His
                325                 330                 335


Pro Thr Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met
            340                 345                 350


Glu Trp Cys Asn Glu Lys Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn
        355                 360                 365


Thr His Ser Ser Leu Val Cys Leu Tyr His Ser Asp Phe
    370                 375                 380
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<210> 233 <211> 891 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(891) <223> G1521

<400> 233
atg cct cca tta ccg tcc tcc acg gcg cct tcg tct tcg aga cat ctt
48
Met Pro Pro Leu Pro Ser Ser Thr Ala Pro Ser Ser Ser Arg His Leu

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1                 5                        10                       15

cga tcg ccg gaa agt atc gcg aaa ttt gca ggg aga gca ata ttt cct
96
Arg Ser Pro Glu Ser Ile Ala Lys Phe Ala Gly Arg Ala Ile Phe Pro
          20                  25                  30

gct tta cag ggg aaa tcg tgt ccg ata tgc ctc gaa aat cta acc gag
144
Ala Leu Gln Gly Lys Ser Cys Pro Ile Cys Leu Glu Asn Leu Thr Glu
          35                  40                  45

cga aga tcc gcc gcc gtg atc acg gtg tgc aag cac gga tac tgc ctt
192
Arg Arg Ser Ala Ala Val Ile Thr Val Cys Lys His Gly Tyr Cys Leu
          50                  55                  60

gct tgt att cgg aag tgg agc agc ttc aag agg aat tgt cct ctt tgt
240
Ala Cys Ile Arg Lys Trp Ser Ser Phe Lys Arg Asn Cys Pro Leu Cys
65                  70                  75                  80

aac act cgt ttt gat tcc tgg ttt atc gtt agt gat ttt gct tct aga
288
Asn Thr Arg Phe Asp Ser Trp Phe Ile Val Ser Asp Phe Ala Ser Arg
                85                  90                  95

aaa tac cat aag gag caa tta cca att ctt cgt gat cgt gag act tta
336
Lys Tyr His Lys Glu Gln Leu Pro Ile Leu Arg Asp Arg Glu Thr Leu
          100                 105                 110

act tat cat cgg aat aat cct tcc gat cgc cgg agg ata att caa agg
384
Thr Tyr His Arg Asn Asn Pro Ser Asp Arg Arg Arg Ile Ile Gln Arg
          115                 120                 125

tcg agg gat gtt ttg gaa aac tct agc tca aga tca agg cca ttg cca
432
Ser Arg Asp Val Leu Glu Asn Ser Ser Ser Arg Ser Arg Pro Leu Pro
    130                 135                 140

tgg cgg aga tca ttt gga cga cca ggt tca gtt cct gat tct gtt atc
480
Trp Arg Arg Ser Phe Gly Arg Pro Gly Ser Val Pro Asp Ser Val Ile
145                 150                 155                 160

ttc cag cga aag ctt cag tgg cga gct agc ata tac act aag caa tta
528
Phe Gln Arg Lys Leu Gln Trp Arg Ala Ser Ile Tyr Thr Lys Gln Leu
                165                 170                 175

cga gct gtt cga tta cat tca agg cgc ttg gaa cta agt ttg gcg gtg
576
Arg Ala Val Arg Leu His Ser Arg Arg Leu Glu Leu Ser Leu Ala Val
          180                 185                 190

aat gat tac acc aaa gca aag ata act gaa aga att gag cca tgg att
624
Asn Asp Tyr Thr Lys Ala Lys Ile Thr Glu Arg Ile Glu Pro Trp Ile
          195                 200                 205
```

```
aga aga gag ctt cag gca gtc ctt gga gat cct gat ccc tca gtt att
672
Arg Arg Glu Leu Gln Ala Val Leu Gly Asp Pro Asp Pro Ser Val Ile
    210                 215                 220

gtt cat ttt gcg tca gct ctt ttc atc aaa agg ctt gag aga gag aat
720
Val His Phe Ala Ser Ala Leu Phe Ile Lys Arg Leu Glu Arg Glu Asn
225                 230                 235                 240

aat cga caa acc ggg cag acc ggg atg ttg gtg gaa gat gaa gtc tcc
768
Asn Arg Gln Thr Gly Gln Thr Gly Met Leu Val Glu Asp Glu Val Ser
                245                 250                 255

tct ctt cga aaa ttc ttg tct gat aag gtg gat ata ttt tgg cat gaa
816
Ser Leu Arg Lys Phe Leu Ser Asp Lys Val Asp Ile Phe Trp His Glu
            260                 265                 270

cta aga tgt ttt gcg gag agt ata ctc acg atg gag act tat gat gca
864
Leu Arg Cys Phe Ala Glu Ser Ile Leu Thr Met Glu Thr Tyr Asp Ala
        275                 280                 285

gtg gtt gaa tac aat gag gtg gag taa
891
Val Val Glu Tyr Asn Glu Val Glu
    290                 295


<210>  234 <211>  296 <212>  PRT <213>  Arabidopsis thaliana  <400>
234

Met Pro Pro Leu Pro Ser Ser Thr Ala Pro Ser Ser Ser Arg His Leu
1               5               10                  15


Arg Ser Pro Glu Ser Ile Ala Lys Phe Ala Gly Arg Ala Ile Phe Pro
            20              25                  30


Ala Leu Gln Gly Lys Ser Cys Pro Ile Cys Leu Glu Asn Leu Thr Glu
            35              40                  45


Arg Arg Ser Ala Ala Val Ile Thr Val Cys Lys His Gly Tyr Cys Leu
    50              55                  60


Ala Cys Ile Arg Lys Trp Ser Ser Phe Lys Arg Asn Cys Pro Leu Cys
65              70                  75                  80


Asn Thr Arg Phe Asp Ser Trp Phe Ile Val Ser Asp Phe Ala Ser Arg
                85              90                  95


Lys Tyr His Lys Glu Gln Leu Pro Ile Leu Arg Asp Arg Glu Thr Leu
            100                 105                 110
```

414

Thr Tyr His Arg Asn Asn Pro Ser Asp Arg Arg Arg Ile Ile Gln Arg
        115   120   125

Ser Arg Asp Val Leu Glu Asn Ser Ser Ser Arg Ser Arg Pro Leu Pro
    130   135   140

Trp Arg Arg Ser Phe Gly Arg Pro Gly Ser Val Pro Asp Ser Val Ile
145   150   155   160

Phe Gln Arg Lys Leu Gln Trp Arg Ala Ser Ile Tyr Thr Lys Gln Leu
            165   170   175

Arg Ala Val Arg Leu His Ser Arg Arg Leu Glu Leu Ser Leu Ala Val
        180   185   190

Asn Asp Tyr Thr Lys Ala Lys Ile Thr Glu Arg Ile Glu Pro Trp Ile
        195   200   205

Arg Arg Glu Leu Gln Ala Val Leu Gly Asp Pro Asp Pro Ser Val Ile
    210   215   220

Val His Phe Ala Ser Ala Leu Phe Ile Lys Arg Leu Glu Arg Glu Asn
225   230   235   240

Asn Arg Gln Thr Gly Gln Thr Gly Met Leu Val Glu Asp Glu Val Ser
            245   250   255

Ser Leu Arg Lys Phe Leu Ser Asp Lys Val Asp Ile Phe Trp His Glu
            260   265   270

Leu Arg Cys Phe Ala Glu Ser Ile Leu Thr Met Glu Thr Tyr Asp Ala
        275   280   285

Val Val Glu Tyr Asn Glu Val Glu
    290   295

<210> 235 <211> 3090 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(3090) <223> G1526

 <400> 235
atg gga acg aaa gtc tca gac gat ctt gtt tcc acc gtc aga tca gtc
48
Met Gly Thr Lys Val Ser Asp Asp Leu Val Ser Thr Val Arg Ser Val
1   5   10   15

gtg ggt tcc gat tac tca gat atg gat ata atc agg gct tta cac atg
96

415

```
Val Gly Ser Asp Tyr Ser Asp Met Asp Ile Ile Arg Ala Leu His Met
            20                  25                  30

gcg aat cat gat cca acg gct gct atc aat ata atc ttc gac act cca
144
Ala Asn His Asp Pro Thr Ala Ala Ile Asn Ile Ile Phe Asp Thr Pro
            35                  40                  45

agt ttc gcc aaa cct gat gta gcc act cct acc ccg agc ggc tct aat
192
Ser Phe Ala Lys Pro Asp Val Ala Thr Pro Thr Pro Ser Gly Ser Asn
    50                  55                  60

gga ggg aag cga gtt gat agt gga tta aag ggc tgt act ttt ggt gac
240
Gly Gly Lys Arg Val Asp Ser Gly Leu Lys Gly Cys Thr Phe Gly Asp
65                  70                  75                  80

agc gga agt gtt gga gcg aat cat cgc gtg gag gaa gaa aat gag agt
288
Ser Gly Ser Val Gly Ala Asn His Arg Val Glu Glu Glu Asn Glu Ser
                85                  90                  95

gtt aat ggt gga gga gaa gag agt gtt tca ggg aat gag tgg tgg ttt
336
Val Asn Gly Gly Gly Glu Glu Ser Val Ser Gly Asn Glu Trp Trp Phe
            100                 105                 110

gtt ggt tgt tct gaa ttg gct ggg tta tcg aca tgt aaa gga agg aaa
384
Val Gly Cys Ser Glu Leu Ala Gly Leu Ser Thr Cys Lys Gly Arg Lys
            115                 120                 125

ttg aag tct ggt gat gaa ttg gtg ttc acg ttt ccg cat agt aaa gga
432
Leu Lys Ser Gly Asp Glu Leu Val Phe Thr Phe Pro His Ser Lys Gly
    130                 135                 140

tta aag cct gag act acg cct ggg aag cgc ggt ttt ggg cgg gga agg
480
Leu Lys Pro Glu Thr Thr Pro Gly Lys Arg Gly Phe Gly Arg Gly Arg
145                 150                 155                 160

cca gct ttg cgt ggt gct tct gat atc gtt agg ttc tct aca aag gat
528
Pro Ala Leu Arg Gly Ala Ser Asp Ile Val Arg Phe Ser Thr Lys Asp
                165                 170                 175

tca gga gag att ggt aga ata cca aac gag tgg gct cgg tgt ctt cta
576
Ser Gly Glu Ile Gly Arg Ile Pro Asn Glu Trp Ala Arg Cys Leu Leu
            180                 185                 190

cca ctt gtg aga gac aag aaa att agg ata gaa ggc agt tgc aag tcg
624
Pro Leu Val Arg Asp Lys Lys Ile Arg Ile Glu Gly Ser Cys Lys Ser
            195                 200                 205

gcg cct gaa gct ttg agc atc atg gat aca att ctt ctg tct gta agc
672
Ala Pro Glu Ala Leu Ser Ile Met Asp Thr Ile Leu Leu Ser Val Ser
```

416

```
       210                    215                    220

gtg tac att aat agt tcc atg ttt caa aag cat agt gcg act tca ttt
720
Val Tyr Ile Asn Ser Ser Met Phe Gln Lys His Ser Ala Thr Ser Phe
225                 230                 235                 240

aag aca gct agt aat acg gca gag gaa tca atg ttc cat cct ctc cca
768
Lys Thr Ala Ser Asn Thr Ala Glu Glu Ser Met Phe His Pro Leu Pro
                245                 250                 255

aat ctc ttt cgg tta ctc ggt ttg atc ccc ttt aag aag gca gag ttt
816
Asn Leu Phe Arg Leu Leu Gly Leu Ile Pro Phe Lys Lys Ala Glu Phe
            260                 265                 270

act cca gag gat ttt tac tct aag aag cga cct ttg agt tcc aag gat
864
Thr Pro Glu Asp Phe Tyr Ser Lys Lys Arg Pro Leu Ser Ser Lys Asp
            275                 280                 285

ggt tct gct att cct act tcg ttg ctt caa tta aac aag gtc aag aat
912
Gly Ser Ala Ile Pro Thr Ser Leu Leu Gln Leu Asn Lys Val Lys Asn
        290                 295                 300

atg aat caa gat gca aac gga gat gaa aat gag cag tgt atc agc gat
960                      '
Met Asn Gln Asp Ala Asn Gly Asp Glu Asn Glu Gln Cys Ile Ser Asp
305                 310                 315                 320

ggt gat ctt gat aac att gtt ggt gtt ggg gac agt tct gga tta aag
1008     .
Gly Asp Leu Asp Asn Ile Val Gly Val Gly Asp Ser Ser Gly Leu Lys
                325                 330                 335

gaa atg gaa act cca cat aca ctt ctg tgt gag ctt cgt cca tac caa
1056
Glu Met Glu Thr Pro His Thr Leu Leu Cys Glu Leu Arg Pro Tyr Gln
            340                 345                 350

aag cag gca ctt cat tgg atg acc caa ctg gag aaa gga aat tgc act
1104
Lys Gln Ala Leu His Trp Met Thr Gln Leu Glu Lys Gly Asn Cys Thr
            355                 360                 365

gat gag gca gca aca atg ctt cac ccg tgt tgg gaa gca tac tgt tta
1152
Asp Glu Ala Ala Thr Met Leu His Pro Cys Trp Glu Ala Tyr Cys Leu
        370                 375                 380

gca gac aag agg gaa ctg gtt gtc tac ctg aat tct ttt act ggt gat
1200
Ala Asp Lys Arg Glu Leu Val Val Tyr Leu Asn Ser Phe Thr Gly Asp
385                 390                 395                 400

gct aca ata cac ttc cct agc aca ctt caa atg gca aga gga gga ata
1248
Ala Thr Ile His Phe Pro Ser Thr Leu Gln Met Ala Arg Gly Gly Ile
                405                 410                 415
```

417

```
tta gca gac gca atg ggt ctt gga aag act gta atg acc ata tcc ctt
1296
Leu Ala Asp Ala Met Gly Leu Gly Lys Thr Val Met Thr Ile Ser Leu
        420             425             430

ttg ctt gcc cat tct tgg aaa gct gca tca act ggg ttt cta tgc ccc
1344
Leu Leu Ala His Ser Trp Lys Ala Ala Ser Thr Gly Phe Leu Cys Pro
        435             440             445

aac tat gaa gga gac aaa gtg atc agc agt tct gta gat gat ctc act
1392
Asn Tyr Glu Gly Asp Lys Val Ile Ser Ser Ser Val Asp Asp Leu Thr
    450             455             460

agt ccc ccg gtg aag gca acc aaa ttt cta ggc ttt gat aag agg ctt
1440
Ser Pro Pro Val Lys Ala Thr Lys Phe Leu Gly Phe Asp Lys Arg Leu
465             470             475             480

ctt gaa caa aaa agt gta ctt caa aat ggt ggt aac ctg att gta tgt
1488
Leu Glu Gln Lys Ser Val Leu Gln Asn Gly Gly Asn Leu Ile Val Cys
            485             490             495

ccg atg aca ctt tta gga cag tgg aag aca gag att gaa atg cat gca
1536
Pro Met Thr Leu Leu Gly Gln Trp Lys Thr Glu Ile Glu Met His Ala
        500             505             510

aag cct ggg tct cta tct gtc tat gtt cac tat ggg caa agc agg ccg
1584
Lys Pro Gly Ser Leu Ser Val Tyr Val His Tyr Gly Gln Ser Arg Pro
        515             520             525

aag gat gca aaa ctt ctt tcc cag agt gat gtg gta atc acc aca tat
1632
Lys Asp Ala Lys Leu Leu Ser Gln Ser Asp Val Val Ile Thr Thr Tyr
    530             535             540

gga gtt cta aca tcc gaa ttc tcg caa gag aac tca gca gac cat gaa
1680
Gly Val Leu Thr Ser Glu Phe Ser Gln Glu Asn Ser Ala Asp His Glu
545             550             555             560

gga att tat gca gtt cga tgg ttt agg att gtt ctt gac gag gca cat
1728
Gly Ile Tyr Ala Val Arg Trp Phe Arg Ile Val Leu Asp Glu Ala His
            565             570             575

acc atc aaa aac tca aaa agc caa att tcc ttg gct gct gca gct ctg
1776
Thr Ile Lys Asn Ser Lys Ser Gln Ile Ser Leu Ala Ala Ala Ala Leu
            580             585             590

gtt gct gat agg cgt tgg tgt ctt acg ggt act cct att cag aac aat
1824
Val Ala Asp Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Gln Asn Asn
        595             600             605
```

418

ctg gag gat tta tac agc ctt cta cgg ttt ttg agg att gaa cca tgg
1872
Leu Glu Asp Leu Tyr Ser Leu Leu Arg Phe Leu Arg Ile Glu Pro Trp
    610   615   620

gga act tgg gca tgg tgg aat aaa ctt gtc caa aag cca ttt gaa gag
1920
Gly Thr Trp Ala Trp Trp Asn Lys Leu Val Gln Lys Pro Phe Glu Glu
625   630   635   640

ggt gat gag aga ggg tta aag cta gtg cag tct atc tta aaa cct atc
1968
Gly Asp Glu Arg Gly Leu Lys Leu Val Gln Ser Ile Leu Lys Pro Ile
                645   650   655

atg ctt agg aga aca aag tct agc aca gac cga gaa gga agg ccg att
2016
Met Leu Arg Arg Thr Lys Ser Ser Thr Asp Arg Glu Gly Arg Pro Ile
                660   665   670

ctt gtt cta ccc cct gct gat gca cgg gtc att tac tgt gaa ctt tcg
2064
Leu Val Leu Pro Pro Ala Asp Ala Arg Val Ile Tyr Cys Glu Leu Ser
            675   680   685

gag tct gag agg gat ttc tac gac gcg cta ttt aaa aga tcc aag gtc
2112
Glu Ser Glu Arg Asp Phe Tyr Asp Ala Leu Phe Lys Arg Ser Lys Val
    690   695   700

aaa ttt gat caa ttt gtt gaa caa ggc aaa gtt ctt cat aac tat gct
2160
Lys Phe Asp Gln Phe Val Glu Gln Gly Lys Val Leu His Asn Tyr Ala
705   710   715   720

tcg atc ctg gaa ctg ctt ttg cgt ctt cga caa tgt tgt gat cac cca
2208
Ser Ile Leu Glu Leu Leu Leu Arg Leu Arg Gln Cys Cys Asp His Pro
                725   730   735

ttt tta gta atg agt cga ggg gat aca gcg gaa tac tct gat ctg aat
2256
Phe Leu Val Met Ser Arg Gly Asp Thr Ala Glu Tyr Ser Asp Leu Asn
                740   745   750

aag ctt tct aaa cgt ttc ctt agt gga aag tct tct ggc tta gaa agg
2304
Lys Leu Ser Lys Arg Phe Leu Ser Gly Lys Ser Ser Gly Leu Glu Arg
            755   760   765

gaa gga aaa gat gta ccg tca gag gct ttt gtt cag gag gtg gta gag
2352
Glu Gly Lys Asp Val Pro Ser Glu Ala Phe Val Gln Glu Val Val Glu
    770   775   780

gaa ctg cgc aaa gga gag caa gga gag tgt cca ata tgc ctt gaa gca
2400
Glu Leu Arg Lys Gly Glu Gln Gly Glu Cys Pro Ile Cys Leu Glu Ala
785   790   795   800

419

```
ctt gag gat gct gta tta acg cca tgt gct cat aga tta tgt cgt gag
2448
Leu Glu Asp Ala Val Leu Thr Pro Cys Ala His Arg Leu Cys Arg Glu
                805                 810                 815

tgt ctc ttg gca agt tgg aga aat tct act tct ggg tta tgt cct gtg
2496
Cys Leu Leu Ala Ser Trp Arg Asn Ser Thr Ser Gly Leu Cys Pro Val
                820                 825                 830

tgt agg aac act gta agc aaa caa gaa ctc atc aca gca cca acc gaa
2544
Cys Arg Asn Thr Val Ser Lys Gln Glu Leu Ile Thr Ala Pro Thr Glu
            835                 840                 845

agt aga ttc cag gtt gac gtg gaa aag aat tgg gtg gaa tca tcg aaa
2592
Ser Arg Phe Gln Val Asp Val Glu Lys Asn Trp Val Glu Ser Ser Lys
        850                 855                 860

atc act gct ctt ctg gaa gag ctt gaa ggt ctt cgt tct tca ggc tct
2640
Ile Thr Ala Leu Leu Glu Glu Leu Glu Gly Leu Arg Ser Ser Gly Ser
865                 870                 -   875                 880

aag agc att ctc ttt agc cag tgg acc gct ttc ctc gat ctc ctc caa
2688
Lys Ser Ile Leu Phe Ser Gln Trp Thr Ala Phe Leu Asp Leu Leu Gln
                885                 890                 895

att ccc ctc tct cgg aat aac ttt tca ttt gtc cgt ctt gat ggc acg
2736
Ile Pro Leu Ser Arg Asn Asn Phe Ser Phe Val Arg Leu Asp Gly Thr
            900                 905                 910

cta agt cag cag caa cga gag aag gtc ctt aaa gaa ttt tcc gaa gat
2784
Leu Ser Gln Gln Gln Arg Glu Lys Val Leu Lys Glu Phe Ser Glu Asp
        915                 920                 925

ggc agt atc ctg gta ctg ttg atg tct cta aaa gct ggt ggc gtt ggg
2832
Gly Ser Ile Leu Val Leu Leu Met Ser Leu Lys Ala Gly Gly Val Gly
    930                 935                 940

ata aat cta aca gct gcg tcc aat gct ttt gtc atg gat cca tgg tgg
2880
Ile Asn Leu Thr Ala Ala Ser Asn Ala Phe Val Met Asp Pro Trp Trp
945                 950                 955                 960

aac cca gcg gta gag gaa caa gct gtt atg cgt att cat cgt ata ggg
2928
Asn Pro Ala Val Glu Glu Gln Ala Val Met Arg Ile His Arg Ile Gly
                965                 970                 975

caa act aag gaa gtc aaa atc aga aga ttc atc gtt aag gga acg gtt
2976
Gln Thr Lys Glu Val Lys Ile Arg Arg Phe Ile Val Lys Gly Thr Val
            980                 985                 990
```

420

```
gaa gag aga atg gag gcg gtt cag  gcg agg aag cag aga  atg atc tct
3024
Glu Glu Arg Met Glu Ala Val Gln  Ala Arg Lys Gln Arg  Met Ile Ser
        995               1000               1005


ggg gct  tta acc gat caa gaa  gta cga agt gca cgt  ata gag gaa
3069
Gly Ala  Leu Thr Asp Gln Glu  Val Arg Ser Ala Arg  Ile Glu Glu
    1010               1015               1020


ctc aag  atg tta ttt acc tga
3090
Leu Lys  Met Leu Phe Thr
    1025
```

<210> 236 <211> 1029 <212> PRT <213> Arabidopsis thaliana <400> 236

```
Met Gly Thr Lys Val Ser Asp Asp Leu Val Ser Thr Val Arg Ser Val
1               5               10              15


Val Gly Ser Asp Tyr Ser Asp Met Asp Ile Ile Arg Ala Leu His Met
            20              25              30


Ala Asn His Asp Pro Thr Ala Ala Ile Asn Ile Ile Phe Asp Thr Pro
        35              40              45


Ser Phe Ala Lys Pro Asp Val Ala Thr Pro Thr Pro Ser Gly Ser Asn
    50              55              60


Gly Gly Lys Arg Val Asp Ser Gly Leu Lys Gly Cys Thr Phe Gly Asp
65              70              75              80


Ser Gly Ser Val Gly Ala Asn His Arg Val Glu Glu Glu Asn Glu Ser
            85              90              95


Val Asn Gly Gly Gly Glu Glu Ser Val Ser Gly Asn Glu Trp Trp Phe
        100             105             110


Val Gly Cys Ser Glu Leu Ala Gly Leu Ser Thr Cys Lys Gly Arg Lys
        115             120             125


Leu Lys Ser Gly Asp Glu Leu Val Phe Thr Phe Pro His Ser Lys Gly
    130             135             140


Leu Lys Pro Glu Thr Thr Pro Gly Lys Arg Gly Phe Gly Arg Gly Arg
145             150             155             160


Pro Ala Leu Arg Gly Ala Ser Asp Ile Val Arg Phe Ser Thr Lys Asp
            165             170             175
```

```
Ser Gly Glu Ile Gly Arg Ile Pro Asn Glu Trp Ala Arg Cys Leu Leu
            180                 185              190


Pro Leu Val Arg Asp Lys Lys Ile Arg Ile Glu Gly Ser Cys Lys Ser
            195             200             205


Ala Pro Glu Ala Leu Ser Ile Met Asp Thr Ile Leu Leu Ser Val Ser
    210             215                 220


Val Tyr Ile Asn Ser Ser Met Phe Gln Lys His Ser Ala Thr Ser Phe
225             230             235                 240


Lys Thr Ala Ser Asn Thr Ala Glu Glu Ser Met Phe His Pro Leu Pro
                245             250             255


Asn Leu Phe Arg Leu Leu Gly Leu Ile Pro Phe Lys Lys Ala Glu Phe
            260             265             270


Thr Pro Glu Asp Phe Tyr Ser Lys Lys Arg Pro Leu Ser Ser Lys Asp
            275             280             285


Gly Ser Ala Ile Pro Thr Ser Leu Leu Gln Leu Asn Lys Val Lys Asn
    290             295             300


Met Asn Gln Asp Ala Asn Gly Asp Glu Asn Glu Gln Cys Ile Ser Asp
305             310             315                 320


Gly Asp Leu Asp Asn Ile Val Gly Val Gly Asp Ser Ser Gly Leu Lys
            325             330             335


Glu Met Glu Thr Pro His Thr Leu Leu Cys Glu Leu Arg Pro Tyr Gln
            340             345             350


Lys Gln Ala Leu His Trp Met Thr Gln Leu Glu Lys Gly Asn Cys Thr
            355             360             365


Asp Glu Ala Ala Thr Met Leu His Pro Cys Trp Glu Ala Tyr Cys Leu
    370             375             380


Ala Asp Lys Arg Glu Leu Val Val Tyr Leu Asn Ser Phe Thr Gly Asp
385             390             395                 400


Ala Thr Ile His Phe Pro Ser Thr Leu Gln Met Ala Arg Gly Gly Ile
            405             410             415
```

422

Leu Ala Asp Ala Met Gly Leu Gly Lys Thr Val Met Thr Ile Ser Leu
            420   425   430

Leu Leu Ala His Ser Trp Lys Ala Ala Ser Thr Gly Phe Leu Cys Pro
            435   440   445

Asn Tyr Glu Gly Asp Lys Val Ile Ser Ser Ser Val Asp Asp Leu Thr
    450   455   460

Ser Pro Pro Val Lys Ala Thr Lys Phe Leu Gly Phe Asp Lys Arg Leu
465   470   475   480   .

Leu Glu Gln Lys Ser Val Leu Gln Asn Gly Gly Asn Leu Ile Val Cys
                485   490   495

Pro Met Thr Leu Leu Gly Gln Trp Lys Thr Glu Ile Glu Met His Ala
            500   505   510

Lys Pro Gly Ser Leu Ser Val Tyr Val His Tyr Gly Gln Ser Arg Pro
            515   520   525

Lys Asp Ala Lys Leu Leu Ser Gln Ser Asp Val Val Ile Thr Thr Tyr
    530   535   540

Gly Val Leu Thr Ser Glu Phe Ser Gln Glu Asn Ser Ala Asp His Glu
545   550   555   560

Gly Ile Tyr Ala Val Arg Trp Phe Arg Ile Val Leu Asp Glu Ala His
            565   570   575

Thr Ile Lys Asn Ser Lys Ser Gln Ile Ser Leu Ala Ala Ala Ala Leu
            580   585   590

Val Ala Asp Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Gln Asn Asn
            595   600   605

Leu Glu Asp Leu Tyr Ser Leu Leu Arg Phe Leu Arg Ile Glu Pro Trp
            610   615   620

Gly Thr Trp Ala Trp Trp Asn Lys Leu Val Gln Lys Pro Phe Glu Glu
625   630   635   640

Gly Asp Glu Arg Gly Leu Lys Leu Val Gln Ser Ile Leu Lys Pro Ile
            645   650   655

423

Met Leu Arg Arg Thr Lys Ser Ser Thr Asp Arg Glu Gly Arg Pro Ile
        660   665   670

Leu Val Leu Pro Pro Ala Asp Ala Arg Val Ile Tyr Cys Glu Leu Ser
        675   680   685

Glu Ser Glu Arg Asp Phe Tyr Asp Ala Leu Phe Lys Arg Ser Lys Val
    690   695   700

Lys Phe Asp Gln Phe Val Glu Gln Gly Lys Val Leu His Asn Tyr Ala
705   710   715   720

Ser Ile Leu Glu Leu Leu Leu Arg Leu Arg Gln Cys Cys Asp His Pro
            725   730   735

Phe Leu Val Met Ser Arg Gly Asp Thr Ala Glu Tyr Ser Asp Leu Asn
        740   745   750

Lys Leu Ser Lys Arg Phe Leu Ser Gly Lys Ser Ser Gly Leu Glu Arg
        755   760   765

Glu Gly Lys Asp Val Pro Ser Glu Ala Phe Val Gln Glu Val Val Glu
    770   775   780

Glu Leu Arg Lys Gly Glu Gln Gly Glu Cys Pro Ile Cys Leu Glu Ala
785   790   795   800

Leu Glu Asp Ala Val Leu Thr Pro Cys Ala His Arg Leu Cys Arg Glu
            805   810   815

Cys Leu Leu Ala Ser Trp Arg Asn Ser Thr Ser Gly Leu Cys Pro Val
        820   825   830

Cys Arg Asn Thr Val Ser Lys Gln Glu Leu Ile Thr Ala Pro Thr Glu
        835   840   845

Ser Arg Phe Gln Val Asp Val Glu Lys Asn Trp Val Glu Ser Ser Lys
    850   855   860

Ile Thr Ala Leu Leu Glu Glu Leu Glu Gly Leu Arg Ser Ser Gly Ser
865   870   875   880

Lys Ser Ile Leu Phe Ser Gln Trp Thr Ala Phe Leu Asp Leu Leu Gln
            885   890   895

Ile Pro Leu Ser Arg Asn Asn Phe Ser Phe Val Arg Leu Asp Gly Thr

424

```
                   900                    905                    910
```

```
Leu Ser Gln Gln Gln Arg Glu Lys Val Leu Lys Glu Phe Ser Glu Asp
        915                    920                    925
```

```
Gly Ser Ile Leu Val Leu Leu Met Ser Leu Lys Ala Gly Gly Val Gly
    930                    935                    940
```

```
Ile Asn Leu Thr Ala Ala Ser Asn Ala Phe Val Met Asp Pro Trp Trp
945                    950                    955                    960
```

```
Asn Pro Ala Val Glu Glu Gln Ala Val Met Arg Ile His Arg Ile Gly
                965                    970                    975
```

```
Gln Thr Lys Glu Val Lys Ile Arg Arg Phe Ile Val Lys Gly Thr Val
            980                    985                    990
```

```
Glu Glu Arg Met Glu Ala Val Gln Ala Arg Lys Gln Arg Met Ile Ser
        995                    1000                   1005
```

```
Gly Ala Leu Thr Asp Gln Glu Val Arg Ser Ala Arg Ile Glu Glu
    1010                   1015                   1020
```

```
Leu Lys Met Leu Phe Thr
    1025
```

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<210> 237 <211> 783 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(783) <223> G1537
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 <400>  237
atg gaa aac gaa gta aac gca gga aca gca agc agt tca aga tgg aac
48
Met Glu Asn Glu Val Asn Ala Gly Thr Ala Ser Ser Ser Arg Trp Asn
1               5                   10                  15
```

```
cca acg aaa gat cag atc acg cta ctg gaa aat ctt tac aag gaa gga
96
Pro Thr Lys Asp Gln Ile Thr Leu Leu Glu Asn Leu Tyr Lys Glu Gly
            20                  25                  30
```

```
ata cga act ccg agc gcc gat cag att cag cag atc acc ggt agg ctt
144
Ile Arg Thr Pro Ser Ala Asp Gln Ile Gln Gln Ile Thr Gly Arg Leu
        35                  40                  45
```

```
cgt gcg tac ggc cat atc gaa ggt aaa aac gtc ttt tac tgg ttc cag
192
Arg Ala Tyr Gly His Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln
    50                  55                  60
```

```
aac cat aag gct agg caa cgc caa aag cag aaa cag gag cgc atg gct
240
```

```
Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Arg Met Ala
65              70          75              80

tac ttc aat cgc ctc ctc cac aaa acc tcc cgt ttc ttc tac ccc cct
288
Tyr Phe Asn Arg Leu Leu His Lys Thr Ser Arg Phe Phe Tyr Pro Pro
                85              90              95

cct tgc tca aac gtg ggt tgt gtc agt ccg tac tat tta cag caa gca
336
Pro Cys Ser Asn Val Gly Cys Val Ser Pro Tyr Tyr Leu Gln Gln Ala
            100             105             110

agt gat cat cat atg aat caa cat gga agt gta tac aca aac gat ctt
384
Ser Asp His His Met Asn Gln His Gly Ser Val Tyr Thr Asn Asp Leu
        115             120             125

ctt cac aga aac aat gtg atg att cca agt ggt ggc tac gag aaa cgg
432
Leu His Arg Asn Asn Val Met Ile Pro Ser Gly Gly Tyr Glu Lys Arg
    130             135             140

aca gtc aca caa cat cag aaa caa ctt tca gac ata aga aca aca gca
480
Thr Val Thr Gln His Gln Lys Gln Leu Ser Asp Ile Arg Thr Thr Ala
145             150             155             160

gcc aca aga atg cca att tct ccg agt tca ctc aga ttt gac aga ttt
528
Ala Thr Arg Met Pro Ile Ser Pro Ser Ser Leu Arg Phe Asp Arg Phe
                165             170             175

gcc ctc cgt gat aac tgt tat gcc ggt gag gac att aac gtc aat tcc
576
Ala Leu Arg Asp Asn Cys Tyr Ala Gly Glu Asp Ile Asn Val Asn Ser
            180             185             190

agt gga cgg aaa aca ctc cct ctt ttt cct ctt cag cct ttg aat gca
624
Ser Gly Arg Lys Thr Leu Pro Leu Phe Pro Leu Gln Pro Leu Asn Ala
        195             200             205

agt aat gct gat ggt atg gga agt tcc agt ttt gcc ctt ggt agt gat
672
Ser Asn Ala Asp Gly Met Gly Ser Ser Ser Phe Ala Leu Gly Ser Asp
        210             215             220

tct ccg gtg gat tgt tct agc gat gga gcc ggc cga gag cag ccg ttt
720
Ser Pro Val Asp Cys Ser Ser Asp Gly Ala Gly Arg Glu Gln Pro Phe
225             230             235             240

att gat ttc ttt tct ggt ggt tct act tct act cgt ttc gat agt aat
768
Ile Asp Phe Phe Ser Gly Gly Ser Thr Ser Thr Arg Phe Asp Ser Asn
                245             250             255

ggt aat ggg ttg taa
783
Gly Asn Gly Leu
```

426

260

<210> 238 <211> 260 <212> PRT <213> Arabidopsis thaliana <400>
238

Met Glu Asn Glu Val Asn Ala Gly Thr Ala Ser Ser Ser Arg Trp Asn
1   5   10   15

Pro Thr Lys Asp Gln Ile Thr Leu Leu Glu Asn Leu Tyr Lys Glu Gly
            20   25   30

Ile Arg Thr Pro Ser Ala Asp Gln Ile Gln Gln Ile Thr Gly Arg Leu
        35   40   45

Arg Ala Tyr Gly His Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln
    50   55   60

Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Arg Met Ala
65   70   75   80

Tyr Phe Asn Arg Leu Leu His Lys Thr Ser Arg Phe Phe Tyr Pro Pro
                85   90   95

Pro Cys Ser Asn Val Gly Cys Val Ser Pro Tyr Tyr Leu Gln Gln Ala
            100   105   110

Ser Asp His His Met Asn Gln His Gly Ser Val Tyr Thr Asn Asp Leu
            115   120   125

Leu His Arg Asn Asn Val Met Ile Pro Ser Gly Gly Tyr Glu Lys Arg
    130   135   140

Thr Val Thr Gln His Gln Lys Gln Leu Ser Asp Ile Arg Thr Thr Ala
145   150   155   160

Ala Thr Arg Met Pro Ile Ser Pro Ser Ser Leu Arg Phe Asp Arg Phe
            165   170   175

Ala Leu Arg Asp Asn Cys Tyr Ala Gly Glu Asp Ile Asn Val Asn Ser
            180   185   190

Ser Gly Arg Lys Thr Leu Pro Leu Phe Pro Leu Gln Pro Leu Asn Ala
        195   200   205

Ser Asn Ala Asp Gly Met Gly Ser Ser Ser Phe Ala Leu Gly Ser Asp
    210   215   220

427

Ser Pro Val Asp Cys Ser Ser Asp Gly Ala Gly Arg Glu Gln Pro Phe
225   230   235   240

Ile Asp Phe Phe Ser Gly Gly Ser Thr Ser Thr Arg Phe Asp Ser Asn
                245   250   255

Gly Asn Gly Leu
            260

<210> 239 <211> 828 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(828) <223> G1543

<400> 239
atg ata aaa cta cta ttt acg tac ata tgc aca tac aca tat aaa cta
48
Met Ile Lys Leu Leu Phe Thr Tyr Ile Cys Thr Tyr Thr Tyr Lys Leu
1   5   10   15

tat gct cta tat cat atg gat tac gca tgc gtg tgt atg tat aaa tat
96
Tyr Ala Leu Tyr His Met Asp Tyr Ala Cys Val Cys Met Tyr Lys Tyr
            20   25   30

aaa ggc atc gtc acg ctt caa gtt tgt ctc ttt tat att aaa ctg aga
144
Lys Gly Ile Val Thr Leu Gln Val Cys Leu Phe Tyr Ile Lys Leu Arg
        35   40   45

gtt ttc ctc tca aac ttt acc ttt tct tct tcg atc cta gct ctt aag
192
Val Phe Leu Ser Asn Phe Thr Phe Ser Ser Ser Ile Leu Ala Leu Lys
    50   55   60

aac cct aat aat tca ttg atc aaa ata atg gcg att ttg ccg gaa aac
240
Asn Pro Asn Asn Ser Leu Ile Lys Ile Met Ala Ile Leu Pro Glu Asn
65   70   75   80

tct tca aac ttg gat ctt act atc tcc gtt cca ggc ttc tct tca tcc
288
Ser Ser Asn Leu Asp Leu Thr Ile Ser Val Pro Gly Phe Ser Ser Ser
            85   90   95

cct ctc tcc gat gaa gga agt ggc gga gga aga gac cag cta agg cta
336
Pro Leu Ser Asp Glu Gly Ser Gly Gly Gly Arg Asp Gln Leu Arg Leu
            100   105   110

gac atg aat cgg tta ccg tcg tct gaa gac gga gac gat gaa gaa ttc
384
Asp Met Asn Arg Leu Pro Ser Ser Glu Asp Gly Asp Asp Glu Glu Phe
            115   120   125

agt cac gat gat ggc tct gct cct ccg cga aag aaa ctc cgt cta acc
432
Ser His Asp Asp Gly Ser Ala Pro Pro Arg Lys Lys Leu Arg Leu Thr
            130   135   140

```
aga gaa cag tca cgt ctt ctt gaa gat agt ttc aga cag aat cat acc
480
Arg Glu Gln Ser Arg Leu Leu Glu Asp Ser Phe Arg Gln Asn His Thr
145                 150                 155                 160

ctt aat ccc aaa caa aag gaa gta ctt gcc aag cat ttg atg cta cgg
528
Leu Asn Pro Lys Gln Lys Glu Val Leu Ala Lys His Leu Met Leu Arg
                165                 170                 175

cca aga caa att gaa gtt tgg ttt caa aac cgt aga gca agg agc aaa
576
Pro Arg Gln Ile Glu Val Trp Phe Gln Asn Arg Arg Ala Arg Ser Lys
            180                 185                 190

ttg aag caa acc gag atg gaa tgc gag tat ctc aaa agg tgg ttt ggt
624
Leu Lys Gln Thr Glu Met Glu Cys Glu Tyr Leu Lys Arg Trp Phe Gly
        195                 200                 205

tca tta acg gaa gaa aac cac agg ctc cat aga gaa gta gaa gag ctt
672
Ser Leu Thr Glu Glu Asn His Arg Leu His Arg Glu Val Glu Glu Leu
    210                 215                 220

aga gcc ata aag gtt ggc cca aca acg gtg aac tct gcc tcg agc ctt
720
Arg Ala Ile Lys Val Gly Pro Thr Thr Val Asn Ser Ala Ser Ser Leu
225                 230                 235                 240

act atg tgt cct cgc tgc gag cga gtt acc cct gcc gcg agc cct tcg
768
Thr Met Cys Pro Arg Cys Glu Arg Val Thr Pro Ala Ala Ser Pro Ser
                245                 250                 255

agg gcg gtg gtg ccg gtt ccg gct aag aaa acg ttt ccg ccg caa gag
816
Arg Ala Val Val Pro Val Pro Ala Lys Lys Thr Phe Pro Pro Gln Glu
            260                 265                 270

cgt gat cgt tga
828
Arg Asp Arg
        275


<210> 240 <211> 275 <212> PRT <213> Arabidopsis thaliana <400>
240

Met Ile Lys Leu Leu Phe Thr Tyr Ile Cys Thr Tyr Thr Tyr Lys Leu
1               5                   10                  15


Tyr Ala Leu Tyr His Met Asp Tyr Ala Cys Val Cys Met Tyr Lys Tyr
            20                  25                  30


Lys Gly Ile Val Thr Leu Gln Val Cys Leu Phe Tyr Ile Lys Leu Arg
        35                  40                  45
```

```
Val Phe Leu Ser Asn Phe Thr Phe Ser Ser Ser Ile Leu Ala Leu Lys
    50                  55              60

Asn Pro Asn Asn Ser Leu Ile Lys Ile Met Ala Ile Leu Pro Glu Asn
65                  70              75                  80

Ser Ser Asn Leu Asp Leu Thr Ile Ser Val Pro Gly Phe Ser Ser Ser
                85              90                  95

Pro Leu Ser Asp Glu Gly Ser Gly Gly Gly Arg Asp Gln Leu Arg Leu
            100             105             110

Asp Met Asn Arg Leu Pro Ser Ser Glu Asp Gly Asp Asp Glu Glu Phe
        115             120             125

Ser His Asp Asp Gly Ser Ala Pro Pro Arg Lys Lys Leu Arg Leu Thr
    130             135             140

Arg Glu Gln Ser Arg Leu Leu Glu Asp Ser Phe Arg Gln Asn His Thr
145             150             155             160

Leu Asn Pro Lys Gln Lys Glu Val Leu Ala Lys His Leu Met Leu Arg
            165             170             175

Pro Arg Gln Ile Glu Val Trp Phe Gln Asn Arg Arg Ala Arg Ser Lys
            180             185             190

Leu Lys Gln Thr Glu Met Glu Cys Glu Tyr Leu Lys Arg Trp Phe Gly
        195             200             205

Ser Leu Thr Glu Glu Asn His Arg Leu His Arg Glu Val Glu Glu Leu
    210             215             220

Arg Ala Ile Lys Val Gly Pro Thr Thr Val Asn Ser Ala Ser Ser Leu
225             230             235             240

Thr Met Cys Pro Arg Cys Glu Arg Val Thr Pro Ala Ala Ser Pro Ser
            245             250             255

Arg Ala Val Val Pro Val Pro Ala Lys Lys Thr Phe Pro Pro Gln Glu
            260             265             270

Arg Asp Arg
        275
```

430

<210> 241 <211> 1962 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1962) <223> G1574

<400> 241
atg gat gat aca atg gac atg agt tca ggt agt gat gaa gaa gta caa
48
Met Asp Asp Thr Met Asp Met Ser Ser Gly Ser Asp Glu Glu Val Gln
1   5   10   15

gaa gag aag acc act gtt aac gag agg gtc atc tat cag gct gca tta
96
Glu Glu Lys Thr Thr Val Asn Glu Arg Val Ile Tyr Gln Ala Ala Leu
            20   25   30

caa gat ctg aag caa ccc aag acc gaa aag gat cta cct cct ggt gtt
144
Gln Asp Leu Lys Gln Pro Lys Thr Glu Lys Asp Leu Pro Pro Gly Val
        35   40   45

ctt aca gtt cct ctt atg agg cat cag aaa att gca ttg aac tgg atg
192
Leu Thr Val Pro Leu Met Arg His Gln Lys Ile Ala Leu Asn Trp Met
    50   55   60

cgt aag aaa gaa aaa aga agc agg cac tgt ttg gga ggg ata tta gca
240
Arg Lys Lys Glu Lys Arg Ser Arg His Cys Leu Gly Gly Ile Leu Ala
65   70   75   80

gat gat cag gga ctt ggt aaa acg atc tcg acg atc tct ctt atc ctg
288
Asp Asp Gln Gly Leu Gly Lys Thr Ile Ser Thr Ile Ser Leu Ile Leu
            85   90   95

tta caa aag ttg aag tca caa tca aag cag aga aag cga aaa ggt caa
336
Leu Gln Lys Leu Lys Ser Gln Ser Lys Gln Arg Lys Arg Lys Gly Gln
            100   105   110

aac tct ggt ggt aca ttg att gtt tgt cca gca agt gtt gta aaa caa
384
Asn Ser Gly Gly Thr Leu Ile Val Cys Pro Ala Ser Val Val Lys Gln
        115   120   125

tgg gca aga gaa gtt aaa gag aag gtt tct gat gaa cac aaa ctc tct
432
Trp Ala Arg Glu Val Lys Glu Lys Val Ser Asp Glu His Lys Leu Ser
    130   135   140

gtt tta gtc cac cat gga tct cac aga acc aaa gat cca aca gaa ata
480
Val Leu Val His His Gly Ser His Arg Thr Lys Asp Pro Thr Glu Ile
145   150   155   160

gca ata tat gat gtg gtc atg aca act tac gcc att gtt aca aat gaa
528
Ala Ile Tyr Asp Val Val Met Thr Thr Tyr Ala Ile Val Thr Asn Glu
            165   170   175

gtt cca caa aac cct atg ctg aat cgt tat gat agt atg aga ggc aga
576

431

```
Val Pro Gln Asn Pro Met Leu Asn Arg Tyr Asp Ser Met Arg Gly Arg
        180                 185                 190

gaa agc ctt gac gga tcg agt ttg att cag cct cac gtt ggt gca cta
624
Glu Ser Leu Asp Gly Ser Ser Leu Ile Gln Pro His Val Gly Ala Leu
        195                 200                 205

gga aga gtt agg tgg ttg aga gta gta tta gat gaa gct cat aca att
672
Gly Arg Val Arg Trp Leu Arg Val Val Leu Asp Glu Ala His Thr Ile
        210                 215                 220

aaa aac cat aga acc cta att gca aaa gct tgt ttt agc ctt aga gcc
720
Lys Asn His Arg Thr Leu Ile Ala Lys Ala Cys Phe Ser Leu Arg Ala
225                 230                 235                 240

aaa agg aga tgg tgt ttg act gga acg ccg ata aag aac aaa gta gac
768
Lys Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Lys Asn Lys Val Asp
                245                 250                 255

gat ctt tat agc tat ttc aga ttt ctt aga tat cat cca tat gcc atg
816
Asp Leu Tyr Ser Tyr Phe Arg Phe Leu Arg Tyr His Pro Tyr Ala Met
            260                 265                 270

tgc aat tca ttt cac caa aga atc aaa gct cca att gat aaa aag cct
864
Cys Asn Ser Phe His Gln Arg Ile Lys Ala Pro Ile Asp Lys Lys Pro
            275                 280                 285

ctt cat ggt tac aag aag ctt caa gct att cta agg ggt ata atg ttg
912
Leu His Gly Tyr Lys Lys Leu Gln Ala Ile Leu Arg Gly Ile Met Leu
        290                 295                 300

cgc cgc acc aaa gaa tgg tct ttc tac agg aag ctt gaa ttg aat tca
960
Arg Arg Thr Lys Glu Trp Ser Phe Tyr Arg Lys Leu Glu Leu Asn Ser
305                 310                 315                 320

cgt tgg aag ttt gag gaa tat gct gct gat ggg act ttg cat gaa cac
1008
Arg Trp Lys Phe Glu Glu Tyr Ala Ala Asp Gly Thr Leu His Glu His
                325                 330                 335

atg gct tat ctt ttg gtg atg ctt ttg cga cta cgc caa gct tgt aac
1056
Met Ala Tyr Leu Leu Val Met Leu Leu Arg Leu Arg Gln Ala Cys Asn
            340                 345                 350

cat cca caa ctt gtt aac gga tat agt cac tca gat act aca aga aaa
1104
His Pro Gln Leu Val Asn Gly Tyr Ser His Ser Asp Thr Thr Arg Lys
        355                 360                 365

atg tca gat gga gtt cga gta gcc cct aga gag aat cta atc atg ttc
1152
Met Ser Asp Gly Val Arg Val Ala Pro Arg Glu Asn Leu Ile Met Phe
```

432

         370   375   380

ctc gat ctc ttg aaa tta tcc tca acc acc tgc tct gtt tgt agt gat
1200
Leu Asp Leu Leu Lys Leu Ser Ser Thr Thr Cys Ser Val Cys Ser Asp
385   390   395   400

cca cca aaa gac cct gtt gtt act ttg tgt ggc cat gtg ttt tgt tat
1248
Pro Pro Lys Asp Pro Val Val Thr Leu Cys Gly His Val Phe Cys Tyr
                405   410   415

gag tgt gtg tct gta aac att aac ggg gat aac aat acg tgc cct gca
1296
Glu Cys Val Ser Val Asn Ile Asn Gly Asp Asn Asn Thr Cys Pro Ala
                420   425   430

ctt aat tgc cac agc cag ctt aaa cat gat gtt gtt ttc act gaa tct
1344
Leu Asn Cys His Ser Gln Leu Lys His Asp Val Val Phe Thr Glu Ser
                435   440   445

gca gtt aga agt tgc atc aac gat tat gat gat cct gaa gat aaa aat
1392
Ala Val Arg Ser Cys Ile Asn Asp Tyr Asp Asp Pro Glu Asp Lys Asn
    450   455   460

gct tta gtt gca tca agg cga gtt tat ttc atc gaa aat ccg agc tgt
1440
Ala Leu Val Ala Ser Arg Arg Val Tyr Phe Ile Glu Asn Pro Ser Cys
465   470   475   480

gat aga gat tct tca gtc gct tgc aga gca agg cag tcc aga cac tcc
1488
Asp Arg Asp Ser Ser Val Ala Cys Arg Ala Arg Gln Ser Arg His Ser
                485   490   495

acc aat aaa gac aat agt atc agt gga ctg aat ctc att ttt acg ttt
1536
Thr Asn Lys Asp Asn Ser Ile Ser Gly Leu Asn Leu Ile Phe Thr Phe
                500   505   510

ctc aaa gac aaa tgt aat gat tat gaa aca ggt gcg atg ttg atg tct
1584
Leu Lys Asp Lys Cys Asn Asp Tyr Glu Thr Gly Ala Met Leu Met Ser
                515   520   525

ctt aaa gct gga aac ctt gga ttg aat atg gta gct gca agt cat gtc
1632
Leu Lys Ala Gly Asn Leu Gly Leu Asn Met Val Ala Ala Ser His Val
                530   535   540

att cta ctg gac cta tgg tgg aat cca aca aca gag gat caa gct att
1680
Ile Leu Leu Asp Leu Trp Trp Asn Pro Thr Thr Glu Asp Gln Ala Ile
545   550   555   560

gat cga gct cat cgt atc gga caa act cga gct gtt acg gtc act cgt
1728
Asp Arg Ala His Arg Ile Gly Gln Thr Arg Ala Val Thr Val Thr Arg
                565   570   575

433

```
att gcc atc aaa aat acc gtt gag gaa cga att ttg act ctt cat gaa
1776
Ile Ala Ile Lys Asn Thr Val Glu Glu Arg Ile Leu Thr Leu His Glu
            580             585             590

cgt aaa agg aac att gtt gca tct gca ttg ggt gaa aaa aac tgg caa
1824
Arg Lys Arg Asn Ile Val Ala Ser Ala Leu Gly Glu Lys Asn Trp Gln
            595             600             605

aag ttc tgc gat tca act aac act aga aga tct cga ata tct gtt ttt
1872
Lys Phe Cys Asp Ser Thr Asn Thr Arg Arg Ser Arg Ile Ser Val Phe
        610             615             620

tgg tgt gta gaa tat ccc aga gtt ttt att gat aag agg aat aaa acc
1920
Trp Cys Val Glu Tyr Pro Arg Val Phe Ile Asp Lys Arg Asn Lys Thr
625             630             635             640

ttt agc tat tta ata agt cac aag tgt gaa tgt aat gaa taa
1962
Phe Ser Tyr Leu Ile Ser His Lys Cys Glu Cys Asn Glu
            645             650
```

<210> 242 <211> 653 <212> PRT <213> Arabidopsis thaliana <400>
242

```
Met Asp Asp Thr Met Asp Met Ser Ser Gly Ser Asp Glu Glu Val Gln
1               5               10              15

Glu Glu Lys Thr Thr Val Asn Glu Arg Val Ile Tyr Gln Ala Ala Leu
            20              25              30

Gln Asp Leu Lys Gln Pro Lys Thr Glu Lys Asp Leu Pro Pro Gly Val
        35              40              45

Leu Thr Val Pro Leu Met Arg His Gln Lys Ile Ala Leu Asn Trp Met
    50              55              60

Arg Lys Lys Glu Lys Arg Ser Arg His Cys Leu Gly Gly Ile Leu Ala
65              70              75              80

Asp Asp Gln Gly Leu Gly Lys Thr Ile Ser Thr Ile Ser Leu Ile Leu
            85              90              95

Leu Gln Lys Leu Lys Ser Gln Ser Lys Gln Arg Lys Arg Lys Gly Gln
            100             105             110

Asn Ser Gly Gly Thr Leu Ile Val Cys Pro Ala Ser Val Val Lys Gln
            115             120             125
```

434

Trp Ala Arg Glu Val Lys Glu Lys Val Ser Asp Glu His Lys Leu Ser
    130   135   140

Val Leu Val His His Gly Ser His Arg Thr Lys Asp Pro Thr Glu Ile
145   150   155   160

Ala Ile Tyr Asp Val Val Met Thr Thr Tyr Ala Ile Val Thr Asn Glu
            165   170   175

Val Pro Gln Asn Pro Met Leu Asn Arg Tyr Asp Ser Met Arg Gly Arg
            180   185   190

Glu Ser Leu Asp Gly Ser Ser Leu Ile Gln Pro His Val Gly Ala Leu
        195   200   205

Gly Arg Val Arg Trp Leu Arg Val Val Leu Asp Glu Ala His Thr Ile
    210   215   220

Lys Asn His Arg Thr Leu Ile Ala Lys Ala Cys Phe Ser Leu Arg Ala
225   230   235   240

Lys Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Lys Asn Lys Val Asp
            245   250   255

Asp Leu Tyr Ser Tyr Phe Arg Phe Leu Arg Tyr His Pro Tyr Ala Met
        260   265   270

Cys Asn Ser Phe His Gln Arg Ile Lys Ala Pro Ile Asp Lys Lys Pro
        275   280   285

Leu His Gly Tyr Lys Lys Leu Gln Ala Ile Leu Arg Gly Ile Met Leu
    290   295   300

Arg Arg Thr Lys Glu Trp Ser Phe Tyr Arg Lys Leu Glu Leu Asn Ser
305   310   315   320

Arg Trp Lys Phe Glu Glu Tyr Ala Ala Asp Gly Thr Leu His Glu His
            325   330   335

Met Ala Tyr Leu Leu Val Met Leu Leu Arg Leu Arg Gln Ala Cys Asn
        340   345   350

His Pro Gln Leu Val Asn Gly Tyr Ser His Ser Asp Thr Thr Arg Lys
        355   360   365

435

```
Met Ser Asp Gly Val Arg Val Ala Pro Arg Glu Asn Leu Ile Met Phe
    370                 375             380


Leu Asp Leu Leu Lys Leu Ser Ser Thr Thr Cys Ser Val Cys Ser Asp
385                 390             395                 400


Pro Pro Lys Asp Pro Val Val Thr Leu Cys Gly His Val Phe Cys Tyr
            405             410             415


Glu Cys Val Ser Val Asn Ile Asn Gly Asp Asn Asn Thr Cys Pro Ala
            420             425             430


Leu Asn Cys His Ser Gln Leu Lys His Asp Val Val Phe Thr Glu Ser
        435             440             445


Ala Val Arg Ser Cys Ile Asn Asp Tyr Asp Asp Pro Glu Asp Lys Asn
    450             455             460


Ala Leu Val Ala Ser Arg Arg Val Tyr Phe Ile Glu Asn Pro Ser Cys
465             470             475             480


Asp Arg Asp Ser Ser Val Ala Cys Arg Ala Arg Gln Ser Arg His Ser
            485             490             495


Thr Asn Lys Asp Asn Ser Ile Ser Gly Leu Asn Leu Ile Phe Thr Phe
            500             505             510


Leu Lys Asp Lys Cys Asn Asp Tyr Glu Thr Gly Ala Met Leu Met Ser
        515             520             525


Leu Lys Ala Gly Asn Leu Gly Leu Asn Met Val Ala Ala Ser His Val
    530             535             540


Ile Leu Leu Asp Leu Trp Trp Asn Pro Thr Thr Glu Asp Gln Ala Ile
545             550             555             560


Asp Arg Ala His Arg Ile Gly Gln Thr Arg Ala Val Thr Val Thr Arg
            565             570             575


Ile Ala Ile Lys Asn Thr Val Glu Glu Arg Ile Leu Thr Leu His Glu
        580             585             590


Arg Lys Arg Asn Ile Val Ala Ser Ala Leu Gly Glu Lys Asn Trp Gln
    595             600             605


Lys Phe Cys Asp Ser Thr Asn Thr Arg Arg Ser Arg Ile Ser Val Phe
```

436

```
        610                   615                   620
```

```
Trp Cys Val Glu Tyr Pro Arg Val Phe Ile Asp Lys Arg Asn Lys Thr
625             ,           630                 635                 640
```

```
Phe Ser Tyr Leu Ile Ser His Lys Cys Glu Cys Asn Glu
                645                 650
```

<210> 243 <211> 807 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(807) <223> G1586

<400> 243
```
atg aat caa gaa ggt gct tca cat agc cca tcc tcc act tcc acc gaa
48
Met Asn Gln Glu Gly Ala Ser His Ser Pro Ser Ser Thr Ser Thr Glu
1               5                   10                  15
```

```
cca gtc cgg gca cgt tgg tca cct aaa ccg gag caa atc ttg ata ctc
96
Pro Val Arg Ala Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu
            20                  25                  30
```

```
gaa tcc atc ttc aac agt ggt act gtt aac cca cca aaa gat gaa acg
144
Glu Ser Ile Phe Asn Ser Gly Thr Val Asn Pro Pro Lys Asp Glu Thr
        35                  40                  45
```

```
gtg agg ata aga aag atg ctt gag aaa ttc ggt gct gtg gga gac gca
192
Val Arg Ile Arg Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala
    50                  55                  60
```

```
aac gtc ttc tac tgg ttt caa aac cga cgg tca aga tct cgc cgg aga
240
Asn Val Phe Tyr Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg.
65                  70                  75                  80
```

```
cac cgg cag ctt tta gca gcc acc acc gca gcc gcc acc tcc ata gga
288
His Arg Gln Leu Leu Ala Ala Thr Thr Ala Ala Ala Thr Ser Ile Gly
                85                  90                  95
```

```
gct gaa gac cac cag cac atg acg gcc atg agc atg cat caa tat cct
336
Ala Glu Asp His Gln His Met Thr Ala Met Ser Met His Gln Tyr Pro
            100                 105                 110
```

```
tgc agc aac aac gag att gat ttg ggg ttt gga agt tgt agc aac tta
384
Cys Ser Asn Asn Glu Ile Asp Leu Gly Phe Gly Ser Cys Ser Asn Leu
            115                 120                 125
```

```
tca gct aat tac ttc ctt aat gga tcg tcg tca tct caa atc cct tcc
432
Ser Ala Asn Tyr Phe Leu Asn Gly Ser Ser Ser Ser Gln Ile Pro Ser
    130                 135                 140
```

```
ttt ttc ctc ggc ctc tct tct tca agt ggt ggg tgt gag aac aac aat
480
Phe Phe Leu Gly Leu Ser Ser Ser Ser Gly Gly Cys Glu Asn Asn Asn
145                     150             155                 160

ggt atg gag aat ctc ttc aaa atg tat ggc cat gaa tct gat cat aat
528
Gly Met Glu Asn Leu Phe Lys Met Tyr Gly His Glu Ser Asp His Asn
                165             170             175

cat cag cag cag cat cat agc tca aat gct gca tca gtt tta aac cca
576
His Gln Gln Gln His His Ser Ser Asn Ala Ala Ser Val Leu Asn Pro
            180             185             190

tct gat caa aac tcc aac tcc caa tac gaa caa gaa ggg ttt atg acg
624
Ser Asp Gln Asn Ser Asn Ser Gln Tyr Glu Gln Glu Gly Phe Met Thr
            195             200             205

gtg ttt ata aac gga gtt cct atg gaa gta aca aaa gga gca ata gac
672
Val Phe Ile Asn Gly Val Pro Met Glu Val Thr Lys Gly Ala Ile Asp
    210             215             --  220

atg aaa aca atg ttc ggt gat gat tcg gtg tta ctt cat tcc tct ggt
720
Met Lys Thr Met Phe Gly Asp Asp Ser Val Leu Leu His Ser Ser Gly
225             230             235                 240

ctt cct ctt ccc act gat gag ttt ggt ttc ttg atg cat tct tta caa
768
Leu Pro Leu Pro Thr Asp Glu Phe Gly Phe Leu Met His Ser Leu Gln
            245             250             255

cat gga caa act tat ttc ctg gta ccg aga cag aca tga
807
His Gly Gln Thr Tyr Phe Leu Val Pro Arg Gln Thr
            260             265


<210>  244 <211>  268 <212>  PRT <213>  Arabidopsis thaliana  <400>
244

Met Asn Gln Glu Gly Ala Ser His Ser Pro Ser Ser Thr Ser Thr Glu
1               5               10              15


Pro Val Arg Ala Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu
            20              25              30


Glu Ser Ile Phe Asn Ser Gly Thr Val Asn Pro Pro Lys Asp Glu Thr
            35              40              45


Val Arg Ile Arg Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala
    50              55              60


Asn Val Phe Tyr Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg
```

```
    65                    70                    75                    80

His Arg Gln Leu Leu Ala Ala Thr Thr Ala Ala Ala Thr Ser Ile Gly
            85                    90                    95

Ala Glu Asp His Gln His Met Thr Ala Met Ser Met His Gln Tyr Pro
            100                   105                   110

Cys Ser Asn Asn Glu Ile Asp Leu Gly Phe Gly Ser Cys Ser Asn Leu
            115                   120                   125

Ser Ala Asn Tyr Phe Leu Asn Gly Ser Ser Ser Ser Gln Ile Pro Ser
    130                   135                    140

Phe Phe Leu Gly Leu Ser Ser Ser Ser Gly Gly Cys Glu Asn Asn Asn
145                   150                   155                   160

Gly Met Glu Asn Leu Phe Lys Met Tyr Gly His Glu Ser Asp His Asn
                165                   170                   175

His Gln Gln Gln His His Ser Ser Asn Ala Ala Ser Val Leu Asn Pro
            180                   185                   190

Ser Asp Gln Asn Ser Asn Ser Gln Tyr Glu Gln Glu Gly Phe Met Thr
            195                   200                   205

Val Phe Ile Asn Gly Val Pro Met Glu Val Thr Lys Gly Ala Ile Asp
    210                   215                   220

Met Lys Thr Met Phe Gly Asp Asp Ser Val Leu Leu His Ser Ser Gly
225                   230                   235                   240

Leu Pro Leu Pro Thr Asp Glu Phe Gly Phe Leu Met His Ser Leu Gln
                245                   250                   255

His Gly Gln Thr Tyr Phe Leu Val Pro Arg Gln Thr
            260                   265
```

<210> 245 <211> 896 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (22)..(855) <223> G1634

```
 <400> 245
ttatctcgta gcctttaaac g atg gag act ctg cat cca cta ctc tcg cac
51
                          Met Glu Thr Leu His Pro Leu Leu Ser His
                          1             5                     10
```

gtg cca act tct gac cac cgg ttt gta gtt caa gag atg atg tgc ttg
99
Val Pro Thr Ser Asp His Arg Phe Val Val Gln Glu Met Met Cys Leu
            15   20   25

caa agc tcg agc tgg act aaa gaa gag aac aag aag ttt gag cga gct
147
Gln Ser Ser Ser Trp Thr Lys Glu Glu Asn Lys Lys Phe Glu Arg Ala
        30   35   40

ctt gct gtc tac gct gat gac acg cct gat cgc tgg ttc aaa gtt gct
195
Leu Ala Val Tyr Ala Asp Asp Thr Pro Asp Arg Trp Phe Lys Val Ala
        45   50   55

gct atg atc cct gga aag acc ata tca gat gtc atg agg caa tac tct
243
Ala Met Ile Pro Gly Lys Thr Ile Ser Asp Val Met Arg Gln Tyr Ser
    60   65   70

aag ctt gaa gaa gac ctc ttc gat atc gaa gca gga ctt gtc ccg atc
291
Lys Leu Glu Glu Asp Leu Phe Asp Ile Glu Ala Gly Leu Val Pro Ile
75   80   85   90

ccg ggt tac cgt tca gtt act cct tgt gga ttt gat cag gtt gtg agt
339
Pro Gly Tyr Arg Ser Val Thr Pro Cys Gly Phe Asp Gln Val Val Ser
            95   100   105

cca cgt gac ttt gat gcg tat cgt aaa ctt cct aat gga gcc aga gga
387
Pro Arg Asp Phe Asp Ala Tyr Arg Lys Leu Pro Asn Gly Ala Arg Gly
        110   115   120

ttt gat caa gac cgt agg aaa gga gtt cca tgg acg gag gaa gaa cac
435
Phe Asp Gln Asp Arg Arg Lys Gly Val Pro Trp Thr Glu Glu Glu His
        125   130   135

agg aga ttc ttg tta ggg ctt ctc aag tat ggg aaa gga gat tgg aga
483
Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr Gly Lys Gly Asp Trp Arg
    140   145   150

aac ata tcg agg aac ttt gtg gga tca aaa aca cca act cag gtt gca
531
Asn Ile Ser Arg Asn Phe Val Gly Ser Lys Thr Pro Thr Gln Val Ala
155   160   165   170

agt cat gcc caa aag tac tac caa aga cag ctt tcc ggt gcg aaa gac
579
Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln Leu Ser Gly Ala Lys Asp
            175   180   185

aaa cga cgg cct agc att cac gac atc acc acc gtc aat ctt ctc aat
627
Lys Arg Arg Pro Ser Ile His Asp Ile Thr Thr Val Asn Leu Leu Asn
        190   195   200

440

```
gcc aat ctt agc cgt cca tcg tct gat cac ggt tgc tta gtc tca aaa
675
Ala Asn Leu Ser Arg Pro Ser Ser Asp His Gly Cys Leu Val Ser Lys
        205              210              215

cag gcc gag ccg aaa cta ggg ttc acc gac agg gat aat gca gag gag
723
Gln Ala Glu Pro Lys Leu Gly Phe Thr Asp Arg Asp Asn Ala Glu Glu
        220              225              230

gga gtt atg ttt ctt ggt cag aat cta tcc tcg gtc ttc tct tcc tac
771
Gly Val Met Phe Leu Gly Gln Asn Leu Ser Ser Val Phe Ser Ser Tyr
235              240              245              250

gat cct gcc att aag ttt tcc gga gca aat gtt tac ggt gaa gga ggt
819
Asp Pro Ala Ile Lys Phe Ser Gly Ala Asn Val Tyr Gly Glu Gly Gly
            255              260              265

tac tgt atc tca caa gat ctt gaa acg aga aaa tga gaattttgaa
865
Tyr Cys Ile Ser Gln Asp Leu Glu Thr Arg Lys
            270              275

attttaacta ttgcaacgaa accataattg c
896


<210> 246 <211> 277 <212> PRT <213> Arabidopsis thaliana <400>
246

Met Glu Thr Leu His Pro Leu Leu Ser His Val Pro Thr Ser Asp His
1               5               10              15


Arg Phe Val Val Gln Glu Met Met Cys Leu Gln Ser Ser Ser Trp Thr
            20              25              30


Lys Glu Glu Asn Lys Lys Phe Glu Arg Ala Leu Ala Val Tyr Ala Asp
        35              40              45


Asp Thr Pro Asp Arg Trp Phe Lys Val Ala Ala Met Ile Pro Gly Lys
    50              55              60


Thr Ile Ser Asp Val Met Arg Gln Tyr Ser Lys Leu Glu Glu Asp Leu
65              70              75              80


Phe Asp Ile Glu Ala Gly Leu Val Pro Ile Pro Gly Tyr Arg Ser Val
            85              90              95


Thr Pro Cys Gly Phe Asp Gln Val Val Ser Pro Arg Asp Phe Asp Ala
        100             105             110


Tyr Arg Lys Leu Pro Asn Gly Ala Arg Gly Phe Asp Gln Asp Arg Arg
```

```
           115                    120                    125

Lys Gly Val Pro Trp Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly
    130                    135                    140


Leu Leu Lys Tyr Gly Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe
145                    150                    155                    160


Val Gly Ser Lys Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr
                   165                    170                    175


Tyr Gln Arg Gln Leu Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile
               180                    185                    190


His Asp Ile Thr Thr Val Asn Leu Leu Asn Ala Asn Leu Ser Arg Pro
           195                    200                    205


Ser Ser Asp His Gly Cys Leu Val Ser Lys Gln Ala Glu Pro Lys Leu
    210                    215                    220


Gly Phe Thr Asp Arg Asp Asn Ala Glu Glu Gly Val Met Phe Leu Gly
225                    230                    235                    240


Gln Asn Leu Ser Ser Val Phe Ser Ser Tyr Asp Pro Ala Ile Lys Phe
                   245                    250                    255


Ser Gly Ala Asn Val Tyr Gly Glu Gly Gly Tyr Cys Ile Ser Gln Asp
                   260                    265                    270


Leu Glu Thr Arg Lys
        275
```

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<210>  247 <211>  1164 <212>  DNA <213>  Arabidopsis thaliana  <220>
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 <400>  247
atg gcg tcg tct ccg ttg act gca aat gtt cag ggt acc aac gct tct
48
Met Ala Ser Ser Pro Leu Thr Ala Asn Val Gln Gly Thr Asn Ala Ser
1               5                    10                    15


ttg agg aat aga gat gaa gaa act gca gac aag cag ata caa ttc aat
96
Leu Arg Asn Arg Asp Glu Glu Thr Ala Asp Lys Gln Ile Gln Phe Asn
               20                    25                    30


gac caa agt ttt ggg gga aat gac tat gca ccc aag gta cgg aag cca
144
Asp Gln Ser Phe Gly Gly Asn Asp Tyr Ala Pro Lys Val Arg Lys Pro
           35                    40                    45
```

442

```
tac acg ata aca aaa gag aga gag aga tgg aca gat gaa gag cac aag
192
Tyr Thr Ile Thr Lys Glu Arg Glu Arg Trp Thr Asp Glu Glu His Lys
    50              55              60

aag ttt gtt gaa gcc ttg aaa tta tac ggg cga gct tgg aga cga ata
240
Lys Phe Val Glu Ala Leu Lys Leu Tyr Gly Arg Ala Trp Arg Arg Ile
65              70              75              80

gaa gaa cat gtg ggc tca aag acc gca gtt cag att cga agc cat gct
288
Glu Glu His Val Gly Ser Lys Thr Ala Val Gln Ile Arg Ser His Ala
                85              90              95

cag aag ttt ttc tct aag gtt gct cga gaa gca act gga ggt gat ggg
336
Gln Lys Phe Phe Ser Lys Val Ala Arg Glu Ala Thr Gly Gly Asp Gly
            100             105             110

agc tca gta gag ccg att gta ata cct cct cct cgt ccc aag aga aag
384
Ser Ser Val Glu Pro Ile Val Ile Pro Pro Pro Arg Pro Lys Arg Lys
            115             120             125

cca gcg cat ccg tac cct cgt aag ttt ggg aac gag gca gat caa aca
432
Pro Ala His Pro Tyr Pro Arg Lys Phe Gly Asn Glu Ala Asp Gln Thr
        130             135             140

agt aga tcg gtt tct ccc tca gaa cgt gat act caa tct cca acc tct
480
Ser Arg Ser Val Ser Pro Ser Glu Arg Asp Thr Gln Ser Pro Thr Ser
145             150             155             160

gtg ttg tcc act gtt gga tca gaa gca ttg tgt tcc ctt gat tcg agt
528
Val Leu Ser Thr Val Gly Ser Glu Ala Leu Cys Ser Leu Asp Ser Ser
                165             170             175

tca ccc aat cga agc ttg tcc cca gtt tct tct gca tca cca cca gct
576
Ser Pro Asn Arg Ser Leu Ser Pro Val Ser Ser Ala Ser Pro Pro Ala
            180             185             190

gct ctt aca acc act gca aat gca cct gaa gag ctt gag act ctg aag
624
Ala Leu Thr Thr Thr Ala Asn Ala Pro Glu Glu Leu Glu Thr Leu Lys
            195             200             205

ctg gag ttg ttt cct agt gag aga ctc tta aac agg gag agc tcg atc
672
Leu Glu Leu Phe Pro Ser Glu Arg Leu Leu Asn Arg Glu Ser Ser Ile
        210             215             220

aag gaa cca acg aag caa agt ctt aaa ctc ttt ggg aag aca gtt ttg
720
Lys Glu Pro Thr Lys Gln Ser Leu Lys Leu Phe Gly Lys Thr Val Leu
225             230             235             240
```

gta tct gat tca ggc atg tcc tct tct cta aca act tca aca tat tgt
768
Val Ser Asp Ser Gly Met Ser Ser Ser Leu Thr Thr Ser Thr Tyr Cys
            245   250   255

aaa tcc cca att cag cca tta cca cgg aaa ctc tca tca tcc aag aca
816
Lys Ser Pro Ile Gln Pro Leu Pro Arg Lys Leu Ser Ser Ser Lys Thr
            260   265   270

cta ccc ata ata aga aac tca caa gaa gaa ctc ttg agc tgc tgg ata
864
Leu Pro Ile Ile Arg Asn Ser Gln Glu Glu Leu Leu Ser Cys Trp Ile
            275   280   285

caa gtc cct ctt aag caa gaa gat gtg gaa aat aga tgt ttg gat tca
912
Gln Val Pro Leu Lys Gln Glu Asp Val Glu Asn Arg Cys Leu Asp Ser
    290   295   300

gga aag gct gtc caa aac gaa gga tca tcg act gga tca aac act ggt
960
Gly Lys Ala Val Gln Asn Glu Gly Ser Ser Thr Gly Ser Asn Thr Gly
305   310   315   320

tcg gtg gat gat acg gga cac acg gaa aag acc aca gaa ccc gaa aca
1008
Ser Val Asp Asp Thr Gly His Thr Glu Lys Thr Thr Glu Pro Glu Thr
            325   330   335

atg cta tgt caa tgg gag ttt aaa cca agt gag agg tct gca ttt tct
1056
Met Leu Cys Gln Trp Glu Phe Lys Pro Ser Glu Arg Ser Ala Phe Ser
            340   345   350

gag ctc aga aga aca aac tcc gag tca aat tca aga gga ttt ggt cca
1104
Glu Leu Arg Arg Thr Asn Ser Glu Ser Asn Ser Arg Gly Phe Gly Pro
            355   360   365

tac aag aag aga aag atg gta aca gaa gaa gaa gag cat gag att cat
1152
Tyr Lys Lys Arg Lys Met Val Thr Glu Glu Glu Glu His Glu Ile His
    370   375   380

ctc cac tta taa
1164
Leu His Leu
385

<210> 248 <211> 387 <212> PRT <213> Arabidopsis thaliana <400>
248

Met Ala Ser Ser Pro Leu Thr Ala Asn Val Gln Gly Thr Asn Ala Ser
1   5   10   15

Leu Arg Asn Arg Asp Glu Glu Thr Ala Asp Lys Gln Ile Gln Phe Asn
            20   25   30

444

```
Asp Gln Ser Phe Gly Gly Asn Asp Tyr Ala Pro Lys Val Arg Lys Pro
        35                  40              45


Tyr Thr Ile Thr Lys Glu Arg Glu Arg Trp Thr Asp Glu Glu His Lys
    50              55              60


Lys Phe Val Glu Ala Leu Lys Leu Tyr Gly Arg Ala Trp Arg Arg Ile
65              70              75                          80


Glu Glu His Val Gly Ser Lys Thr Ala Val Gln Ile Arg Ser His Ala
                85              90                  95


Gln Lys Phe Phe Ser Lys Val Ala Arg Glu Ala Thr Gly Gly Asp Gly
            100             105             110


Ser Ser Val Glu Pro Ile Val Ile Pro Pro Pro Arg Pro Lys Arg Lys
        115             120             125


Pro Ala His Pro Tyr Pro Arg Lys Phe Gly Asn Glu Ala Asp Gln Thr
    130             135             140


Ser Arg Ser Val Ser Pro Ser Glu Arg Asp Thr Gln Ser Pro Thr Ser
145             150             155             160


Val Leu Ser Thr Val Gly Ser Glu Ala Leu Cys Ser Leu Asp Ser Ser
            165             170             175


Ser Pro Asn Arg Ser Leu Ser Pro Val Ser Ser Ala Ser Pro Pro Ala
            180             185             190


Ala Leu Thr Thr Thr Ala Asn Ala Pro Glu Glu Leu Glu Thr Leu Lys
        195             200             205


Leu Glu Leu Phe Pro Ser Glu Arg Leu Leu Asn Arg Glu Ser Ser Ile
    210             215             220


Lys Glu Pro Thr Lys Gln Ser Leu Lys Leu Phe Gly Lys Thr Val Leu
225             230             235             240


Val Ser Asp Ser Gly Met Ser Ser Ser Leu Thr Thr Ser Thr Tyr Cys
            245             250             255


Lys Ser Pro Ile Gln Pro Leu Pro Arg Lys Leu Ser Ser Ser Lys Thr
            260             265             270
```

```
        Leu Pro Ile Ile Arg Asn Ser Gln Glu Glu Leu Leu Ser Cys Trp Ile
                275             280             285


        Gln Val Pro Leu Lys Gln Glu Asp Val Glu Asn Arg Cys Leu Asp Ser
            290             295             300


        Gly Lys Ala Val Gln Asn Glu Gly Ser Ser Thr Gly Ser Asn Thr Gly
        305             310             315             320


        Ser Val Asp Asp Thr Gly His Thr Glu Lys Thr Thr Glu Pro Glu Thr
                    325             330             335


        Met Leu Cys Gln Trp Glu Phe Lys Pro Ser Glu Arg Ser Ala Phe Ser
                340             345             350


        Glu Leu Arg Arg Thr Asn Ser Glu Ser Asn Ser Arg Gly Phe Gly Pro
                355             360             365


        Tyr Lys Lys Arg Lys Met Val Thr Glu Glu Glu Glu His Glu Ile His
            370             375             380


        Leu His Leu
        385



        <210> 249 <211> 668 <212> DNA <213> Arabidopsis thaliana <220>
        <221> CDS <222> (19)..(666) <223> G1636

        <400> 249
        gagtaatcat caacgatt atg gcg tca agt cag tgg acg agg tcg gag gat
        51
                        Met Ala Ser Ser Gln Trp Thr Arg Ser Glu Asp
                        1               5                   10

        aag atg ttt gag caa gct ttg gtt ctt ttt cct gaa gga tct cct aat
        99
        Lys Met Phe Glu Gln Ala Leu Val Leu Phe Pro Glu Gly Ser Pro Asn
                    15              20              25

        cgg tgg gag aga atc gct gat cag ctt cat aaa tct gct ggt gaa gtt
        147
        Arg Trp Glu Arg Ile Ala Asp Gln Leu His Lys Ser Ala Gly Glu Val
                30              35              40

        agg gag cat tac gag gtc ttg gtt cat gat gtt ttc gag att gat tct
        195
        Arg Glu His Tyr Glu Val Leu Val His Asp Val Phe Glu Ile Asp Ser
            45              50              55

        ggt cga gtt gat gtc cct gat tac atg gat gac tcg gcg gct gcg gcg
        243
        Gly Arg Val Asp Val Pro Asp Tyr Met Asp Asp Ser Ala Ala Ala Ala
        60              65              70              75
```

gcg ggt tgg gat tcc gct ggt cag atc tct ttt ggg tct aaa cat ggc
291
Ala Gly Trp Asp Ser Ala Gly Gln Ile Ser Phe Gly Ser Lys His Gly
                80   85   90

gag agt gaa cgc aaa aga gga act cct tgg aca gag aac gaa cac aaa
339
Glu Ser Glu Arg Lys Arg Gly Thr Pro Trp Thr Glu Asn Glu His Lys
                95   100   105

ttg ttt ctg atc gga tta aag aga tat ggt aag gga gat tgg agg agt
387
Leu Phe Leu Ile Gly Leu Lys Arg Tyr Gly Lys Gly Asp Trp Arg Ser
            110   115   120

atc tcg aga aac gtt gtg gtg acg agg aca ccg acg caa gtc gcg agt
435
Ile Ser Arg Asn Val Val Val Thr Arg Thr Pro Thr Gln Val Ala Ser
        125   130   135

cac gct cag aag tat ttt ctg aga cag aac tcg gtg aag aag gag agg
483
His Ala Gln Lys Tyr Phe Leu Arg Gln Asn Ser Val Lys Lys Glu Arg
140   145   150   155

aaa agg tcg agc atc cat gat ata act acg gtt gat gct act ttg gct
531
Lys Arg Ser Ser Ile His Asp Ile Thr Thr Val Asp Ala Thr Leu Ala
                160   165   170

atg cct ggg tct aac atg gac tgg act ggc caa cac ggg agt cct gtt
579
Met Pro Gly Ser Asn Met Asp Trp Thr Gly Gln His Gly Ser Pro Val
            175   180   185

cag gcg ccg cag cag caa cag att atg tct gag ttc ggt cag caa ttg
627
Gln Ala Pro Gln Gln Gln Gln Ile Met Ser Glu Phe Gly Gln Gln Leu
            190   195   200

aat cct ggt cat ttc gag gat ttt ggg ttt cgg atg tga tg
668
Asn Pro Gly His Phe Glu Asp Phe Gly Phe Arg Met
        205   210   215

<210>   250 <211>   215 <212>   PRT <213>   Arabidopsis thaliana   <400>
250

Met Ala Ser Ser Gln Trp Thr Arg Ser Glu Asp Lys Met Phe Glu Gln
1   5   10   15

Ala Leu Val Leu Phe Pro Glu Gly Ser Pro Asn Arg Trp Glu Arg Ile
            20   25   30

Ala Asp Gln Leu His Lys Ser Ala Gly Glu Val Arg Glu His Tyr Glu
            35   40   45

447

Val Leu Val His Asp Val Phe Glu Ile Asp Ser Gly Arg Val Asp Val
    50   55   60

Pro Asp Tyr Met Asp Asp Ser Ala Ala Ala Ala Gly Trp Asp Ser
65   70   75   80

Ala Gly Gln Ile Ser Phe Gly Ser Lys His Gly Glu Ser Glu Arg Lys
                85   90   95

Arg Gly Thr Pro Trp Thr Glu Asn Glu His Lys Leu Phe Leu Ile Gly
            100   105   110

Leu Lys Arg Tyr Gly Lys Gly Asp Trp Arg Ser Ile Ser Arg Asn Val
        115   120   125

Val Val Thr Arg Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr
    130   135   140

Phe Leu Arg Gln Asn Ser Val Lys Lys Glu Arg Lys Arg Ser Ser Ile
145   150   155   160

His Asp Ile Thr Thr Val Asp Ala Thr Leu Ala Met Pro Gly Ser Asn
            165   170   175

Met Asp Trp Thr Gly Gln His Gly Ser Pro Val Gln Ala Pro Gln Gln
            180   185   190

Gln Gln Ile Met Ser Glu Phe Gly Gln Gln Leu Asn Pro Gly His Phe
        195   200   205

Glu Asp Phe Gly Phe Arg Met
    210   215

<210> 251 <211> 1300 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (168)..(1196) <223> G1640

 <400> 251
ttcgccagat ccttcctcta tataaggaag ttcatttcat ttggagaggt ttcgctgaca
60

agctgctcta gcttatctgg taccgtcgac ctctcactca agggtccaaa agtgttttct
120

cttttcagt ttctctttct cttttgaca gaagagaccg agaagca atg gga agg
176
                                                    Met Gly Arg
                                                     1

gct ccg tgt tgt gag aaa atc ggg ttg aag aga ggg aga tgg aca gcc
224

Ala Pro Cys Cys Glu Lys Ile Gly Leu Lys Arg Gly Arg Trp Thr Ala
    5   10   15

gag gaa gat gag atc ctc acc aag tat att cag acc aat ggt gaa ggt
272
Glu Glu Asp Glu Ile Leu Thr Lys Tyr Ile Gln Thr Asn Gly Glu Gly
20   25   30   35

tct tgg cga tct ttg cct aag aaa gct gga ttg ttg aga tgt gga aag
320
Ser Trp Arg Ser Leu Pro Lys Lys Ala Gly Leu Leu Arg Cys Gly Lys
            40   45   50

agc tgt aga cta agg tgg ata aac tac tta aga aga gac tta aaa aga
368
Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Arg Asp Leu Lys Arg
            55   60   65

gga aat att act tcc gac gaa gaa gaa ata atc gtc aag ttg cat tcc
416
Gly Asn Ile Thr Ser Asp Glu Glu Glu Ile Ile Val Lys Leu His Ser
        70   75   80

ctt ctc ggc aac aga tgg tca ctt att gca aca cat cta cca gga aga
464
Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Thr His Leu Pro Gly Arg
        85   90   95

aca gac aac gaa att aaa aac tat tgg aac tca cat ctc agc cgc aaa
512
Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu Ser Arg Lys
100   105   110   115

atc tat gcc ttc act gcc gtt tcc gga gat gga cac aat cta ctc gtc
560
Ile Tyr Ala Phe Thr Ala Val Ser Gly Asp Gly His Asn Leu Leu Val
                120   125   130

aac gat gta gtc ttg aag aaa tct tgt tca tcg tct tct gga gcc aag
608
Asn Asp Val Val Leu Lys Lys Ser Cys Ser Ser Ser Ser Gly Ala Lys
                135   140   145

aac aat aac aag acc aag aag aag aag aag gga agg act agt agg tca
656
Asn Asn Asn Lys Thr Lys Lys Lys Lys Lys Gly Arg Thr Ser Arg Ser
            150   155   160

tcc atg aag aaa cac aag caa atg gtg acg gcc tca caa tgt ttc tca
704
Ser Met Lys Lys His Lys Gln Met Val Thr Ala Ser Gln Cys Phe Ser
            165   170   175

caa cct aag gag cta gag agt gat ttc agt gag gga ggg caa aat ggt
752
Gln Pro Lys Glu Leu Glu Ser Asp Phe Ser Glu Gly Gly Gln Asn Gly
180   185   190   195

aat ttt gaa gga gag tct ttg ggg cct tat gag tgg ttg gat ggt gag
800
Asn Phe Glu Gly Glu Ser Leu Gly Pro Tyr Glu Trp Leu Asp Gly Glu

449

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                    200                    205                    210

tta gaa cgg ctc ttg agt agt tgt gtc tgg gaa tgc act agt gaa gag
848
Leu Glu Arg Leu Leu Ser Ser Cys Val Trp Glu Cys Thr Ser Glu Glu
            215                    220                    225

gct gtg att gga gta aat gat gaa aag gtg tgt gag agt ggg gac aat
896
Ala Val Ile Gly Val Asn Asp Glu Lys Val Cys Glu Ser Gly Asp Asn
            230                    235                    240

agt agt tgt tgt gtt aat ttg ttt gaa gaa gaa caa gga agc gag aca
944
Ser Ser Cys Cys Val Asn Leu Phe Glu Glu Glu Gln Gly Ser Glu Thr
        245                    250                    255

aag att ggt cac gta gga atc aca gag gtt gat cat gat atg acg gtg
992
Lys Ile Gly His Val Gly Ile Thr Glu Val Asp His Asp Met Thr Val
260                    265                    270                    275

gaa aga gaa aga gag gga agt ttt tta agt tcg aat tca aat gaa aat
1040
Glu Arg Glu Arg Glu Gly Ser Phe Leu Ser Ser Asn Ser Asn Glu Asn
                280                    285                    290

aat gat aaa gat tgg tgg gtt ggt cta tgt aat tct tca gaa gtt ggg
1088
Asn Asp Lys Asp Trp Trp Val Gly Leu Cys Asn Ser Ser Glu Val Gly
            295                    300                    305

ttt ggg gtt gat gag gag ttg ctt gat tgg gag ttt caa ggt aat gtc
1136
Phe Gly Val Asp Glu Glu Leu Leu Asp Trp Glu Phe Gln Gly Asn Val
        310                    315                    320

act tgt caa agt gat gat cta tgg gat ctc tca gat att gga gag ata
1184
Thr Cys Gln Ser Asp Asp Leu Trp Asp Leu Ser Asp Ile Gly Glu Ile
        325                    330                    335

aca ttg gag tga ttgtaccgag caagtggatt ggcggccgct ctagacaggc
1236
Thr Leu Glu
340

ctcgtaccgg atctctagct agagctttcg ttcgtatcat cggtttcgac aacgttcgtc
1296

aagt
1300


<210> 252 <211> 342 <212> PRT <213> Arabidopsis thaliana <400>
252


Met Gly Arg Ala Pro Cys Cys Glu Lys Ile Gly Leu Lys Arg Gly Arg
1               5                   10                  15
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Trp Thr Ala Glu Glu Asp Glu Ile Leu Thr Lys Tyr Ile Gln Thr Asn
            20   25   30

Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Lys Ala Gly Leu Leu Arg
            35   40   45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Arg Asp
            50   55   60

Leu Lys Arg Gly Asn Ile Thr Ser Asp Glu Glu Glu Ile Ile Val Lys
65   70   75   80

Leu His Ser Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Thr His Leu
            85   90   95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu
            100   105   110

Ser Arg Lys Ile Tyr Ala Phe Thr Ala Val Ser Gly Asp Gly His Asn
            115   120   125

Leu Leu Val Asn Asp Val Val Leu Lys Lys Ser Cys Ser Ser Ser Ser
            130   135   140

Gly Ala Lys Asn Asn Asn Lys Thr Lys Lys Lys Lys Gly Arg Thr
145   150   155   160

Ser Arg Ser Ser Met Lys Lys His Lys Gln Met Val Thr Ala Ser Gln
            165   170   175

Cys Phe Ser Gln Pro Lys Glu Leu Glu Ser Asp Phe Ser Glu Gly Gly
            180   185   190

Gln Asn Gly Asn Phe Glu Gly Glu Ser Leu Gly Pro Tyr Glu Trp Leu
            195   200   205

Asp Gly Glu Leu Glu Arg Leu Leu Ser Ser Cys Val Trp Glu Cys Thr
            210   215   220

Ser Glu Glu Ala Val Ile Gly Val Asn Asp Glu Lys Val Cys Glu Ser
225   230   235   240

Gly Asp Asn Ser Ser Cys Cys Val Asn Leu Phe Glu Glu Glu Gln Gly
            245   250   255

Ser Glu Thr Lys Ile Gly His Val Gly Ile Thr Glu Val Asp His Asp

451

```
          260                    265                    270
```

Met Thr Val Glu Arg Glu Arg Glu Gly Ser Phe Leu Ser Ser Asn Ser
        275   280   285

Asn Glu Asn Asn Asp Lys Asp Trp Trp Val Gly Leu Cys Asn Ser Ser
    290   295   300

Glu Val Gly Phe Gly Val Asp Glu Glu Leu Leu Asp Trp Glu Phe Gln
305   310   315   320

Gly Asn Val Thr Cys Gln Ser Asp Asp Leu Trp Asp Leu Ser Asp Ile
                325   330   335

Gly Glu Ile Thr Leu Glu
                340

<210> 253 <211> 867 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(867) <223> G1641

<400> 253
atg gag gtt atg aga ccg tcg acg tca cac gtg tca ggt ggg aac tgg
48
Met Glu Val Met Arg Pro Ser Thr Ser His Val Ser Gly Gly Asn Trp
1   5   10   15

ctc atg gag gaa act aag agc ggc gtc gca gct tct ggt gaa ggt gcc
96
Leu Met Glu Glu Thr Lys Ser Gly Val Ala Ala Ser Gly Glu Gly Ala
            20   25   30

acg tgg acg gcg gca gag aac aag gca ttc gag aat gct ttg gcg gtt
144
Thr Trp Thr Ala Ala Glu Asn Lys Ala Phe Glu Asn Ala Leu Ala Val
        35   40   45

tac gac gac aac act cct gat cgg tgg cag aag gtg gct gcg gtg att
192
Tyr Asp Asp Asn Thr Pro Asp Arg Trp Gln Lys Val Ala Ala Val Ile
    50   55   60

ccg ggg aag aca gtg agt gac gta att aga cag tat aac gat ttg gaa
240
Pro Gly Lys Thr Val Ser Asp Val Ile Arg Gln Tyr Asn Asp Leu Glu
65   70   75   80

gct gat gtc agc agc atc gag gcc ggt tta atc ccg gtc ccc ggt tac
288
Ala Asp Val Ser Ser Ile Glu Ala Gly Leu Ile Pro Val Pro Gly Tyr
                85   90   95

atc acc tcg ccg cct ttc act cta gat tgg gcc ggc ggc ggt ggc gga
336
Ile Thr Ser Pro Pro Phe Thr Leu Asp Trp Ala Gly Gly Gly Gly Gly
            100   105   110
```

452

```
tgt aac ggg ttt aaa ccg ggt cat cag gtt tgt aat aaa cgg tcg cag
384
Cys Asn Gly Phe Lys Pro Gly His Gln Val Cys Asn Lys Arg Ser Gln
        115             120             125

gcc ggt aga tcg ccg gag ctg gag cgg aag aaa ggc gtt cct tgg acg
432
Ala Gly Arg Ser Pro Glu Leu Glu Arg Lys Lys Gly Val Pro Trp Thr
        130             135             140

gag gaa gaa cac aag cta ttt cta atg ggt ttg aag aaa tat ggg aaa
480
Glu Glu Glu His Lys Leu Phe Leu Met Gly Leu Lys Lys Tyr Gly Lys
145             150             155             160

gga gat tgg aga aac ata tct cgg aac ttt gtg ata acg cga acg cca
528
Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Ile Thr Arg Thr Pro
            165             170             175

aca caa gta gct agc cac gcc caa aag tac ttc atc cgg caa ctt tcc
576
Thr Gln Val Ala Ser His Ala Gln Lys Tyr Phe Ile Arg Gln Leu Ser
        180             185             190

ggc ggc aag gac aag aga cga gca agc att cac gac ata acc acc gta
624
Gly Gly Lys Asp Lys Arg Arg Ala Ser Ile His Asp Ile Thr Thr Val
        195             200             205

aat ctc gaa gag gag gct tct ttg gag acc aat aag agc tcc att gtt
672
Asn Leu Glu Glu Glu Ala Ser Leu Glu Thr Asn Lys Ser Ser Ile Val
    210             215             220

gtt gga gat cag cgt tca agg cta acc gcg ttt cct tgg aac caa acg
720
Val Gly Asp Gln Arg Ser Arg Leu Thr Ala Phe Pro Trp Asn Gln Thr
225             230             235             240

gac aac aat gga aca cag gca gac gct ttc aat ata acg att gga aac
768
Asp Asn Asn Gly Thr Gln Ala Asp Ala Phe Asn Ile Thr Ile Gly Asn
            245             250             255

gct att agt ggc gtt cat tca tac ggc cag gtt atg att gga ggg tat
816
Ala Ile Ser Gly Val His Ser Tyr Gly Gln Val Met Ile Gly Gly Tyr
            260             265             270

aac aat gca gat tct tgc tat gac gcc caa aac aca atg ttt caa cta
864
Asn Asn Ala Asp Ser Cys Tyr Asp Ala Gln Asn Thr Met Phe Gln Leu
        275             280             285

tag
867
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<210> 254 <211> 288 <212> PRT <213> Arabidopsis thaliana <400>
254

Met Glu Val Met Arg Pro Ser Thr Ser His Val Ser Gly Gly Asn Trp
1   5   10   15

Leu Met Glu Glu Thr Lys Ser Gly Val Ala Ala Ser Gly Glu Gly Ala
            20   25 ,   30

Thr Trp Thr Ala Ala Glu Asn Lys Ala Phe Glu Asn Ala Leu Ala Val
        35   40   45

Tyr Asp Asp Asn Thr Pro Asp Arg Trp Gln Lys Val Ala Ala Val Ile
    50   55   60

Pro Gly Lys Thr Val Ser Asp Val Ile Arg Gln Tyr Asn Asp Leu Glu
65   70   75   80

Ala Asp Val Ser Ser Ile Glu Ala Gly Leu Ile Pro Val Pro Gly Tyr
                85   90   95

Ile Thr Ser Pro Pro Phe Thr Leu Asp Trp Ala Gly Gly Gly Gly Gly
            100   105   110

Cys Asn Gly Phe Lys Pro Gly His Gln Val Cys Asn Lys Arg Ser Gln
        115   120   125

Ala Gly Arg Ser Pro Glu Leu Glu Arg Lys Lys Gly Val Pro Trp Thr
    130   135   140

Glu Glu Glu His Lys Leu Phe Leu Met Gly Leu Lys Lys Tyr Gly Lys
145   150   155   160

Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Ile Thr Arg Thr Pro
            165   170   175

Thr Gln Val Ala Ser His Ala Gln Lys Tyr Phe Ile Arg Gln Leu Ser
        180   185   190

Gly Gly Lys Asp Lys Arg Arg Ala Ser Ile His Asp Ile Thr Thr Val
        195   200   205

Asn Leu Glu Glu Glu Ala Ser Leu Glu Thr Asn Lys Ser Ser Ile Val
    210   215   220

Val Gly Asp Gln Arg Ser Arg Leu Thr Ala Phe Pro Trp Asn Gln Thr
225   230   235   240

454

Asp Asn Asn Gly Thr Gln Ala Asp Ala Phe Asn Ile Thr Ile Gly Asn
            245   250   255

Ala Ile Ser Gly Val His Ser Tyr Gly Gln Val Met Ile Gly Gly Tyr
            260   265   270

Asn Asn Ala Asp Ser Cys Tyr Asp Ala Gln Asn Thr Met Phe Gln Leu
            275   280   285

<210> 255 <211> 800 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (34)..(786) <223> G1646

<400> 255
gatcttttga tccaatcaca aggcaaagat cca atg gac aat aac aac aac aac
54
                                    Met Asp Asn Asn Asn Asn Asn
                                    1   5

aac aac cag caa cca cca cca acc tcc gtc tat cca cct ggc tcc gcc
102
Asn Asn Gln Gln Pro Pro Pro Thr Ser Val Tyr Pro Pro Gly Ser Ala
        10   15   20

gtc aca acc gta atc cct cct cca cca tct gga tct gca tca ata gtc
150
Val Thr Thr Val Ile Pro Pro Pro Pro Ser Gly Ser Ala Ser Ile Val
    25   30   35

acc gga gga gga gcg aca tac cac cac ctc ctc cag caa caa cag caa
198
Thr Gly Gly Gly Ala Thr Tyr His His Leu Leu Gln Gln Gln Gln Gln
40   45   50   55

cag ctt caa atg ttc tgg aca tac cag aga caa gag atc gaa cag gta
246
Gln Leu Gln Met Phe Trp Thr Tyr Gln Arg Gln Glu Ile Glu Gln Val
                60   65   70

aac gat ttc aaa aac cat cag ctc cct cta gct cgt atc aaa aaa atc
294
Asn Asp Phe Lys Asn His Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile
                75   80   85

atg aaa gct gat gaa gat gtg cgt atg atc tcc gcc gaa gca ccg att
342
Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Ile
            90   95   100

ctc ttc gcg aaa gct tgt gag ctt ttc att ctc gaa ctt acg att aga
390
Leu Phe Ala Lys Ala Cys Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg
        105   110   115

tct tgg ctt cac gct gaa gag aac aaa cgt cgt acg ctt cag aaa aac
438
Ser Trp Leu His Ala Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn

455

```
        120                    125                    130                    135

gat atc gct gct gcg att act aga acc gat atc ttc gat ttc ctt gtt
486
Asp Ile Ala Ala Ala Ile Thr Arg Thr Asp Ile Phe Asp Phe Leu Val
                    140                    145                    150

gat att gtt cct agg gaa gag atc aag gaa gag gaa gat gca gca tcg
534
Asp Ile Val Pro Arg Glu Glu Ile Lys Glu Glu Glu Asp Ala Ala Ser
                155                    160                    165

gct ctt ggt gga gga ggt atg gtt gct ccc gcc gcg agc ggt gtt cct
582
Ala Leu Gly Gly Gly Gly Met Val Ala Pro Ala Ala Ser Gly Val Pro
            170                    175                    180

tat tat tat cca ccg atg gga caa ccg gcg gtt cct gga ggg atg atg
630
Tyr Tyr Tyr Pro Pro Met Gly Gln Pro Ala Val Pro Gly Gly Met Met
        185                    190                    195

att gga aga ccg gcg atg gat cct agc ggt gtt tat gct cag cct cct
678
Ile Gly Arg Pro Ala Met Asp Pro Ser Gly Val Tyr Ala Gln Pro Pro
200                    205                    210                    215

tct cag gca tgg caa agc gtt tgg cag aat tca gct ggt ggt ggt gat
726
Ser Gln Ala Trp Gln Ser Val Trp Gln Asn Ser Ala Gly Gly Gly Asp
                    220                    225                    230

gat gtg tct tat gga agt gga gga agt agc ggc cat ggt aat ctc gat
774
Asp Val Ser Tyr Gly Ser Gly Gly Ser Ser Gly His Gly Asn Leu Asp
                235                    240                    245

agc caa ggg taa gtgaattcta gtag
800
Ser Gln Gly
        250
```

<210> 256 <211> 250 <212> PRT <213> Arabidopsis thaliana <400>
256

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Met Asp Asn Asn Asn Asn Asn Asn Gln Gln Pro Pro Pro Thr Ser
1               5                   10                  15


Val Tyr Pro Pro Gly Ser Ala Val Thr Thr Val Ile Pro Pro Pro Pro
            20                  25                  30


Ser Gly Ser Ala Ser Ile Val Thr Gly Gly Gly Ala Thr Tyr His His
        35                  40                  45


Leu Leu Gln Gln Gln Gln Gln Gln Leu Gln Met Phe Trp Thr Tyr Gln
    50                  55                  60
```

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Arg Gln Glu Ile Glu Gln Val Asn Asp Phe Lys Asn His Gln Leu Pro
65                  70                  75                  80


Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met
                85                  90                  95


Ile Ser Ala Glu Ala Pro Ile Leu Phe Ala Lys Ala Cys Glu Leu Phe
                100                 105                 110


Ile Leu Glu Leu Thr Ile Arg Ser Trp Leu His Ala Glu Glu Asn Lys
                115                 120                 125


Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala Ala Ile Thr Arg Thr
    130                 135                 140


Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro Arg Glu Glu Ile Lys
145                 150                 155                 160


Glu Glu Glu Asp Ala Ala Ser Ala Leu Gly Gly Gly Gly Met Val Ala
                165                 170                 175


Pro Ala Ala Ser Gly Val Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro
                180                 185                 190


Ala Val Pro Gly Gly Met Met Ile Gly Arg Pro Ala Met Asp Pro Ser
                195                 200                 205


Gly Val Tyr Ala Gln Pro Pro Ser Gln Ala Trp Gln Ser Val Trp Gln
    210                 215                 220


Asn Ser Ala Gly Gly Gly Asp Asp Val Ser Tyr Gly Ser Gly Gly Ser
225                 230                 235                 240


Ser Gly His Gly Asn Leu Asp Ser Gln Gly
                245                 250
```

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<210> 257 <211> 938 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (142)..(903) <223> G1667
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<400> 257
tcgacccatc cctactcctc acaatcattc ttttggtgtc tctaccattt aataattcac
60

caaaatctcc ttacttaaac tcacaaactc ctcacaaatt ttctgaatct ttcagttgaa
120

catataacaa cattcataac a atg gct gga ggt aca gct cta act cca acc
171
```

```
                               Met Ala Gly Gly Thr Ala Leu Thr Pro Thr
                               1               5                   10

tct gta gga tcc aag tct gtt cca atg agg aac cat gaa gca aca gag
219
Ser Val Gly Ser Lys Ser Val Pro Met Arg Asn His Glu Ala Thr Glu
                15                  20                  25

aga ggc aac acc aac aac aac ctg aga gca tta ccc aaa gcc gtc caa
267
Arg Gly Asn Thr Asn Asn Asn Leu Arg Ala Leu Pro Lys Ala Val Gln
            30                  35                  40

ccg gtt tca tca atc gaa gga gag atg gct aag agg cca cgt ggc aga
315
Pro Val Ser Ser Ile Glu Gly Glu Met Ala Lys Arg Pro Arg Gly Arg
            45                  50                  55

ccc gct ggc tcc aag aac aaa ccc aaa cca cca atc att gtg act cac
363
Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Val Thr His
    60                  65                  70

gac agt cca aat tcc ctc aga gct aac gcc gtt gag atc agc tca ggt
411
Asp Ser Pro Asn Ser Leu Arg Ala Asn Ala Val Glu Ile Ser Ser Gly
75                  80                  85                  90

tgt gac atc tgt gag act tta tcg gat ttt gca aga agg aaa cag aga
459
Cys Asp Ile Cys Glu Thr Leu Ser Asp Phe Ala Arg Arg Lys Gln Arg
                95                  100                 105

ggt ctc tgc att ctc agt gcc aat ggt tgt gtc acc aat gtg aca tta
507
Gly Leu Cys Ile Leu Ser Ala Asn Gly Cys Val Thr Asn Val Thr Leu
            110                 115                 120

agg caa cca gct tca tca gga gca att gtc aca tta cac gga cgt tac
555
Arg Gln Pro Ala Ser Ser Gly Ala Ile Val Thr Leu His Gly Arg Tyr
            125                 130                 135

gag atc ctc tca ttg ctt gga tca atc ttg cct cca cca gca cca ctt
603
Glu Ile Leu Ser Leu Leu Gly Ser Ile Leu Pro Pro Pro Ala Pro Leu
    140                 145                 150

gga ata act ggt ctg acc att tac tta gcc gga cct caa gga cag gtt
651
Gly Ile Thr Gly Leu Thr Ile Tyr Leu Ala Gly Pro Gln Gly Gln Val
155                 160                 165                 170

gtt ggt gga gga gtg gtt ggt ggg cta atc gca tct ggt cct gtt gtt
699
Val Gly Gly Gly Val Val Gly Gly Leu Ile Ala Ser Gly Pro Val Val
                175                 180                 185

ctc atg gct gca tct ttc atg aat gct gtt ttt gat cgt ctt cct atg
747
Leu Met Ala Ala Ser Phe Met Asn Ala Val Phe Asp Arg Leu Pro Met
```

458

                    190   195   200

gat gat gat gaa gct gcc tct atg cag aac cag cag tac tac cag aat
795
Asp Asp Asp Glu Ala Ala Ser Met Gln Asn Gln Gln Tyr Tyr Gln Asn
        205   210   215

gga aga tcc cgt cct tta gat gac att cat gga ctg cct caa aat ctg
843
Gly Arg Ser Arg Pro Leu Asp Asp Ile His Gly Leu Pro Gln Asn Leu
    220   225   230

ctc act aat gga aac tcg gct tct gat atc tac tct tgg ggg cct tgg
891
Leu Thr Asn Gly Asn Ser Ala Ser Asp Ile Tyr Ser Trp Gly Pro Trp
235   240   245   250

aat caa aga taa atgtgtctgt aggttgagag agaaccgtaa gtctg
938
Asn Gln Arg

<210> 258 <211> 253 <212> PRT <213> Arabidopsis thaliana <400>
258

Met Ala Gly Gly Thr Ala Leu Thr Pro Thr Ser Val Gly Ser Lys Ser
1   5   10   15

Val Pro Met Arg Asn His Glu Ala Thr Glu Arg Gly Asn Thr Asn Asn
            20   25   30

Asn Leu Arg Ala Leu Pro Lys Ala Val Gln Pro Val Ser Ser Ile Glu
        35   40   45

Gly Glu Met Ala Lys Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn
    50   55   60

Lys Pro Lys Pro Pro Ile Ile Val Thr His Asp Ser Pro Asn Ser Leu
65   70   75   80

Arg Ala Asn Ala Val Glu Ile Ser Ser Gly Cys Asp Ile Cys Glu Thr
            85   90   95

Leu Ser Asp Phe Ala Arg Arg Lys Gln Arg Gly Leu Cys Ile Leu Ser
        100   105   110

Ala Asn Gly Cys Val Thr Asn Val Thr Leu Arg Gln Pro Ala Ser Ser
        115   120   125

Gly Ala Ile Val Thr Leu His Gly Arg Tyr Glu Ile Leu Ser Leu Leu
    130   135   140

```
Gly Ser Ile Leu Pro Pro Pro Ala Pro Leu Gly Ile Thr Gly Leu Thr
145             150             155                 160


Ile Tyr Leu Ala Gly Pro Gln Gly Gln Val Val Gly Gly Gly Val Val
                165             170             175


Gly Gly Leu Ile Ala Ser Gly Pro Val Val Leu Met Ala Ala Ser Phe
            180             185             190


Met Asn Ala Val Phe Asp Arg Leu Pro Met Asp Asp Asp Glu Ala Ala
        195             200             205


Ser Met Gln Asn Gln Gln Tyr Tyr Gln Asn Gly Arg Ser Arg Pro Leu
    210             215             220


Asp Asp Ile His Gly Leu Pro Gln Asn Leu Leu Thr Asn Gly Asn Ser
225             230             235             240


Ala Ser Asp Ile Tyr Ser Trp Gly Pro Trp Asn Gln Arg
            245             250
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<210> 259 <211> 1221 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1221) <223> G1706

<400> 259

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atg aaa aat aaa acc caa aaa tat ata gat aag aag acg tgg aac tat
48
Met Lys Asn Lys Thr Gln Lys Tyr Ile Asp Lys Lys Thr Trp Asn Tyr
1               5               10                  15


ata aat atg gac cac cat cac gcc ttt gca tca cat tca tac aac tca
96
Ile Asn Met Asp His His His Ala Phe Ala Ser His Ser Tyr Asn Ser
            20              25              30


gtt ttc ata agc aaa aag gca atg gaa gag tca cga tcc tac aga aag
144
Val Phe Ile Ser Lys Lys Ala Met Glu Glu Ser Arg Ser Tyr Arg Lys
        35              40              45


gag agg aag cag aca aag aag aaa acg ggt cgt ggg tca gga tcc agg
192
Glu Arg Lys Gln Thr Lys Lys Lys Thr Gly Arg Gly Ser Gly Ser Arg
    50              55              60


tcg atc cat ata aag atg agg aag ctt cga gtg ctt ata ccg ggt gga
240
Ser Ile His Ile Lys Met Arg Lys Leu Arg Val Leu Ile Pro Gly Gly
65              70              75              80


cga aga ttg aac caa ccg gat ctg ctt cta tca aag act gct gat tat
288
Arg Arg Leu Asn Gln Pro Asp Leu Leu Leu Ser Lys Thr Ala Asp Tyr
```

                    85   90   95

att atg cat ttg gag ttg agg att agc att cta cat ttg ttg gtc aga
336
Ile Met His Leu Glu Leu Arg Ile Ser Ile Leu His Leu Leu Val Arg
                100   105   110

tat tac tta aag aag aaa aga tca aac ctt tcg tca tca cca aac gaa
384
Tyr Tyr Leu Lys Lys Lys Arg Ser Asn Leu Ser Ser Ser Pro Asn Glu
                115   120   125

tct aat caa aac cca gaa ttt tcc gac tcc gat act tac caa aga cag
432
Ser Asn Gln Asn Pro Glu Phe Ser Asp Ser Asp Thr Tyr Gln Arg Gln
                130   135   140

ctt caa cag ctc ttt cat ctc cat gat tca ggt cta gat caa gct tta
480
Leu Gln Gln Leu Phe His Leu His Asp Ser Gly Leu Asp Gln Ala Leu
145   150   155   160

atc gat gct ctt cct gtg ttt ctt tac aaa gag atc aaa ggt acg aaa
528
Ile Asp Ala Leu Pro Val Phe Leu Tyr Lys Glu Ile Lys Gly Thr Lys
                        165   170   175

gag cct ttt gat tgt gca gtg tgt ctc tgt gaa ttc tcg gaa gat gat
576
Glu Pro Phe Asp Cys Ala Val Cys Leu Cys Glu Phe Ser Glu Asp Asp
                180   185   190

aag ctt aga ttg ctt ccg aat tgt agt cac gct ttt cac ata gat tgt
624
Lys Leu Arg Leu Leu Pro Asn Cys Ser His Ala Phe His Ile Asp Cys
                195   200   205

atc gat act tgg ctt ctc tcg aat tcg act tgt cca ctt tgt aga gga
672
Ile Asp Thr Trp Leu Leu Ser Asn Ser Thr Cys Pro Leu Cys Arg Gly
                210   215   220

acc ctt ttc tct tta ggt cat caa ttt gaa tac cct gat ttc aat ttc
720
Thr Leu Phe Ser Leu Gly His Gln Phe Glu Tyr Pro Asp Phe Asn Phe
225   230   235   240

ggg ttt ttc gcc gga gat gat gga gga gga gga gtt agg gtt tct ccg
768
Gly Phe Phe Ala Gly Asp Asp Gly Gly Gly Gly Val Arg Val Ser Pro
                        245   250   255

gtt cag aaa cca gct gag aat gag att ggg aag aga gtg ttt tca gtg
816
Val Gln Lys Pro Ala Glu Asn Glu Ile Gly Lys Arg Val Phe Ser Val
                260   265   270

agg ctt ggt aag ttt agg agc agt aat att gtc aac aat ggt gaa gta
864
Arg Leu Gly Lys Phe Arg Ser Ser Asn Ile Val Asn Asn Gly Glu Val
                275   280   285

                                461

gta gta gga gga gga gga gag aca agt agt agt agt ctt gat aat aga
912
Val Val Gly Gly Gly Gly Glu Thr Ser Ser Ser Ser Leu Asp Asn Arg
    290   295   300

aga tgt ttc tca atg ggg tct tat cag tac ata gtg gct gaa tca gat
960
Arg Cys Phe Ser Met Gly Ser Tyr Gln Tyr Ile Val Ala Glu Ser Asp
305   310   315   320

ctg gtt gtt gct ttg tgt cct aat aat gaa gga ttg aag aat aat aag
1008
Leu Val Val Ala Leu Cys Pro Asn Asn Glu Gly Leu Lys Asn Asn Lys
            325   330   335

gat gtt gaa ggg aag aag att aat atg aga agt aaa ggt gag agc ttt
1056
Asp Val Glu Gly Lys Lys Ile Asn Met Arg Ser Lys Gly Glu Ser Phe
        340   345   350

tct gtg tca aag att tgg caa tgg tct aat aag aga tca aag ttt cct
1104
Ser Val Ser Lys Ile Trp Gln Trp Ser Asn Lys Arg Ser Lys Phe Pro
        355   360   365

aat aat cat cca tca gag act aat ctt gtg gtt ggt ggt tct tct tct
1152
Asn Asn His Pro Ser Glu Thr Asn Leu Val Val Gly Gly Ser Ser Ser
    370   375   380

tct tct tct tat gtt tgt tct gga tct gat ggg tta tca ttg aat gga
1200
Ser Ser Ser Tyr Val Cys Ser Gly Ser Asp Gly Leu Ser Leu Asn Gly
385   390   395   400

agg aga ttt cag ggt cca tga
1221
Arg Arg Phe Gln Gly Pro
            405

<210> 260 <211> 406 <212> PRT <213> Arabidopsis thaliana <400>
260

Met Lys Asn Lys Thr Gln Lys Tyr Ile Asp Lys Lys Thr Trp Asn Tyr
1   5   10   15

Ile Asn Met Asp His His His Ala Phe Ala Ser His Ser Tyr Asn Ser
            20   25   30

Val Phe Ile Ser Lys Lys Ala Met Glu Glu Ser Arg Ser Tyr Arg Lys
        35   40   45

Glu Arg Lys Gln Thr Lys Lys Lys Thr Gly Arg Gly Ser Gly Ser Arg
    50   55   60

462

```
Ser Ile His Ile Lys Met Arg Lys Leu Arg Val Leu Ile Pro Gly Gly
65               70              75              80


Arg Arg Leu Asn Gln Pro Asp Leu Leu Leu Ser Lys Thr Ala Asp Tyr
            85              90              95


Ile Met His Leu Glu Leu Arg Ile Ser Ile Leu His Leu Leu Val Arg
        100             105             110


Tyr Tyr Leu Lys Lys Lys Arg Ser Asn Leu Ser Ser Ser Pro Asn Glu
        115             120             125


Ser Asn Gln Asn Pro Glu Phe Ser Asp Ser Asp Thr Tyr Gln Arg Gln
    130             135             140


Leu Gln Gln Leu Phe His Leu His Asp Ser Gly Leu Asp Gln Ala Leu
145             150             155             160


Ile Asp Ala Leu Pro Val Phe Leu Tyr Lys Glu Ile Lys Gly Thr Lys
            165             170             175


Glu Pro Phe Asp Cys Ala Val Cys Leu Cys Glu Phe Ser Glu Asp Asp
            180             185             190


Lys Leu Arg Leu Leu Pro Asn Cys Ser His Ala Phe His Ile Asp Cys
        195             200             205


Ile Asp Thr Trp Leu Leu Ser Asn Ser Thr Cys Pro Leu Cys Arg Gly
    210             215             220


Thr Leu Phe Ser Leu Gly His Gln Phe Glu Tyr Pro Asp Phe Asn Phe
225             230             235             240


Gly Phe Phe Ala Gly Asp Asp Gly Gly Gly Val Arg Val Ser Pro
            245             250             255


Val Gln Lys Pro Ala Glu Asn Glu Ile Gly Lys Arg Val Phe Ser Val
            260             265             270


Arg Leu Gly Lys Phe Arg Ser Ser Asn Ile Val Asn Asn Gly Glu Val
        275             280             285


Val Val Gly Gly Gly Gly Glu Thr Ser Ser Ser Ser Leu Asp Asn Arg
    290             295             300


Arg Cys Phe Ser Met Gly Ser Tyr Gln Tyr Ile Val Ala Glu Ser Asp
```

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305              310              315              320
```

Leu Val Val Ala Leu Cys Pro Asn Asn Glu Gly Leu Lys Asn Asn Lys
                325   330   335

Asp Val Glu Gly Lys Lys Ile Asn Met Arg Ser Lys Gly Glu Ser Phe
                340   345   350

Ser Val Ser Lys Ile Trp Gln Trp Ser Asn Lys Arg Ser Lys Phe Pro
                355   360   365

Asn Asn His Pro Ser Glu Thr Asn Leu Val Val Gly Gly Ser Ser Ser
        370   375   380

Ser Ser Ser Tyr Val Cys Ser Gly Ser Asp Gly Leu Ser Leu Asn Gly
385   390   395   400

Arg Arg Phe Gln Gly Pro
                405

<210> 261 <211> 1410 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (32)..(1216) <223> G1766

  <400> 261
aggctattct cggaaaaaca aagaataaag a atg aat tcg ttt tca caa gta
52
                                  Met Asn Ser Phe Ser Gln Val
                                  1   5

cct cct ggc ttc aga ttt cat cct act gat gaa gaa ctt gta gac tac
100
Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Asp Tyr
        10   15   20

tac ttg agg aaa aaa gtt gca tca aag aga ata gaa atc gat atc atc
148
Tyr Leu Arg Lys Lys Val Ala Ser Lys Arg Ile Glu Ile Asp Ile Ile
    25   30   35

aag gat gtt gat ctt tac aag att gag cca tgt gat ctt caa gag tta
196
Lys Asp Val Asp Leu Tyr Lys Ile Glu Pro Cys Asp Leu Gln Glu Leu
40   45   50   55

tgc aag ata gga aac gaa gag cag agc gaa tgg tac ttc ttt agt cat
244
Cys Lys Ile Gly Asn Glu Glu Gln Ser Glu Trp Tyr Phe Phe Ser His
                60   65   70

aaa gac aag aag tat ccc acg gga act cga acc aat aga gcc acg aaa
292
Lys Asp Lys Lys Tyr Pro Thr Gly Thr Arg Thr Asn Arg Ala Thr Lys
                75   80   85
```

```
gca gga ttt tgg aaa gcc act gga aga gac aag gct ata tat ata aga
340
Ala Gly Phe Trp Lys Ala Thr Gly Arg Asp Lys Ala Ile Tyr Ile Arg
        90              95                  100

cat agt ctt atc ggt atg agg aaa aca ctt gtg ttt tac aaa gga aga
388
His Ser Leu Ile Gly Met Arg Lys Thr Leu Val Phe Tyr Lys Gly Arg
    105             110                 115

gcc cca aat ggt cag aaa tcc gat tgg atc atg cac gaa tat cgc tta
436
Ala Pro Asn Gly Gln Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu
120             125             130                 135

gaa aca agt gaa aat gga acc cct cag gaa gaa gga tgg gta gta tgt
484
Glu Thr Ser Glu Asn Gly Thr Pro Gln Glu Glu Gly Trp Val Val Cys
            140             145                 150

agg gta ttc aag aag aaa ttg gca gcg aca gtg agg aaa atg gga gat
532
Arg Val Phe Lys Lys Lys Leu Ala Ala Thr Val Arg Lys Met Gly Asp
        155             160                 165

tac cat tca tca cca tcg cag cat tgg tac gat gat cag ctc tct ttt
580
Tyr His Ser Ser Pro Ser Gln His Trp Tyr Asp Asp Gln Leu Ser Phe
        170             175                 180

atg gcc tcc gag atc att tct agt tct cca cga cag ttt ctt ccc aat
628
Met Ala Ser Glu Ile Ile Ser Ser Ser Pro Arg Gln Phe Leu Pro Asn
    185             190                 195

cat cat tat aac cgc cac cat cac cag cag aca ttg cct tgt ggc ctc
676
His His Tyr Asn Arg His His His Gln Gln Thr Leu Pro Cys Gly Leu
200             205             210                 215

aat gca ttc aac aac aac aat cct aac ttg caa tgc aag caa gag ctc
724
Asn Ala Phe Asn Asn Asn Asn Pro Asn Leu Gln Cys Lys Gln Glu Leu
            220             225                 230

gag tta cat tac aat caa atg gta caa cat caa caa caa aac cat cat
772
Glu Leu His Tyr Asn Gln Met Val Gln His Gln Gln Gln Asn His His
        235             240                 245

ctt cgt gaa tct atg ttt ctc cag ctt cct cag ctc gaa agc cct acc
820
Leu Arg Glu Ser Met Phe Leu Gln Leu Pro Gln Leu Glu Ser Pro Thr
        250             255                 260

agt aat tgc aat tct gac aac aac aat aac aca aga aat att agt aac
868
Ser Asn Cys Asn Ser Asp Asn Asn Asn Asn Thr Arg Asn Ile Ser Asn
    265             270                 275
```

465

ttg cag aaa tca tca aat ata tct cat gag gaa caa ttg caa caa ggg
916
Leu Gln Lys Ser Ser Asn Ile Ser His Glu Glu Gln Leu Gln Gln Gly
280   285   290   295

aat caa agt ttc agc tct ctg tat tac gat caa gga gta gag caa atg
964
Asn Gln Ser Phe Ser Ser Leu Tyr Tyr Asp Gln Gly Val Glu Gln Met
                300   305   310

act act gac tgg aga gtt ctc gat aaa ttt gtt gct tca cag ctt agc
1012
Thr Thr Asp Trp Arg Val Leu Asp Lys Phe Val Ala Ser Gln Leu Ser
                315   320   325

aat gat gaa gag gct gca gcc gtg gtt tct tct tct tct cat caa aac
1060
Asn Asp Glu Glu Ala Ala Ala Val Val Ser Ser Ser Ser His Gln Asn
            330   335   340

aac gtc aag att gac acg aga aac acg ggt tat cat gtg ata gat gag
1108
Asn Val Lys Ile Asp Thr Arg Asn Thr Gly Tyr His Val Ile Asp Glu
        345   350   355

gga ata aat ttg ccg gag aat gat tct gaa agg gtt gtt gaa atg gga
1156
Gly Ile Asn Leu Pro Glu Asn Asp Ser Glu Arg Val Val Glu Met Gly
360   365   370   375

gaa gag tat tca aat gct cat gct gct tct act tct tca agt tgt cag
1204
Glu Glu Tyr Ser Asn Ala His Ala Ala Ser Thr Ser Ser Ser Cys Gln
                380   385   390

att gat ctc tag aaatagtgat agagagatga aaaagatgca aggtgaatat
1256
Ile Asp Leu

atatgaaaat acatgcacac tagtgttatt tatacttaaa gatggaaggg gaaaaacaag
1316

gagttatttc ctggatttat ggaggttttg tacataataa aaacctacaa ccatatggta
1376

ttttcttttg aaaaaaaaaa aaaaaaaaaa aaaa
1410

<210> 262 <211> 394 <212> PRT <213> Arabidopsis thaliana <400>
262

Met Asn Ser Phe Ser Gln Val Pro Pro Gly Phe Arg Phe His Pro Thr
1   5   10   15

Asp Glu Glu Leu Val Asp Tyr Tyr Leu Arg Lys Lys Val Ala Ser Lys
            20   25   30

466

```
Arg Ile Glu Ile Asp Ile Ile Lys Asp Val Asp Leu Tyr Lys Ile Glu
        35              40              45

Pro Cys Asp Leu Gln Glu Leu Cys Lys Ile Gly Asn Glu Glu Gln Ser
     50              55              60

Glu Trp Tyr Phe Phe Ser His Lys Asp Lys Lys Tyr Pro Thr Gly Thr
65              70              75              80

Arg Thr Asn Arg Ala Thr Lys Ala Gly Phe Trp Lys Ala Thr Gly Arg
             85              90              95

Asp Lys Ala Ile Tyr Ile Arg His Ser Leu Ile Gly Met Arg Lys Thr
             100             105             110

Leu Val Phe Tyr Lys Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp
        115             120             125

Ile Met His Glu Tyr Arg Leu Glu Thr Ser Glu Asn Gly Thr Pro Gln
    130             135             140

Glu Glu Gly Trp Val Val Cys Arg Val Phe Lys Lys Lys Leu Ala Ala
145             150             155             160

Thr Val Arg Lys Met Gly Asp Tyr His Ser Ser Pro Ser Gln His Trp
             165             170             175

Tyr Asp Asp Gln Leu Ser Phe Met Ala Ser Glu Ile Ile Ser Ser Ser
             180             185             190

Pro Arg Gln Phe Leu Pro Asn His His Tyr Asn Arg His His His Gln
    195             200             205

Gln Thr Leu Pro Cys Gly Leu Asn Ala Phe Asn Asn Asn Asn Pro Asn
    210             215             220

Leu Gln Cys Lys Gln Glu Leu Glu Leu His Tyr Asn Gln Met Val Gln
225             230             235             240

His Gln Gln Gln Asn His His Leu Arg Glu Ser Met Phe Leu Gln Leu
             245             250             255

Pro Gln Leu Glu Ser Pro Thr Ser Asn Cys Asn Ser Asp Asn Asn Asn
    260             265             270

Asn Thr Arg Asn Ile Ser Asn Leu Gln Lys Ser Ser Asn Ile Ser His
```

```
            275                   280                   285


Glu Glu Gln Leu Gln Gln Gly Asn Gln Ser Phe Ser Ser Leu Tyr Tyr
    290                   295                   300


Asp Gln Gly Val Glu Gln Met Thr Thr Asp Trp Arg Val Leu Asp Lys
305                   310                   315                   320


Phe Val Ala Ser Gln Leu Ser Asn Asp Glu Glu Ala Ala Ala Val Val
                325                   330                   335


Ser Ser Ser Ser His Gln Asn Asn Val Lys Ile Asp Thr Arg Asn Thr
            340                   345                   350


Gly Tyr His Val Ile Asp Glu Gly Ile Asn Leu Pro Glu Asn Asp Ser
            355                   360                   365


Glu Arg Val Val Glu Met Gly Glu Glu Tyr Ser Asn Ala His Ala Ala
    370                   375                   380


Ser Thr Ser Ser Ser Cys Gln Ile Asp Leu
385                   390
```

<210> 263 <211> 927 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(927) <223> G1782

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<400> 263
atg caa gtg ttt caa agg aaa gaa gat tca tct tgg gga aac tca atg
48
Met Gln Val Phe Gln Arg Lys Glu Asp Ser Ser Trp Gly Asn Ser Met
1               5                   10                  15

cct aca aca aat tca aat att caa gga tct gaa tct ttc agc ttg act
96
Pro Thr Thr Asn Ser Asn Ile Gln Gly Ser Glu Ser Phe Ser Leu Thr
            20                  25                  30

aag gat atg ata atg tct aca aca caa tta ccc gcg atg aaa cat tcg
144
Lys Asp Met Ile Met Ser Thr Thr Gln Leu Pro Ala Met Lys His Ser
        35                  40                  45

ggt ttg cag ctg caa aat caa gat tca acc tca tca caa tct act gaa
192
Gly Leu Gln Leu Gln Asn Gln Asp Ser Thr Ser Ser Gln Ser Thr Glu
    50                  55                  60

gaa gaa tca ggc ggc ggt gaa gtt gca agc ttt gga gaa tat aag cgt
240
Glu Glu Ser Gly Gly Gly Glu Val Ala Ser Phe Gly Glu Tyr Lys Arg
65                  70                  75                  80
```

468

tat gga tgc agc att gtt aat aac aat ctc tca ggt tac atc gaa aac
288
Tyr Gly Cys Ser Ile Val Asn Asn Asn Leu Ser Gly Tyr Ile Glu Asn
                    85   90   95

ttg gga aag cct att gaa aat tat act aag tca att act acc tcg tcg
336
Leu Gly Lys Pro Ile Glu Asn Tyr Thr Lys Ser Ile Thr Thr Ser Ser
            100   105   110

atg gtg tct caa gac tct gtg ttt cct gct cct act tct ggt caa ata
384
Met Val Ser Gln Asp Ser Val Phe Pro Ala Pro Thr Ser Gly Gln Ile
            115   120   125

tct tgg tct ctt caa tgt gct gaa acg tca cat ttc aat ggt ttc ttg
432
Ser Trp Ser Leu Gln Cys Ala Glu Thr Ser His Phe Asn Gly Phe Leu
        130   135   140

gct cct gaa tat gca tca aca cca acg gcg ctg cca cat tta gag atg
480
Ala Pro Glu Tyr Ala Ser Thr Pro Thr Ala Leu Pro His Leu Glu Met
145   150   155   160

atg ggt ttg gtt tct tca aga gtg cca ttg cct cat cac att caa gag
528
Met Gly Leu Val Ser Ser Arg Val Pro Leu Pro His His Ile Gln Glu
                165   170   175

aat gaa cca ata ttt gtc aat gcg aaa cag tat cat gcg att ctc cgt
576
Asn Glu Pro Ile Phe Val Asn Ala Lys Gln Tyr His Ala Ile Leu Arg
            180   185   190

cgc agg aag cac cgt gct aaa ctc gaa gct cag aac aaa ctc atc aaa
624
Arg Arg Lys His Arg Ala Lys Leu Glu Ala Gln Asn Lys Leu Ile Lys
            195   200   205

tgc cgt aaa ccg tac ctt cat gag tct cgc cat ctt cat gct tta aag
672
Cys Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His Ala Leu Lys
        210   215   220

aga gct aga ggc tcc ggt gga cgt ttc ctc aat aca aag aag ctt caa
720
Arg Ala Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Lys Leu Gln
225   230   235   240

gaa tca tca aac tca ctg tgt tct tct caa atg gca aat gga caa aat
768
Glu Ser Ser Asn Ser Leu Cys Ser Ser Gln Met Ala Asn Gly Gln Asn
                245   250   255

ttc tct atg agc cct cac ggt ggt gga agc gga atc ggg tct agt tcg
816
Phe Ser Met Ser Pro His Gly Gly Gly Ser Gly Ile Gly Ser Ser Ser
                260   265   270

atc tca ccg agc tcc aat tca aac tgt atc aac atg ttc caa aac ccg
864
Ile Ser Pro Ser Ser Asn Ser Asn Cys Ile Asn Met Phe Gln Asn Pro
         275   280   285

cag ttc aga ttc tca ggt tat ccg tca aca cac cat gcc tca gct ctc
912
Gln Phe Arg Phe Ser Gly Tyr Pro Ser Thr His His Ala Ser Ala Leu
     290   295   300

atg tca ggg act tga
927
Met Ser Gly Thr
305

<210> 264 <211> 308 <212> PRT <213> Arabidopsis thaliana <400>
264

Met Gln Val Phe Gln Arg Lys Glu Asp Ser Ser Trp Gly Asn Ser Met
1   5   10   15

Pro Thr Thr Asn Ser Asn Ile Gln Gly Ser Glu Ser Phe Ser Leu Thr
             20   25   30

Lys Asp Met Ile Met Ser Thr Thr Gln Leu Pro Ala Met Lys His Ser
         35   40   45

Gly Leu Gln Leu Gln Asn Gln Asp Ser Thr Ser Ser Gln Ser Thr Glu
     50   55   60

Glu Glu Ser Gly Gly Gly Glu Val Ala Ser Phe Gly Glu Tyr Lys Arg
65   70   75   80

Tyr Gly Cys Ser Ile Val Asn Asn Asn Leu Ser Gly Tyr Ile Glu Asn
                 85   90   95

Leu Gly Lys Pro Ile Glu Asn Tyr Thr Lys Ser Ile Thr Thr Ser Ser
             100   105   110

Met Val Ser Gln Asp Ser Val Phe Pro Ala Pro Thr Ser Gly Gln Ile
         115   120   125

Ser Trp Ser Leu Gln Cys Ala Glu Thr Ser His Phe Asn Gly Phe Leu
     130   135   140

Ala Pro Glu Tyr Ala Ser Thr Pro Thr Ala Leu Pro His Leu Glu Met
145   150   155   160

Met Gly Leu Val Ser Ser Arg Val Pro Leu Pro His His Ile Gln Glu
                 165   170   175

470

```
Asn Glu Pro Ile Phe Val Asn Ala Lys Gln Tyr His Ala Ile Leu Arg
            180                 185             190


Arg Arg Lys His Arg Ala Lys Leu Glu Ala Gln Asn Lys Leu Ile Lys
            195             200                 205


Cys Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His Ala Leu Lys
            210             215             220


Arg Ala Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Lys Leu Gln
225             230                 235                 240


Glu Ser Ser Asn Ser Leu Cys Ser Ser Gln Met Ala Asn Gly Gln Asn
            245                 250                 255


Phe Ser Met Ser Pro His Gly Gly Gly Ser Gly Ile Gly Ser Ser Ser
            260                 265                 270


Ile Ser Pro Ser Ser Asn Ser Asn Cys Ile Asn Met Phe Gln Asn Pro
            275                 280                 285


Gln Phe Arg Phe Ser Gly Tyr Pro Ser Thr His His Ala Ser Ala Leu
    290                 295                 300


Met Ser Gly Thr
305


<210>  265 <211>  450 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (27)..(422) <223>  G1795

 <400>  265
acaaacacgc aaaaagtcat taatat atg gat caa gga ggt cga ggt gtc ggt
53
                            Met Asp Gln Gly Gly Arg Gly Val Gly
                            1               5


gcc gag cat gga aag tac cgg gga gtt cgg aga cga cct tgg gga aaa
101
Ala Glu His Gly Lys Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys
10                  15                  20                  25


tat gca gca gag ata cga gat tcg agg aag cac ggt gaa cgt gtg tgg
149
Tyr Ala Ala Glu Ile Arg Asp Ser Arg Lys His Gly Glu Arg Val Trp
                    30              35                  40


ctt gga acg ttc gat acg gca gag gaa gcg gct aga gcc tat gac caa
197
Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Gln
                45                  50                  55
```

471

```
gct gct tac tcc atg aga ggc caa gca gca atc ctt aac ttc cct cat
245
Ala Ala Tyr Ser Met Arg Gly Gln Ala Ala Ile Leu Asn Phe Pro His
        60              65              70

gag tat aac atg ggg agt ggt gtc tct tct tcc acc gcc atg gct gga
293
Glu Tyr Asn Met Gly Ser Gly Val Ser Ser Ser Thr Ala Met Ala Gly
    75              80              .       85

tct tcc tcc gcc tcc gcc tcc gct tct tct tct tct agg caa gtt ttt       .
341
Ser Ser Ser Ala Ser Ala Ser Ala Ser Ser Ser Ser Arg Gln Val Phe
90              95              100             105

gaa ttt gag tac ttg gat gat agt gtt ttg gag gag ctc ctt gag gaa
389
Glu Phe Glu Tyr Leu Asp Asp Ser Val Leu Glu Glu Leu Leu Glu Glu
            110             115             120

gga gag aaa cct aac aag ggc aag aag aaa tga gcgagatata attcatgatt
442
Gly Glu Lys Pro Asn Lys Gly Lys Lys Lys
            125             130

atttctaa
450


<210>  266 <211>  131 <212>   PRT <213>   Arabidopsis thaliana  <400>
266

Met Asp Gln Gly Gly Arg Gly Val Gly Ala Glu His Gly Lys Tyr Arg
1               5               10              15


Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile Arg Asp
            20              25              30


Ser Arg Lys His Gly Glu Arg Val Trp Leu Gly Thr Phe Asp Thr Ala
    .       35      .       40              45


Glu Glu Ala Ala Arg Ala Tyr Asp Gln Ala Ala Tyr Ser Met Arg Gly
    50          .       55              60


Gln Ala Ala Ile Leu Asn Phe Pro His Glu Tyr Asn Met Gly Ser Gly
65              70              75              80


Val Ser Ser Ser Thr Ala Met Ala Gly Ser Ser Ser Ala Ser Ala Ser
            85              90              95


Ala Ser Ser Ser Ser Arg Gln Val Phe Glu Phe Glu Tyr Leu Asp Asp
            100             105             110
```

Ser Val Leu Glu Glu·Leu Leu Glu Glu Gly Glu Lys Pro Asn Lys Gly
        115   ·   120   125

Lys Lys Lys
    130

<210> 267 <211> 1716 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (169)..(1497) <223> G1804

<400> 267
tatctctctc tttctcaaaa cctttcagtc aaaattctcc ggcggctttt aaactatgtg
60

aaggaggaga acctccataa caagaagcgg attctctcag ttttccggcg gcggaggaac
120

acaaagccac cggttttttag acacacagat ttcattttca gttgttaa atg gta act
177
                                                                Met Val Thr
                                                                1

aga gaa acg aag ttg acg tca gag cga gaa gta gag tcg tcc atg gcg
225
Arg Glu Thr Lys Leu Thr Ser Glu Arg Glu Val Glu Ser Ser Met Ala
    5   10   15

caa gcg aga cat aat gga gga ggt ggt ggt gag aat cat ccg ttt act
273
Gln Ala Arg His Asn Gly Gly Gly Gly Gly Glu Asn His Pro Phe Thr
20   25   30   .   35

tct ttg gga aga caa tcc tct atc tac tca ttg acc ctt gac gag ttc
321
Ser Leu Gly Arg Gln Ser Ser Ile Tyr Ser Leu Thr Leu Asp Glu Phe
                40   45   50 ·

caa cat gct tta tgt gag aac ggc aag aac ttt ggg tcc atg aac atg
369
Gln His Ala Leu Cys Glu Asn Gly Lys Asn Phe Gly Ser Met Asn Met
            55   60   65

gac gag ttt ctt gtc tct att tgg aac gca gag gag aat aat aac aat
417
Asp Glu Phe Leu Val Ser Ile Trp Asn Ala Glu Glu Asn Asn Asn Asn
        70   75   80

caa caa caa gca gca gca gct gca ggt tca cat tct gtt ccg gct aat
465
Gln Gln Gln Ala Ala Ala Ala Ala Gly Ser His Ser Val Pro Ala Asn
    85   90   95

cac aat ggt ttc aac aac aac aat aac aat gga ggc gag ggt ggt gtt
513
His Asn Gly Phe Asn Asn Asn Asn Asn Asn Gly Gly Glu Gly Gly Val
100   105   110   115

ggt gtc ttt agt ggt ggt tct aga ggc aac gaa gat gct aac aat aag
561
Gly Val Phe Ser Gly Gly Ser Arg Gly Asn Glu Asp Ala Asn Asn Lys

473

```
                   120                  125                  130

aga ggg ata gcg aac gag tct agt ctt cct cga caa ggc tct ttg aca
609
Arg Gly Ile Ala Asn Glu Ser Ser Leu Pro Arg Gln Gly Ser Leu Thr
            135                  140                  145

ctt cca gct ccg ctt tgt agg aag act gtt gat gag gtt tgg tct gag
657
Leu Pro Ala Pro Leu Cys Arg Lys Thr Val Asp Glu Val Trp Ser Glu
        150                  155                  160

ata cat aga ggt ggt ggt agc ggt aat gga gga gac agc aat gga cgt
705
Ile His Arg Gly Gly Gly Ser Gly Asn Gly Gly Asp Ser Asn Gly Arg
    165                  170                  175

agt agt agt agt aat gga cag aac aat gct cag aac ggc ggt gag act
753
Ser Ser Ser Ser Asn Gly Gln Asn Asn Ala Gln Asn Gly Gly Glu Thr
180                  185                  190                  195

gcg gct aga caa ccg act ttt gga gag atg aca ctt gag gat ttc ttg
801
Ala Ala Arg Gln Pro Thr Phe Gly Glu Met Thr Leu Glu Asp Phe Leu
            200                  205                  210

gtg aag gct ggt gtg gtt aga gaa cat ccc act aat cct aaa cct aat
849
Val Lys Ala Gly Val Val Arg Glu His Pro Thr Asn Pro Lys Pro Asn
        215                  220                  225

cca aac ccg aac caa aac caa aac ccg tct agt gta ata ccc gca gct
897
Pro Asn Pro Asn Gln Asn Gln Asn Pro Ser Ser Val Ile Pro Ala Ala
        230                  235                  240

gca cag caa cag ctt tat ggt gtg ttt caa gga acc ggt gat cct tca
945
Ala Gln Gln Gln Leu Tyr Gly Val Phe Gln Gly Thr Gly Asp Pro Ser
    245                  250                  255

ttc ccg ggt caa gct atg ggt gtg ggt gac cca tca ggt tat gct aaa
993
Phe Pro Gly Gln Ala Met Gly Val Gly Asp Pro Ser Gly Tyr Ala Lys
260                  265                  270                  275

agg aca gga gga gga ggg tat cag cag gcg cca cca gtt cag gca ggt
1041
Arg Thr Gly Gly Gly Gly Tyr Gln Gln Ala Pro Pro Val Gln Ala Gly
            280                  285                  290

gtt tgc tat gga ggt ggc gtt ggg ttt gga gcg ggt gga cag caa atg
1089
Val Cys Tyr Gly Gly Gly Val Gly Phe Gly Ala Gly Gly Gln Gln Met
            295                  300                  305

gga atg gtt gga ccg tta agc ccg gtg tct tca gat gga tta gga cat
1137
Gly Met Val Gly Pro Leu Ser Pro Val Ser Ser Asp Gly Leu Gly His
            310                  315                  320
```

474

gga caa gtg gat aac ata gga ggt cag tat gga gta gat atg gga ggg
1185
Gly Gln Val Asp Asn Ile Gly Gly Gln Tyr Gly Val Asp Met Gly Gly
    325   330   335

cta agg gga agg aaa aga gta gtg gat ggt cca gtg gag aaa gta gtg
1233
Leu Arg Gly Arg Lys Arg Val Val Asp Gly Pro Val Glu Lys Val Val
340   345   350   355

gag aga aga cag agg agg atg atc aag aac cgc gag tct gct gct aga
1281
Glu Arg Arg Gln Arg Arg Met Ile Lys Asn Arg Glu Ser Ala Ala Arg
                360   365   370

tct aga gca aga aaa caa gca tat aca gtg gaa ttg gaa gct gaa ctt
1329
Ser Arg Ala Arg Lys Gln Ala Tyr Thr Val Glu Leu Glu Ala Glu Leu
            375   380   385

aac cag ttg aaa gaa gag aat gcg cag cta aaa cat gca ttg gcg gag
1377
Asn Gln Leu Lys Glu Glu Asn Ala Gln Leu Lys His Ala Leu Ala Glu
        390   395   400

ttg gag agg aag agg aag caa cag tat ttt gag agt ttg aag tca agg
1425
Leu Glu Arg Lys Arg Lys Gln Gln Tyr Phe Glu Ser Leu Lys Ser Arg
    405   410   415

gca caa ccg aaa ttg ccg aaa tcg aac ggg aga ttg cgg aca ttg atg
1473
Ala Gln Pro Lys Leu Pro Lys Ser Asn Gly Arg Leu Arg Thr Leu Met
420   425   430   435

agg aac ccg agt tgt cca ctc taa acaaacaata ggaagatgga gaagaagtcg
1527
Arg Asn Pro Ser Cys Pro Leu
                440

gagacagaac gagggaaaaa ctgatgattt tctacgttgt tgttttgtct ttgaggaatg
1587

aggttataga atctttatac tttgatgttt tctgtgttgg taggaggaac accatctgat
1647

ctgctttact agtgttccct gtgaacaaag aaagtgattc tgtgtttcaa catcatcaat
1707

ctttggaaa
1716

<210> 268 <211> 442 <212> PRT <213> Arabidopsis thaliana <400>
268

Met Val Thr Arg Glu Thr Lys Leu Thr Ser Glu Arg Glu Val Glu Ser
1   5   10   15

Ser Met Ala Gln Ala Arg His Asn Gly Gly Gly Gly Gly Glu Asn His
            20   25   30

Pro Phe Thr Ser Leu Gly Arg Gln Ser Ser Ile Tyr Ser Leu Thr Leu
            35   40   45

Asp Glu Phe Gln His Ala Leu Cys Glu Asn Gly Lys Asn Phe Gly Ser
    50   55   60

Met Asn Met Asp Glu Phe Leu Val Ser Ile Trp Asn Ala Glu Glu Asn
65   70   75   80

Asn Asn Asn Gln Gln Gln Ala Ala Ala Ala Gly Ser His Ser Val
            85   90   95

Pro Ala Asn His Asn Gly Phe Asn Asn Asn Asn Asn Gly Gly Glu
            100   105   110

Gly Gly Val Gly Val Phe Ser Gly Gly Ser Arg Gly Asn Glu Asp Ala
            115   120   125

Asn Asn Lys Arg Gly Ile Ala Asn Glu Ser Ser Leu Pro Arg Gln Gly
    130   135   140

Ser Leu Thr Leu Pro Ala Pro Leu Cys Arg Lys Thr Val Asp Glu Val
145   150   155   160

Trp Ser Glu Ile His Arg Gly Gly Gly Ser Gly Asn Gly Gly Asp Ser
            165   170   175

Asn Gly Arg Ser Ser Ser Ser Asn Gly Gln Asn Asn Ala Gln Asn Gly
            180   185   190

Gly Glu Thr Ala Ala Arg Gln Pro Thr Phe Gly Glu Met Thr Leu Glu
            195   200   205

Asp Phe Leu Val Lys Ala Gly Val Val Arg Glu His Pro Thr Asn Pro
    210   215   220

Lys Pro Asn Pro Asn Pro Asn Gln Asn Gln Asn Pro Ser Ser Val Ile
225   230   235   240

Pro Ala Ala Ala Gln Gln Gln Leu Tyr Gly Val Phe Gln Gly Thr Gly
            245   250   255

Asp Pro Ser Phe Pro Gly Gln Ala Met Gly Val Gly Asp Pro Ser Gly

```
          260                   265                   270


Tyr Ala Lys Arg Thr Gly Gly Gly Gly Tyr Gln Gln Ala Pro Pro Val
        275.                  280                   285


Gln Ala Gly Val Cys Tyr Gly Gly Gly Val Gly Phe Gly Ala Gly Gly
    290                   295                   300


Gln Gln Met Gly Met Val Gly Pro Leu Ser Pro Val Ser Ser Asp Gly
305                   310                   315                   320


Leu Gly His Gly Gln Val Asp Asn Ile Gly Gly Gln Tyr Gly Val Asp
                  325                   330                   335


Met Gly Gly Leu Arg Gly Arg Lys Arg Val Val Asp Gly Pro Val Glu
              340                   345                   350


Lys Val Val Glu Arg Arg Gln Arg Arg Met Ile Lys Asn Arg Glu Ser
        355                   360                   365


Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Val Glu Leu Glu
    370                   375 ·                 380


Ala Glu Leu Asn Gln Leu Lys Glu Glu Asn Ala Gln Leu Lys His Ala
385                 ·   390                   395                   400


Leu Ala Glu Leu Glu Arg Lys Arg Lys Gln Gln Tyr Phe Glu Ser Leu
                  405                   410                   415


Lys Ser Arg Ala Gln Pro Lys Leu Pro Lys Ser Asn Gly Arg Leu Arg
              420                   425                   430


Thr Leu Met Arg Asn Pro Ser Cys Pro Leu
        435                   440
```

<210> 269 <211> 1662 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1662) <223> G1807

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 <400>  269
atg ggt gat aca gag aag tgt aac agt gat atg atc cag aga ctt cat
48
Met Gly Asp Thr Glu Lys Cys Asn Ser Asp Met Ile Gln Arg Leu His
1                 5                   10                  15


tca tct ttc ggc act act tct tct tcc att ccc aaa aat ccc att tct
96
Ser Ser Phe Gly Thr Thr Ser Ser Ser Ile Pro Lys Asn Pro Ile Ser
              20                  25                  30
```

```
cag ctc gat tta aac cct aat ttc atc cgc tca tca gct cct caa ttc
144
Gln Leu Asp Leu Asn Pro Asn Phe Ile Arg Ser Ser Ala Pro Gln Phe
        35              40              45

tcc aag cct ttc agt gac agt ggc aaa cga atc ggt gtt cct ccg tcg
192
Ser Lys Pro Phe Ser Asp Ser Gly Lys Arg Ile Gly Val Pro Pro Ser
    50              55              60

cac ccc aac tta atc cca ccg act tct ccg ttt tct cag atc ccg acc
240
His Pro Asn Leu Ile Pro Pro Thr Ser Pro Phe Ser Gln Ile Pro Thr
65              70              75              80

acc cga caa ccc ggt tcg cat aat ttt aac ccg gga gga gct aat cat
288
Thr Arg Gln Pro Gly Ser His Asn Phe Asn Pro Gly Gly Ala Asn His
                85              90              95

tca cgg tca atg tca cag ccc aac tct ttc ttc tct ttt gac tcc tta
336
Ser Arg Ser Met Ser Gln Pro Asn Ser Phe Phe Ser Phe Asp Ser Leu
            100             105             110

cct ccg tta agc cct tct ccg ttt cga gat cac gat gtt tca atg gag
384
Pro Pro Leu Ser Pro Ser Pro Phe Arg Asp His Asp Val Ser Met Glu
            115             120             125

gat aga gat tcc ggc gtg ttt aac agc aac cat tcg ttg cct cca tcg
432
Asp Arg Asp Ser Gly Val Phe Asn Ser Asn His Ser Leu Pro Pro Ser
    130             135             140

ccg ttc acg agg tgt aat tcg acc tct tct agc tcc ttg aga gtc ggt
480
Pro Phe Thr Arg Cys Asn Ser Thr Ser Ser Ser Ser Leu Arg Val Gly
145             150             155             160

gag agt tta cct ccg aga aag tct cat aga cgc tcc aac agt gat atc
528
Glu Ser Leu Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Ile
            165             170             175

ccc agt ggg ttt aat tcg atg cct ttg atc cct ccg aga cca ttg gag
576
Pro Ser Gly Phe Asn Ser Met Pro Leu Ile Pro Pro Arg Pro Leu Glu
            180             185             190

agg tct ttt tct ggt ggg gag tgt gct gat tgg tca aag tct aat cct
624
Arg Ser Phe Ser Gly Gly Glu Cys Ala Asp Trp Ser Lys Ser Asn Pro
            195             200             205

ttt gtg aag aag gaa tcg agc tgc gaa agg gaa ggt gtc gga gag aga
672
Phe Val Lys Lys Glu Ser Ser Cys Glu Arg Glu Gly Val Gly Glu Arg
    210             215             220
```

478

```
gaa gct atg gat gat ctc ttc tca gca tat atg aat ctt gaa aac att
720
Glu Ala Met Asp Asp Leu Phe Ser Ala Tyr Met Asn Leu Glu Asn Ile
225             230             235             240

gat gtg ttg aac tcc tct gaa gct gat gat agc aag aac ggt aat gag
768
Asp Val Leu Asn Ser Ser Glu Ala Asp Asp Ser Lys Asn Gly Asn Glu
        245             250             255

aat agg gat gat atg gag agc agc aga gca agc ggg acc aag act aac
816
Asn Arg Asp Asp Met Glu Ser Ser Arg Ala Ser Gly Thr Lys Thr Asn
        260             265             270

ggt agt gat acg gaa gga gag agc agc agt gtc aat gag agt gcc aat
864
Gly Ser Asp Thr Glu Gly Glu Ser Ser Ser Val Asn Glu Ser Ala Asn
        275             280             285

aat aat atg aat tct tct ggt gaa aag aga gag agc gtg aag aga aga
912
Asn Asn Met Asn Ser Ser Gly Glu Lys Arg Glu Ser Val Lys Arg Arg
    290             295             300

gcg gct gga gga gat att gct cct acc acc aga cat tac agg agt gtt
960
Ala Ala Gly Gly Asp Ile Ala Pro Thr Thr Arg His Tyr Arg Ser Val
305             310             315             320

tca gtg gac agt tgt ttc atg gag aag ttg tct ttt ggt gat gaa tct
1008
Ser Val Asp Ser Cys Phe Met Glu Lys Leu Ser Phe Gly Asp Glu Ser
            325             330             335

cta aag ccg cct cct tct cct gga tct atg tca agg aaa gtt tcc cct
1056
Leu Lys Pro Pro Pro Ser Pro Gly Ser Met Ser Arg Lys Val Ser Pro
            340             345             350

acc aat tcg gtt gat ggg aac tcg ggt gct gct ttt agc atc gag ttc
1104
Thr Asn Ser Val Asp Gly Asn Ser Gly Ala Ala Phe Ser Ile Glu Phe
            355             360             365

aat aac ggt gag ttt act gca gcg gaa atg aag aag atc atg gca aat
1152
Asn Asn Gly Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Met Ala Asn
    370             375             380

gat aaa cta gca gag atg gcc atg tct gac cct aaa cgt gtc aaa agg
1200
Asp Lys Leu Ala Glu Met Ala Met Ser Asp Pro Lys Arg Val Lys Arg
385             390             395             400

aat gat cct ctt ttc aga atc tta gcg aac cgt caa tcc gca gca cgg
1248
Asn Asp Pro Leu Phe Arg Ile Leu Ala Asn Arg Gln Ser Ala Ala Arg
            405             410             415
```

479

tca aag gag agg aag atg cgg tac ata gta gaa ttg gaa cac aaa gtg
1296
Ser Lys Glu Arg Lys Met Arg Tyr Ile Val Glu Leu Glu His Lys Val
            420   425   430

cag act ctt cag acc gag gct acc aca ttg tct gct cag ctc aca ctt
1344
Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu Thr Leu
            435   440   445

ttg cag cgc gat atg atg ggg ttg aca aat cag aac aat gag ctt aag
1392
Leu Gln Arg Asp Met Met Gly Leu Thr Asn Gln Asn Asn Glu Leu Lys
            450   455   460

ttc cgg ctt caa gca atg gag caa caa gcg cgt ctt cgc gat gct ctg
1440
Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Arg Leu Arg Asp Ala Leu
465   470   475   480

aac gaa gca ctg aat gga gaa gtc cag cga ctg aaa ctg gca atc ggt
1488
Asn Glu Ala Leu Asn Gly Glu Val Gln Arg Leu Lys Leu Ala Ile Gly
            485   490   495

gag agc agt cag aac gaa tca gag aga tca aag atg caa tca ctc aac
1536
Glu Ser Ser Gln Asn Glu Ser Glu Arg Ser Lys Met Gln Ser Leu Asn
            500   505   510

gct gag atg ttc cag caa ctc aac atc agc cag tta aga cag cag cca
1584
Ala Glu Met Phe Gln Gln Leu Asn Ile Ser Gln Leu Arg Gln Gln Pro
            515   520   525

caa cag atg cag caa cag tct cat cag cag aac cac cag aat gga acc
1632
Gln Gln Met Gln Gln Gln Ser His Gln Gln Asn His Gln Asn Gly Thr
            530   535   540

atg gca aca aaa tct gaa tca aat gaa tag
1662
Met Ala Thr Lys Ser Glu Ser Asn Glu
545   550

<210> 270 <211> 553 <212> PRT <213> Arabidopsis thaliana <400>
270

Met Gly Asp Thr Glu Lys Cys Asn Ser Asp Met Ile Gln Arg Leu His
1   5   10   15

Ser Ser Phe Gly Thr Thr Ser Ser Ile Pro Lys Asn Pro Ile Ser
            20   25   30

Gln Leu Asp Leu Asn Pro Asn Phe Ile Arg Ser Ser Ala Pro Gln Phe
            35   40   45

480

```
Ser Lys Pro Phe Ser Asp Ser Gly Lys Arg Ile Gly Val Pro Pro Ser
    50              55                  60

His Pro Asn Leu Ile Pro Pro Thr Ser Pro Phe Ser Gln Ile Pro Thr
65              70              75                  80

Thr Arg Gln Pro Gly Ser His Asn Phe Asn Pro Gly Gly Ala Asn His
                85              90                  95

Ser Arg Ser Met Ser Gln Pro Asn Ser Phe Phe Ser Phe Asp Ser Leu
            100             105             110

Pro Pro Leu Ser Pro Ser Pro Phe Arg Asp His Asp Val Ser Met Glu
        115             120             125

Asp Arg Asp Ser Gly Val Phe Asn Ser Asn His Ser Leu Pro Pro Ser
    130             135             140

Pro Phe Thr Arg Cys Asn Ser Thr Ser Ser Ser Leu Arg Val Gly
145             150             155             160

Glu Ser Leu Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Ile
            165             170             175

Pro Ser Gly Phe Asn Ser Met Pro Leu Ile Pro Pro Arg Pro Leu Glu
            180             185             190

Arg Ser Phe Ser Gly Gly Glu Cys Ala Asp Trp Ser Lys Ser Asn Pro
        195             200             205

Phe Val Lys Lys Glu Ser Ser Cys Glu Arg Glu Gly Val Gly Glu Arg
    210             215             220

Glu Ala Met Asp Asp Leu Phe Ser Ala Tyr Met Asn Leu Glu Asn Ile
225             230             235             240

Asp Val Leu Asn Ser Ser Glu Ala Asp Asp Ser Lys Asn Gly Asn Glu
            245             250             255

Asn Arg Asp Asp Met Glu Ser Ser Arg Ala Ser Gly Thr Lys Thr Asn
        260             265             270

Gly Ser Asp Thr Glu Gly Glu Ser Ser Ser Val Asn Glu Ser Ala Asn
    275             280             285

Asn Asn Met Asn Ser Ser Gly Glu Lys Arg Glu Ser Val Lys Arg Arg
```

481

```
         290                    295                    300


Ala Ala Gly Gly Asp Ile Ala Pro Thr Thr Arg His Tyr Arg Ser Val
305                 310             315             320


Ser Val Asp Ser Cys Phe Met Glu Lys Leu Ser Phe Gly Asp Glu Ser
                325             330             335


Leu Lys Pro Pro Pro Ser Pro Gly Ser Met Ser Arg Lys Val Ser Pro
            340             345             350


Thr Asn Ser Val Asp Gly Asn Ser Gly Ala Ala Phe Ser Ile Glu Phe
        355             360             365


Asn Asn Gly Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Met Ala Asn
    370             375             380


Asp Lys Leu Ala Glu Met Ala Met Ser Asp Pro Lys Arg Val Lys Arg
385             390             395             400


Asn Asp Pro Leu Phe Arg Ile Leu Ala Asn Arg Gln Ser Ala Ala Arg
            405             410             415


Ser Lys Glu Arg Lys Met Arg Tyr Ile Val Glu Leu Glu His Lys Val
            420             425             430


Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu Thr Leu
        435             440             445


Leu Gln Arg Asp Met Met Gly Leu Thr Asn Gln Asn Asn Glu Leu Lys
    450             455             460


Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Arg Leu Arg Asp Ala Leu
465             470             475             480


Asn Glu Ala Leu Asn Gly Glu Val Gln Arg Leu Lys Leu Ala Ile Gly
            485             490             495


Glu Ser Ser Gln Asn Glu Ser Glu Arg Ser Lys Met Gln Ser Leu Asn
        500             505             510


Ala Glu Met Phe Gln Gln Leu Asn Ile Ser Gln Leu Arg Gln Gln Pro
        515             520             525


Gln Gln Met Gln Gln Gln Ser His Gln Gln Asn His Gln Asn Gly Thr
    530             535             540
```

482

Met Ala Thr Lys Ser Glu Ser Asn Glu
545   ·   550   ·¹   ·   ·

<210> 271 <211> 969 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(969) <223> G1835

<400> 271
atg att gga aca agc ttc ccc gag gat ctt gat tgt ggc aac ttc ttt
48
Met Ile Gly Thr Ser Phe Pro Glu Asp Leu Asp Cys Gly Asn Phe Phe
1   5   10   15

gac aac atg gat gat ctc atg gac ttt ccc ggt gga gat atc gat gtc
96
Asp Asn Met Asp Asp Leu Met Asp Phe Pro Gly Gly Asp Ile Asp Val
            20   25   ·   30

ggt ttc ggc ata ggt gac tcc gac tct ttc cct acc atc tgg acc act
144
Gly Phe Gly Ile Gly Asp Ser Asp Ser Phe Pro Thr Ile Trp Thr Thr
            35   40   45

cat cac gac acg tgg cct gcc gct tct gat cct ctc ttc tct tcc aac
192
His His Asp Thr Trp Pro Ala Ala Ser Asp Pro Leu Phe Ser Ser Asn
    50   55   60

acc aac tct gat tca tca cct gag ctc tat gtt ccg ttt gag gac att
240
Thr Asn Ser Asp Ser Ser Pro Glu Leu Tyr Val Pro Phe Glu Asp Ile
65   70   75   80

gtt aag gtg gaa aga cct cca agc ttt gta gag gaa aca ttg gtt gag
288
Val Lys Val Glu Arg Pro Pro Ser Phe Val Glu Glu Thr Leu Val Glu
                85   90   95

aag aag gaa gat tcg ttt tcg aca aac act gat tca tca tct tct cat
336
Lys Lys Glu Asp Ser Phe Ser Thr Asn Thr Asp Ser Ser Ser Ser His
            100   105   110

agc caa ttc agg agc tca agt cca gtg tcg gtt ctc gag agc agc tcc
384
Ser Gln Phe Arg Ser Ser Ser Pro Val Ser Val Leu Glu Ser Ser Ser
            115   120   125

tcc tcg tct caa acc acc aac aca acc tcc ctt gtt ctc cct gga aag
432
Ser Ser Ser Gln Thr Thr Asn Thr Thr Ser Leu Val Leu Pro Gly Lys
    130   135   140

cac ggt cgt cca cgc aca aaa cgc cct cgt cca cct gtc cag gat aaa
480
His Gly Arg Pro Arg Thr Lys Arg Pro Arg Pro Pro Val Gln Asp Lys
145   150   155   160

```
gat aga gtc aaa gac aat gtg tgc ggt ggt gac tcg cgc ctc atc att
528
Asp Arg Val Lys Asp Asn Val Cys Gly Gly Asp Ser Arg Leu Ile Ile
            165             170             175

aga ata ccg aaa cag ttt ctc tct gat cac aac aag atg atc aac aag
576
Arg Ile Pro Lys Gln Phe Leu Ser Asp His Asn Lys Met Ile Asn Lys
            180             185             190

aag aag aag aag aag gcc aag att act tct tcc tct tct tcg tcc ggg
624
Lys Lys Lys Lys Lys Ala Lys Ile Thr Ser Ser Ser Ser Ser Ser Gly
            195             200             205

att gat ctt gaa gtc aat gga aac aac gtc gat tcg tat tct tca gag
672
Ile Asp Leu Glu Val Asn Gly Asn Asn Val Asp Ser Tyr Ser Ser Glu
        210             215             220

caa tat ccg ctt agg aaa tgt atg cac tgt gag gtc acc aag act cca
720
Gln Tyr Pro Leu Arg Lys Cys Met His Cys Glu Val Thr Lys Thr Pro
225             230             235             240

cag tgg agg ctt ggt cca atg ggt cca aag aca ctt tgc aat gcg tgc
768
Gln Trp Arg Leu Gly Pro Met Gly Pro Lys Thr Leu Cys Asn Ala Cys
            245             250             255

ggt gta cgt tac aaa tca ggg agg ctt ttc ccg gag tac cgt cca gct
816
Gly Val Arg Tyr Lys Ser Gly Arg Leu Phe Pro Glu Tyr Arg Pro Ala
            260             265             270

gct agt cca aca ttt act cca gct ctt cac tca aac tca cac aag aaa
864
Ala Ser Pro Thr Phe Thr Pro Ala Leu His Ser Asn Ser His Lys Lys
            275             280             285

gtg gct gaa atg aga aac aag aga tgc agt gat ggt agc tac ata acc
912
Val Ala Glu Met Arg Asn Lys Arg Cys Ser Asp Gly Ser Tyr Ile Thr
        290             295             300

gaa gag aat gat ctg caa ggg ctg att ccg aac aat gcc tac att ggc
960
Glu Glu Asn Asp Leu Gln Gly Leu Ile Pro Asn Asn Ala Tyr Ile Gly
305             310             315             320

gta gac taa
969
Val Asp
```

<210> 272 <211> 322 <212> PRT <213> Arabidopsis thaliana <400>
272

```
Met Ile Gly Thr Ser Phe Pro Glu Asp Leu Asp Cys Gly Asn Phe Phe
1               5               10              15
```

```
Asp Asn Met Asp Asp Leu Met Asp Phe Pro Gly Gly Asp Ile Asp Val
            20                  25                  30

Gly Phe Gly Ile Gly Asp Ser Asp Ser Phe Pro Thr Ile Trp Thr Thr
            35                  40                  45

His His Asp Thr Trp Pro Ala Ala Ser Asp Pro Leu Phe Ser Ser Asn
    50                  55                  60

Thr Asn Ser Asp Ser Ser Pro Glu Leu Tyr Val Pro Phe Glu Asp Ile
65                  70                  75                  80

Val Lys Val Glu Arg Pro Pro Ser Phe Val Glu Glu Thr Leu Val Glu
            85                  90                  95

Lys Lys Glu Asp Ser Phe Ser Thr Asn Thr Asp Ser Ser Ser Ser His
            100                 105                 110

Ser Gln Phe Arg Ser Ser Ser Pro Val Ser Val Leu Glu Ser Ser Ser
            115                 120                 125

Ser Ser Ser Gln Thr Thr Asn Thr Thr Ser Leu Val Leu Pro Gly Lys
    130                 135                 140

His Gly Arg Pro Arg Thr Lys Arg Pro Arg Pro Pro Val Gln Asp Lys
145                 150                 155                 160

Asp Arg Val Lys Asp Asn Val Cys Gly Gly Asp Ser Arg Leu Ile Ile
                165                 170                 175

Arg Ile Pro Lys Gln Phe Leu Ser Asp His Asn Lys Met Ile Asn Lys
            180                 185                 190

Lys Lys Lys Lys Lys Ala Lys Ile Thr Ser Ser Ser Ser Ser Ser Gly
            195                 200                 205

Ile Asp Leu Glu Val Asn Gly Asn Asn Val Asp Ser Tyr Ser Ser Glu
    210                 215                 220

Gln Tyr Pro Leu Arg Lys Cys Met His Cys Glu Val Thr Lys Thr Pro
225                 230                 235                 240

Gln Trp Arg Leu Gly Pro Met Gly Pro Lys Thr Leu Cys Asn Ala Cys
                245                 250                 255
```

```
Gly Val Arg Tyr Lys Ser Gly Arg Leu Phe Pro Glu Tyr Arg Pro Ala
            260                 265                 270


Ala Ser Pro Thr Phe Thr Pro Ala Leu His Ser Asn Ser His Lys Lys
            275                 280                 285


Val Ala Glu Met Arg Asn Lys Arg Cys Ser Asp Gly Ser Tyr Ile Thr
        290                 295                 300


Glu Glu Asn Asp Leu Gln Gly Leu Ile Pro Asn Asn Ala Tyr Ile Gly
305                 310                 315                 320


Val Asp
```

<210> 273 <211> 668 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (47)..(610) <223> G1836

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<400> 273
ataacaagcc tagaacacta gaaacttcaa aaaagaaaaa aatctt atg gag aac
55
                                                    Met Glu Asn
                                                    1


aac aac ggc aac aac cag ctg cca ccg aaa ggt aac gag caa ctg aag
103
Asn Asn Gly Asn Asn Gln Leu Pro Pro Lys Gly Asn Glu Gln Leu Lys
    5                   10                  15


agt ttc tgg tca aaa gag atg gaa ggt aac tta gat ttc aaa aat cac
151
Ser Phe Trp Ser Lys Glu Met Glu Gly Asn Leu Asp Phe Lys Asn His
20                  25                  30                  35


gac ctt cct ata act cgt atc aag aag att atg aag tat gat ccg gat
199
Asp Leu Pro Ile Thr Arg Ile Lys Lys Ile Met Lys Tyr Asp Pro Asp
                40                  45                  50


gtg act atg ata gct agt gag gct cca atc ctc ctc tcg aaa gca tgt
247
Val Thr Met Ile Ala Ser Glu Ala Pro Ile Leu Leu Ser Lys Ala Cys
                55                  60                  65


gag atg ttt atc atg gat ctc acg atg cgt tcg tgg ctc cat gct cag
295
Glu Met Phe Ile Met Asp Leu Thr Met Arg Ser Trp Leu His Ala Gln
            70                  75                  80


gaa agc aaa cga gtc acg cta cag aaa tct aat gtc gat gcc gca gtg
343
Glu Ser Lys Arg Val Thr Leu Gln Lys Ser Asn Val Asp Ala Ala Val
        85                  90                  95
```

486

```
gct caa act gtt atc ttt gat ttc ttg ctt gat gat gac att gag gta
391
Ala Gln Thr Val Ile Phe Asp Phe Leu Leu Asp Asp Asp Ile Glu Val
100                 105                 110                 115


aag aga gag tct gtt gcc gcc gct gct gat cct gtg gcc atg cca cct
439
Lys Arg Glu Ser Val Ala Ala Ala Ala Asp Pro Val Ala Met Pro Pro
                120                 125                 130


att gac gat gga gag ctg cct cca gga atg gta att gga act cct gtt
487
Ile Asp Asp Gly Glu Leu Pro Pro Gly Met Val Ile Gly Thr Pro Val
            135                 140                 145


tgt tgt agt ctt gga atc cac caa cca caa cca caa atg cag gca tgg
535
Cys Cys Ser Leu Gly Ile His Gln Pro Gln Pro Gln Met Gln Ala Trp
        150                 155                 160


cct gga gct tgg acc tcg gtg tct ggt gag gag gaa gaa gcg cgt ggg
583
Pro Gly Ala Trp Thr Ser Val Ser Gly Glu Glu Glu Glu Ala Arg Gly
    165                 170                 175


aaa aaa gga ggt gac gac gga aac taa taagtggaat acgttttagg
630
Lys Lys Gly Gly Asp Asp Gly Asn
180                 185


gtattttcaa gggaatatgt agtaaatagt catggatc
668
```

<210> 274 <211> 187 <212> PRT <213> Arabidopsis thaliana <400>
274

```
Met Glu Asn Asn Asn Gly Asn Asn Gln Leu Pro Pro Lys Gly Asn Glu
1               5                   10                  15


Gln Leu Lys Ser Phe Trp Ser Lys Glu Met Glu Gly Asn Leu Asp Phe
            20                  25                  30


Lys Asn His Asp Leu Pro Ile Thr Arg Ile Lys Lys Ile Met Lys Tyr
        35                  40                  45


Asp Pro Asp Val Thr Met Ile Ala Ser Glu Ala Pro Ile Leu Leu Ser
    50                  55                  60


Lys Ala Cys Glu Met Phe Ile Met Asp Leu Thr Met Arg Ser Trp Leu
65                  70                  75                  80


His Ala Gln Glu Ser Lys Arg Val Thr Leu Gln Lys Ser Asn Val Asp
                85                  90                  95
```

```
Ala Ala Val Ala Gln Thr Val Ile Phe Asp Phe Leu Leu Asp Asp Asp
            100                 105                 110


Ile Glu Val Lys Arg Glu Ser Val Ala Ala Ala Ala Asp Pro Val Ala
            115                 120                 125


Met Pro Pro Ile Asp Asp Gly Glu Leu Pro Pro Gly Met Val Ile Gly
    130                 135                 140


Thr Pro Val Cys Cys Ser Leu Gly Ile His Gln Pro Gln Pro Gln Met
145                 150                 155                 160


Gln Ala Trp Pro Gly Ala Trp Thr Ser Val Ser Gly Glu Glu Glu Glu
                165                 170                 175


Ala Arg Gly Lys Lys Gly Gly Asp Asp Gly Asn
                180                 185
```

```
<210> 275 <211> 897 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(897) <223> G1900

<400> 275
atg ctg gaa act aaa gat cct gcg ata aag ctc ttt ggt atg aaa att
48
Met Leu Glu Thr Lys Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile
1               5                   10                  15

cct ttc ccg acg gtt tta gag gtt gct gat gaa gaa gaa gaa aag aac
96
Pro Phe Pro Thr Val Leu Glu Val Ala Asp Glu Glu Glu Glu Lys Asn
                20                  25                  30

caa aac aag aca tta act gat caa tcg gag aaa gac aaa acc cta aag
144
Gln Asn Lys Thr Leu Thr Asp Gln Ser Glu Lys Asp Lys Thr Leu Lys
            35                  40                  45

aaa cca acc aag att ctt cca tgt cca aga tgc aac agc atg gag act
192
Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Met Glu Thr
        50                  55                  60

aag ttc tgt tac tac aac aac tac aac gta aac caa cct cgc cat ttt
240
Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg His Phe
65                  70                  75                  80

tgt aaa gct tgt cag aga tat tgg acc tca ggt ggg acc atg aga agt
288
Cys Lys Ala Cys Gln Arg Tyr Trp Thr Ser Gly Gly Thr Met Arg Ser
                85                  90                  95

gtt cca atc gga gca gga cgg cgc aag aac aag aac aac tca cca act
336
Val Pro Ile Gly Ala Gly Arg Arg Lys Asn Lys Asn Asn Ser Pro Thr
```

                    100   105   110

tca cat tac cac cat gtg act atc tcc gaa aca aat ggt ccg gtc ctt
384
Ser His Tyr His His Val Thr Ile Ser Glu Thr Asn Gly Pro Val Leu
        115   120   125

agt ttc agc ctc gga gat gat caa aag gtc tcg agt aat agg ttt ggt
432
Ser Phe Ser Leu Gly Asp Asp Gln Lys Val Ser Ser Asn Arg Phe Gly
        130   135   140

aat caa aag cta gtt gct agg ata gag aac aat gac gag cgc tct aat
480
Asn Gln Lys Leu Val Ala Arg Ile Glu Asn Asn Asp Glu Arg Ser Asn
145   150   155   160

aac aac act tcg aac ggt ttg aat tgt ttt ccg gga gtt tcg tgg ccg
528
Asn Asn Thr Ser Asn Gly Leu Asn Cys Phe Pro Gly Val Ser Trp Pro
                165   170   175

tac acg tgg aat cct gcg ttt tac ccg gtt tac cct tat tgg agc atg
576
Tyr Thr Trp Asn Pro Ala Phe Tyr Pro Val Tyr Pro Tyr Trp Ser Met
                180   185   190

cca gtg ttg tct tct ccg gta agt tca agt cct act tct act ctt ggt
624
Pro Val Leu Ser Ser Pro Val Ser Ser Ser Pro Thr Ser Thr Leu Gly
        195   200   205

aag cat tcg aga gac gaa gac gag acg gtg aag caa aaa cag agg aat
672
Lys His Ser Arg Asp Glu Asp Glu Thr Val Lys Gln Lys Gln Arg Asn
        210   215   220

gga tct gta ttg gtt cca aag act ttg aga att gat gat cct aat gaa
720
Gly Ser Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro Asn Glu
225   230   235   240

gct gca aag agt tcg ata tgg aca aca ctt ggg atc aag aac gaa gtt
768
Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Val
                245   250   255

atg ttc aat ggg ttt ggt tcg aag aaa gag gtt aag ctc agt aac aaa
816
Met Phe Asn Gly Phe Gly Ser Lys Lys Glu Val Lys Leu Ser Asn Lys
                260   265   270

gaa gaa aca gag acc tca ctt gtt ctt tgt gca aac cct gct gcg tta
864
Glu Glu Thr Glu Thr Ser Leu Val Leu Cys Ala Asn Pro Ala Ala Leu
        275   280   285

tca aga tca atc aat ttc cat gag cag atg tga
897
Ser Arg Ser Ile Asn Phe His Glu Gln Met
        290   295

<210> 276 <211> 298 <212> PRT <213> Arabidopsis thaliana <400>
276

Met Leu Glu Thr Lys Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile
1   5   10   15

Pro Phe Pro Thr Val Leu Glu Val Ala Asp Glu Glu Glu Glu Lys Asn
            20   25   30

Gln Asn Lys Thr Leu Thr Asp Gln Ser Glu Lys Asp Lys Thr Leu Lys
        35   40   45

Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Met Glu Thr
    50   55   60

Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg His Phe
65   70   75   80

Cys Lys Ala Cys Gln Arg Tyr Trp Thr Ser Gly Gly Thr Met Arg Ser
            85   90   95

Val Pro Ile Gly Ala Gly Arg Arg Lys Asn Lys Asn Asn Ser Pro Thr
            100   105   110

Ser His Tyr His His Val Thr Ile Ser Glu Thr Asn Gly Pro Val Leu
        115   120   125

Ser Phe Ser Leu Gly Asp Asp Gln Lys Val Ser Ser Asn Arg Phe Gly
    130   135   140

Asn Gln Lys Leu Val Ala Arg Ile Glu Asn Asn Asp Glu Arg Ser Asn
145   150   155   160

Asn Asn Thr Ser Asn Gly Leu Asn Cys Phe Pro Gly Val Ser Trp Pro
                165   170   175

Tyr Thr Trp Asn Pro Ala Phe Tyr Pro Val Tyr Pro Tyr Trp Ser Met
                180   185   190

Pro Val Leu Ser Ser Pro Val Ser Ser Ser Pro Thr Ser Thr Leu Gly
            195   200   205

Lys His Ser Arg Asp Glu Asp Glu Thr Val Lys Gln Lys Gln Arg Asn
        210   215   220

490

```
Gly Ser Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro Asn Glu
225                 230             235             240


Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Val
            245                 250             255


Met Phe Asn Gly Phe Gly Ser Lys Lys Glu Val Lys Leu Ser Asn Lys
            260                 265             270


Glu Glu Thr Glu Thr Ser Leu Val Leu Cys Ala Asn Pro Ala Ala Leu
        275                 280             285


Ser Arg Ser Ile Asn Phe His Glu Gln Met
    290                 295
```

<210> 277 <211> 1200 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1200) <223> G1903

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 <400> 277
atg tct aaa tct aga gat acg gag ata aag ttg ttt ggg agg aca atc
48
Met Ser Lys Ser Arg Asp Thr Glu Ile Lys Leu Phe Gly Arg Thr Ile
1               5               10              15


aca tct ctt tta gat gtg aat tgt tat gat ccg tcg tcg ttg tcc cct
96
Thr Ser Leu Leu Asp Val Asn Cys Tyr Asp Pro Ser Ser Leu Ser Pro
            20              25              30


gtt cac gat gtt tct tct gat cca agc aag gag gat tcg tct tct tct
144
Val His Asp Val Ser Ser Asp Pro Ser Lys Glu Asp Ser Ser Ser Ser
        35              40              45


tca tct tct tgt tct cca act att gga cca atc agg gtt ccg gtt aaa
192
Ser Ser Ser Cys Ser Pro Thr Ile Gly Pro Ile Arg Val Pro Val Lys
    50              55              60


aaa agt gag caa gag agt aac aaa ttc aaa gat cca tat ata tta tcc
240
Lys Ser Glu Gln Glu Ser Asn Lys Phe Lys Asp Pro Tyr Ile Leu Ser
65              70              75              80


gat cta aac gaa cca cca aaa gca gta tct gag att tca tca cca aga
288
Asp Leu Asn Glu Pro Pro Lys Ala Val Ser Glu Ile Ser Ser Pro Arg
                85              90              95


agt tcc aag aac aac tgt gat caa cag agc gag atc aca aca aca act
336
Ser Ser Lys Asn Asn Cys Asp Gln Gln Ser Glu Ile Thr Thr Thr Thr
            100             105             110


acc aca agt act aca tca gga gag aaa tca acg gct ctc aag aaa ccg
384
```

```
Thr Thr Ser Thr Thr Ser Gly Glu Lys Ser Thr Ala Leu Lys Lys Pro
        115                 120             125

gac aag ctt att cca tgt cct aga tgt gaa agc gca aac acc aaa ttc
432
Asp Lys Leu Ile Pro Cys Pro Arg Cys Glu Ser Ala Asn Thr Lys Phe
        130             135                 140

tgt tat tac aac aac tac aac gtg aac cag cca cgt tac ttc tgc agg
480
Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg Tyr Phe Cys Arg
145                 150                 155                 160

aac tgt cag agg tat tgg aca gct ggt gga tct atg agg aac gtt cct
528
Asn Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met Arg Asn Val Pro
                165                 170                 175

gtt ggc tca ggt cgt cgc aag aac aaa gga tgg cct tct tca aac cat
576
Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Pro Ser Ser Asn His
            180                 185                 190

tac ttg caa gtc act tct gag gat tgt gat aat aat aac tcg ggg acg
624
Tyr Leu Gln Val Thr Ser Glu Asp Cys Asp Asn Asn Asn Ser Gly Thr
            195                 200                 205

atc ctt agt ttc ggt tct tcg gag tct tcg gtt aca gag act ggt aag
672
Ile Leu Ser Phe Gly Ser Ser Glu Ser Ser Val Thr Glu Thr Gly Lys
        210                 215                 220

cat cag tca ggt gat aca gca aag ata agt gct gat tca gtt tct caa
720
His Gln Ser Gly Asp Thr Ala Lys Ile Ser Ala Asp Ser Val Ser Gln
225                 230                 235                 240

gaa aat aaa agc tac caa ggg ttt ctt cct ccg caa gta atg tta cct
768
Glu Asn Lys Ser Tyr Gln Gly Phe Leu Pro Pro Gln Val Met Leu Pro
                245                 250                 255

aat aat tct tct cct tgg cct tac caa tgg agt cca acg ggt cct aac
816
Asn Asn Ser Ser Pro Trp Pro Tyr Gln Trp Ser Pro Thr Gly Pro Asn
            260                 265                 270

gct agt ttc tac cct gtc ccc ttc tac tgg gga tgc acg gtt ccg ata
864
Ala Ser Phe Tyr Pro Val Pro Phe Tyr Trp Gly Cys Thr Val Pro Ile
            275                 280                 285

tac cct acc tca gag act tca tca tgt tta gga aaa cgg tca aga gat
912
Tyr Pro Thr Ser Glu Thr Ser Ser Cys Leu Gly Lys Arg Ser Arg Asp
        290                 295                 300

caa act gaa gga aga atc aat gat act aat aca aca ata act act aca
960
Gln Thr Glu Gly Arg Ile Asn Asp Thr Asn Thr Thr Ile Thr Thr Thr
```

305   310 ·   315   320

aga gca aga ttg gtc tca gaa tct ctt aga atg aat atc gaa gct agt
1008
Arg Ala Arg Leu Val Ser Glu Ser Leu Arg Met Asn Ile Glu Ala Ser
            325   330   335

aag agc gct gtg tgg tct aag tta ccg aca aaa ccc gag aaa aaa acg
1056
Lys Ser Ala Val Trp Ser Lys Leu Pro Thr Lys Pro Glu Lys Lys Thr
            340   345   350

caa gga ttc agt ttg ttc aat gga ttt gac aca aag gga aac agc aac
1104
Gln Gly Phe Ser Leu Phe Asn Gly Phe Asp Thr Lys Gly Asn Ser Asn
        · 355   360   365

aga agt agc ttg gtc tcc gaa act tct cac agt cta caa gca aac cct
1152
Arg Ser Ser Leu Val·Ser Glu Thr Ser His Ser Leu Gln Ala Asn Pro
        370   375   380

gca gcg atg tct aga gct atg aac ttc agg gag agc atg caa caa taa
1200
Ala Ala Met Ser Arg Ala Met Asn Phe Arg Glu Ser Met Gln Gln
385   390   395

<210> 278 <211> 399 <212> PRT <213> Arabidopsis thaliana <400>
278

Met Ser Lys Ser Arg Asp Thr Glu Ile Lys Leu Phe Gly Arg Thr Ile
1   5   10   15

Thr Ser Leu Leu Asp Val Asn Cys Tyr Asp Pro Ser Ser Leu Ser Pro
            20   25   30

Val His Asp Val Ser Ser Asp Pro Ser Lys Glu Asp Ser Ser Ser Ser
            35   40   45

Ser Ser Ser Cys Ser Pro Thr Ile Gly Pro Ile Arg Val Pro Val Lys
        50   55   60

Lys Ser Glu Gln Glu Ser Asn Lys Phe Lys Asp Pro Tyr Ile Leu Ser
65   70   75   80

Asp Leu Asn Glu Pro Pro Lys Ala Val Ser Glu Ile Ser Ser Pro Arg
            85   90   95

Ser Ser Lys Asn Asn Cys Asp Gln Gln Ser Glu Ile Thr Thr Thr Thr
            100   105   · 110

Thr Thr Ser Thr Thr Ser Gly Glu Lys Ser Thr Ala Leu Lys Lys Pro
            115   120   125

493

```
Asp Lys Leu Ile Pro Cys Pro Arg Cys Glu Ser Ala Asn Thr Lys Phe
    130             135             140

Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg Tyr Phe Cys Arg
145             150             155             160

Asn Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met Arg Asn Val Pro
            165             170             175

Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Pro Ser Ser Asn His
            180             185             190

Tyr Leu Gln Val Thr Ser Glu Asp Cys Asp Asn Asn Asn Ser Gly Thr
        195             200             205

Ile Leu Ser Phe Gly Ser Ser Glu Ser Ser Val Thr Glu Thr Gly Lys
    210             215             220

His Gln Ser Gly Asp Thr Ala Lys Ile Ser Ala Asp Ser Val Ser Gln
225             230             235             240

Glu Asn Lys Ser Tyr Gln Gly Phe Leu Pro Pro Gln Val Met Leu Pro
            245             250             255

Asn Asn Ser Ser Pro Trp Pro Tyr Gln Trp Ser Pro Thr Gly Pro Asn
            260             265             270

Ala Ser Phe Tyr Pro Val Pro Phe Tyr Trp Gly Cys Thr Val Pro Ile
        275             280             285

Tyr Pro Thr Ser Glu Thr Ser Ser Cys Leu Gly Lys Arg Ser Arg Asp
    290             295             300

Gln Thr Glu Gly Arg Ile Asn Asp Thr Asn Thr Thr Ile Thr Thr Thr
305             310             315             320

Arg Ala Arg Leu Val Ser Glu Ser Leu Arg Met Asn Ile Glu Ala Ser
            325             330             335

Lys Ser Ala Val Trp Ser Lys Leu Pro Thr Lys Pro Glu Lys Lys Thr
            340             345             350

Gln Gly Phe Ser Leu Phe Asn Gly Phe Asp Thr Lys Gly Asn Ser Asn
        355             360             365
```

494

Arg Ser Ser Leu Val Ser Glu Thr Ser His Ser Leu Gln Ala Asn Pro
    370   375   380

Ala Ala Met Ser Arg Ala Met Asn Phe Arg Glu Ser Met Gln Gln
385   . 390   395

<210> 279 <211> 883 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (42)..(764) <223> G1950

<400> 279
ctgaattcga actttggaag aagaagaagc tttgatcaat c atg gaa att gca acc
56
                                              Met Glu Ile Ala Thr
                                              1   5

gat aca gca aag cag atg aga gac gaa gag ttg ttc aaa gca gcg gaa
104
Asp Thr Ala Lys Gln Met Arg Asp Glu Glu Leu Phe Lys Ala Ala Glu
              10   15   20

tgg gga gat tca tcg ttg ttc atg tca tta tct gaa gaa cag ctc tct
152
Trp Gly Asp Ser Ser Leu Phe Met Ser Leu Ser Glu Glu Gln Leu Ser
          25   30   35

aaa tct ctc aat ttc aga aac gaa gat ggt cgc tct ctc ctc cat gtc
200
Lys Ser Leu Asn Phe Arg Asn Glu Asp Gly Arg Ser Leu Leu His Val
          40   45   50

gct gct tcc ttc ggc cat tct caa ata gtg aag ttg tta tca agt tca
248
Ala Ala Ser Phe Gly His Ser Gln Ile Val Lys Leu Leu Ser Ser Ser
    55   60   65

gat gaa gca aag act gta atc aat agc aag gat gat gaa gga tgg gct
296
Asp Glu Ala Lys Thr Val Ile Asn Ser Lys Asp Asp Glu Gly Trp Ala
70   75   80   85

cct ttg cat tcc gct gct agc atc ggt aat gct gag ctc gtt gag gtg
344
Pro Leu His Ser Ala Ala Ser Ile Gly Asn Ala Glu Leu Val Glu Val
          90   95   100

ctt ttg acc aga ggt gct gat gtc aat gcc aaa aat aac ggt ggt cgc
392
Leu Leu Thr Arg Gly Ala Asp Val Asn Ala Lys Asn Asn Gly Gly Arg
          105   110   115

act gct ctt cac tat gct gct agc aaa ggc cgg ttg gag att gct cag
440
Thr Ala Leu His Tyr Ala Ala Ser Lys Gly Arg Leu Glu Ile Ala Gln
          120   125   130

ctt tta tta aca cac ggt gca aag att aac atc aca gac aag gtt ggt
488
Leu Leu Leu Thr His Gly Ala Lys Ile Asn Ile Thr Asp Lys Val Gly

495

```
          135                   140                   145

tgc act ccg ctt cac agg gca gca agc gtg gga aag tta gaa gtt tgt
536
Cys Thr Pro Leu His Arg Ala Ala Ser Val Gly Lys Leu Glu Val Cys
150                 155                 160                 165


gaa ttt ctt att gaa gaa gga gca gag atc gat gct acg gat aaa atg
584
Glu Phe Leu Ile Glu Glu Gly Ala Glu Ile Asp Ala Thr Asp Lys Met
            170                     175                 180


ggt caa act gca ctc atg cat tca gtt atc tgc gat gac aaa cag gtt
632
Gly Gln Thr Ala Leu Met His Ser Val Ile Cys Asp Asp Lys Gln Val
            185                 190                 195


gcg ttc ctg ctt ata aga cat ggt gca gat gtg gat gta gaa gac aag
680
Ala Phe Leu Leu Ile Arg His Gly Ala Asp Val Asp Val Glu Asp Lys
        200                 205                 210


gaa ggc tac act gtt cta ggc cga gct acc aat gaa ttc cga cct gca
728
Glu Gly Tyr Thr Val Leu Gly Arg Ala Thr Asn Glu Phe Arg Pro Ala
    215                 220                 225


ctt atc gat gct gct aag gcc atg ctt gaa gga taa aatgactctg
774
Leu Ile Asp Ala Ala Lys Ala Met Leu Glu Gly
230                 235                 240


gattacttta aaacttacta actctgagag ttgtttagtt acttaaaagg attttcttt
834

actgtatcat gtttgcaaaa tgtttctgcc ttatcaattc atgttctgt
883
```

`<210> 280 <211> 240 <212> PRT <213> Arabidopsis thaliana <400> 280`

```
Met Glu Ile Ala Thr Asp Thr Ala Lys Gln Met Arg Asp Glu Glu Leu
1               5                   10                  15


Phe Lys Ala Ala Glu Trp Gly Asp Ser Ser Leu Phe Met Ser Leu Ser
            20              25                  30


Glu Glu Gln Leu Ser Lys Ser Leu Asn Phe Arg Asn Glu Asp Gly Arg
        35                  40                  45


Ser Leu Leu His Val Ala Ala Ser Phe Gly His Ser Gln Ile Val Lys
    50                  55                  60


Leu Leu Ser Ser Ser Asp Glu Ala Lys Thr Val Ile Asn Ser Lys Asp
65                  70                  75                  80
```

496

```
Asp Glu Gly Trp Ala Pro Leu His Ser Ala Ala Ser Ile Gly Asn Ala
            85                  90                  95

Glu Leu Val Glu Val Leu Leu Thr Arg Gly Ala Asp Val Asn Ala Lys
            100                 105                 110

Asn Asn Gly Gly Arg Thr Ala Leu His Tyr Ala Ala Ser Lys Gly Arg
        115                 120                 125

Leu Glu Ile Ala Gln Leu Leu Leu Thr His Gly Ala Lys Ile Asn Ile
    130                 135                 140

Thr Asp Lys Val Gly Cys Thr Pro Leu His Arg Ala Ala Ser Val Gly
145                 150                 155                 160

Lys Leu Glu Val Cys Glu Phe Leu Ile Glu Glu Gly Ala Glu Ile Asp
                165                 170                 175

Ala Thr Asp Lys Met Gly Gln Thr Ala Leu Met His Ser Val Ile Cys
            180                 185                 190

Asp Asp Lys Gln Val Ala Phe Leu Leu Ile Arg His Gly Ala Asp Val
        195                 200                 205

Asp Val Glu Asp Lys Glu Gly Tyr Thr Val Leu Gly Arg Ala Thr Asn
    210                 215                 220

Glu Phe Arg Pro Ala Leu Ile Asp Ala Ala Lys Ala Met Leu Glu Gly
225                 230                 235                 240
```

<210> 281 <211> 1444 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (107)..(1336) <223> G1958

<400> 281
gtaccgtcga ccgattatcc ccaagaggag aatcctcata atcattttct ccgattcgat
60

tcgtcttcct tggtcctgga ttgcttcatg aatttctagg acaaca atg gag gct
115
                                                    Met Glu Ala
                                                     1

cgt cca gtt cat aga tca ggt tcg aga gac ctc aca cgc act tct tca
163
Arg Pro Val His Arg Ser Gly Ser Arg Asp Leu Thr Arg Thr Ser Ser
    5   10   15

atc cca tct aca caa aaa cct tca cca gta gaa gat agt ttc atg aga
211
Ile Pro Ser Thr Gln Lys Pro Ser Pro Val Glu Asp Ser Phe Met Arg

```
20                   ·25                    30                    35

tca gat aac aac agt cag tta atg tct aga cca tta gga caa acc tac
259
Ser Asp Asn Asn Ser Gln Leu Met Ser Arg Pro Leu Gly Gln Thr Tyr
                40                    45                    50

cat tta ctt tca tct agt aac ggt gga gct gtt gga cat ata tgt tct
307
His Leu Leu Ser Ser Ser Asn Gly Gly Ala Val Gly His Ile Cys Ser
                55                    60                    65   -

tct tca tca tct ggt ttt gca acc aat ctc cat tac tca act atg gta
355
Ser Ser Ser Ser Gly Phe Ala Thr Asn Leu His Tyr Ser Thr Met Val·
                70                    75                    80

tct cat gag aaa caa caa cac tac aca gga agc agc agt aat aat gct
403
Ser His Glu Lys Gln Gln His Tyr Thr Gly Ser Ser Ser Asn Asn Ala
        85             ·      90                    95

gtg cag aca cca agc aac aac gat agt gct tgg tgt cat gat tca ttg
451                                  --
Val Gln Thr Pro Ser Asn Asn Asp Ser Ala Trp Cys His Asp Ser Leu
100                   105                   110                   115

cca gga ggg ttt ctt gac ttc cat gaa acc aac ccg gcg att caa aac
499
Pro Gly Gly Phe Leu Asp Phe His Glu Thr Asn Pro Ala Ile Gln Asn
                120                   125                   130

aac tgt cag att gag gat ggt ggc att gcg gct gct ttt gat gac att
547
Asn Cys Gln Ile Glu Asp Gly Gly Ile Ala Ala Ala Phe Asp Asp Ile
                135                   140                   145

caa aaa cga agt gat tgg cat gaa tgg gct gac cat ttg atc act gat
595
Gln Lys Arg Ser Asp Trp His Glu Trp Ala Asp His Leu Ile Thr Asp
            150                   155                   160

gat gat cct ttg atg tct act aac tgg aat gat ctc ttg ctt gaa aca
643
Asp Asp Pro Leu Met Ser Thr Asn Trp Asn Asp Leu Leu Leu Glu Thr
            165                   170                   175

aat tcc aat tca gat tca aag gac cag aag aca ctg caa att ccg caa
691
Asn Ser Asn Ser Asp Ser Lys Asp Gln Lys Thr Leu Gln Ile Pro Gln
180                   185                   190                   195

cct cag att gtt cag cag caa cct tct ccg tct gtg gaa ttg cga cct
739
Pro Gln Ile Val Gln Gln Gln Pro Ser Pro Ser Val Glu Leu Arg Pro
                200                   205                   210

gtt agc aca aca tct tca aac agc aat aac gga acg ggc aag gca cga
787
Val Ser Thr Thr Ser Ser Asn Ser Asn Asn Gly Thr Gly Lys Ala Arg
                215                   220                   225
```

```
atg cgt tgg acg cca gag ctt cac gag gct ttt gtt gag gct gtc aac
835
Met Arg Trp Thr Pro Glu Leu His Glu Ala Phe Val Glu Ala Val Asn
        230               235               240

agt ctt ggc ggt agt gaa aga gct act cct aaa ggg gta ctg aag att
883
Ser Leu Gly Gly Ser Glu Arg Ala Thr Pro Lys Gly Val Leu Lys Ile
        245               250               255

atg aaa gtt gaa ggc ttg act ata tat cat gtt aaa agc cat tta cag
931
Met Lys Val Glu Gly Leu Thr Ile Tyr His Val Lys Ser His Leu Gln
260               265               270               275

aaa tat agg aca gct aga tat cgg cca gaa cca tca gaa act ggt tcg
979
Lys Tyr Arg Thr Ala Arg Tyr Arg Pro Glu Pro Ser Glu Thr Gly Ser
                280               285               290

cca gaa agg aag ttg aca ccg ctt gaa cat ata aca tct ctt gat ttg
1027
Pro Glu Arg Lys Leu Thr Pro Leu Glu His Ile Thr Ser Leu Asp Leu
            295               300               305

aaa ggt ggg ata ggt att aca gag gct cta cga ctt cag atg gaa gta
1075
Lys Gly Gly Ile Gly Ile Thr Glu Ala Leu Arg Leu Gln Met Glu Val
        310               315               320

cag aag caa ctc cat gag cag ctc gag att caa aga aac ctg caa ctc
1123
Gln Lys Gln Leu His Glu Gln Leu Glu Ile Gln Arg Asn Leu Gln Leu
        325               330               335

cga ata gaa gaa caa ggc aag tac ctg caa atg atg ttc gag aag caa
1171
Arg Ile Glu Glu Gln Gly Lys Tyr Leu Gln Met Met Phe Glu Lys Gln
340               345               350               355

aac tct ggt ctt acc aaa ggg aca gcc tca aca tca gat tcc gca gcc
1219
Asn Ser Gly Leu Thr Lys Gly Thr Ala Ser Thr Ser Asp Ser Ala Ala
            360               365               370

aaa tct gaa caa gaa gac aag aag act gct gat tcg aag gag gtt cca
1267
Lys Ser Glu Gln Glu Asp Lys Lys Thr Ala Asp Ser Lys Glu Val Pro
            375               380               385

gaa gaa gaa acc agg aaa tgt gag gaa cta gaa tct cca cag cca aag
1315
Glu Glu Glu Thr Arg Lys Cys Glu Glu Leu Glu Ser Pro Gln Pro Lys
        390               395               400

cgt ccc aaa atc gat aat tga aagtattggt cttttgctgg ataatctcgg
1366
Arg Pro Lys Ile Asp Asn
        405
```

499

agtttcagag ttaacagtga tagagagaac gagctcttat cttgaggttc ttcaggactt
1426

ctctcgcggc cgctctag
1444

<210> 282 <211> 409 <212> PRT <213> Arabidopsis thaliana <400>
282

Met Glu Ala Arg Pro Val His Arg Ser Gly Ser Arg Asp Leu Thr Arg
1   5   10   15

Thr Ser Ser Ile Pro Ser Thr Gln Lys Pro Ser Pro Val Glu Asp Ser
            20   25   30

Phe Met Arg Ser Asp Asn Asn Ser Gln Leu Met Ser Arg Pro Leu Gly
        35   40   45

Gln Thr Tyr His Leu Leu Ser Ser Ser Asn Gly Gly Ala Val Gly His
    50   55   60

Ile Cys Ser Ser Ser Ser Ser Gly Phe Ala Thr Asn Leu His Tyr Ser
65   70   75   80

Thr Met Val Ser His Glu Lys Gln Gln His Tyr Thr Gly Ser Ser Ser
                85   90   95

Asn Asn Ala Val Gln Thr Pro Ser Asn Asn Asp Ser Ala Trp Cys His
            100   105   110

Asp Ser Leu Pro Gly Gly Phe Leu Asp Phe His Glu Thr Asn Pro Ala
        115   120   125

Ile Gln Asn Asn Cys Gln Ile Glu Asp Gly Gly Ile Ala Ala Ala Phe
    130   135   140

Asp Asp Ile Gln Lys Arg Ser Asp Trp His Glu Trp Ala Asp His Leu
145   150   155   160

Ile Thr Asp Asp Asp Pro Leu Met Ser Thr Asn Trp Asn Asp Leu Leu
                165   170   175

Leu Glu Thr Asn Ser Asn Ser Asp Ser Lys Asp Gln Lys Thr Leu Gln
            180   185   190

Ile Pro Gln Pro Gln Ile Val Gln Gln Gln Pro Ser Pro Ser Val Glu
        195   200   205

500

```
Leu Arg Pro Val Ser Thr Thr Ser Ser Asn Ser Asn Asn Gly Thr Gly
    210             215             220
```

```
Lys Ala Arg Met Arg Trp Thr Pro Glu Leu His Glu Ala Phe Val Glu
225             230             235             240
```

```
Ala Val Asn Ser Leu Gly Gly Ser Glu Arg Ala Thr Pro Lys Gly Val
                245             250             255
```

```
Leu Lys Ile Met Lys Val Glu Gly Leu Thr Ile Tyr His Val Lys Ser
            260             265             270
```

```
His Leu Gln Lys Tyr Arg Thr Ala Arg Tyr Arg Pro Glu Pro Ser Glu
        275             280             285
```

```
Thr Gly Ser Pro Glu Arg Lys Leu Thr Pro Leu Glu His Ile Thr Ser
    290             295             300
```

```
Leu Asp Leu Lys Gly Gly Ile Gly Ile Thr Glu Ala Leu Arg Leu Gln
305             310             315             320
```

```
Met Glu Val Gln Lys Gln Leu His Glu Gln Leu Glu Ile Gln Arg Asn
                325             330             335
```

```
Leu Gln Leu Arg Ile Glu Glu Gln Gly Lys Tyr Leu Gln Met Met Phe
            340             345             350
```

```
Glu Lys Gln Asn Ser Gly Leu Thr Lys Gly Thr Ala Ser Thr Ser Asp
        355             360             365
```

```
Ser Ala Ala Lys Ser Glu Gln Glu Asp Lys Lys Thr Ala Asp Ser Lys
    370             375             380
```

```
Glu Val Pro Glu Glu Glu Thr Arg Lys Cys Glu Glu Leu Glu Ser Pro
385             390             395             400
```

```
Gln Pro Lys Arg Pro Lys Ile Asp Asn
                405
```

```
<210> 283 <211> 1120 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (87)..(923) <223> G2124
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<400> 283
gaacagcaaa accctagatt tcctgttcaa gctcaagacc gtacaaaact ttggaactca
60
```

tatataaaga tctcgagaat agcatt atg aat atc gtc tct tgg aaa gat gca
113

                              Met Asn Ile Val Ser Trp Lys Asp Ala
                              1   5

aac gac gaa gtt gca ggc ggc gct acg aca aga cgt gaa aga gaa gta
161
Asn Asp Glu Val Ala Gly Gly Ala Thr Thr Arg Arg Glu Arg Glu Val
10   15   20   25

aaa gag gat caa gaa gaa acc gaa gtc aga gcc acc agt ggc aaa acc
209
Lys Glu Asp Gln Glu Glu Thr Glu Val Arg Ala Thr Ser Gly Lys Thr
                30   35   40

gta att aaa aag cag cct aca tcg atc tct tct tct tct tct tcg tgg
257
Val Ile Lys Lys Gln Pro Thr Ser Ile Ser Ser Ser Ser Ser Ser Trp
                45   50   55

atg aaa tcc aag gat ccg agg att gtt agg gtt tca cgc gcc ttt gga
305
Met Lys Ser Lys Asp Pro Arg Ile Val Arg Val Ser Arg Ala Phe Gly
            60   65   70

ggc aaa gac cgt cac agc aaa gtg tgt acg tta cgt gga cta cgt gac
353
Gly Lys Asp Arg His Ser Lys Val Cys Thr Leu Arg Gly Leu Arg Asp
        75   80   85

aga cgc gtg aga tta tca gtc cca acg gct att cag ctc tac gat ctt
401
Arg Arg Val Arg Leu Ser Val Pro Thr Ala Ile Gln Leu Tyr Asp Leu
90   95   100   105

caa gaa cgg ctc ggt gtt gac cag cct agc aaa gcc gtt gac tgg ttg
449
Gln Glu Arg Leu Gly Val Asp Gln Pro Ser Lys Ala Val Asp Trp Leu
                110   115   120

ctt gat gca gct aaa gag gag atc gac gag cta cct ccg tta cct atc
497
Leu Asp Ala Ala Lys Glu Glu Ile Asp Glu Leu Pro Pro Leu Pro Ile
                125   130   135

tcg ccg gaa aat ttc agc atc ttc aac cat cat cag tcc ttc ttg aat
545
Ser Pro Glu Asn Phe Ser Ile Phe Asn His His Gln Ser Phe Leu Asn
            140   145   150

ctt ggt caa cgg ccc ggt caa gat ccg acc caa ctc ggg ttt aaa atc
593
Leu Gly Gln Arg Pro Gly Gln Asp Pro Thr Gln Leu Gly Phe Lys Ile
        155   160   165

aat gga tgt gta caa aag tct act act act agc cgc gaa gaa aac gat
641
Asn Gly Cys Val Gln Lys Ser Thr Thr Thr Ser Arg Glu Glu Asn Asp
170   175   180   185

```
aga gag aaa gga gaa aac gat gtc gtt tac aca aac aat cat cat gtt
689
Arg Glu Lys Gly Glu Asn Asp Val Val Tyr Thr Asn Asn His His Val
                190             195             200

ggg tct tat gga act tat cac aac ctg gaa cat cat cat cat cat cac
737
Gly Ser Tyr Gly Thr Tyr His Asn Leu Glu His His His His His His
            205             210             215

caa cat ttg agt tta cag gca gat tat cat agt cat caa cta cat agt
785
Gln His Leu Ser Leu Gln Ala Asp Tyr His Ser His Gln Leu His Ser
        220             225             230

ctt gtc cca ttt cca tca caa att ttg gta tgt cca atg acg aca tca
833
Leu Val Pro Phe Pro Ser Gln Ile Leu Val Cys Pro Met Thr Thr Ser
    235             240             245

cca aca act aca act ata caa tct ttg ttt cca tca tca tcg tca gct
881
Pro Thr Thr Thr Thr Ile Gln Ser Leu Phe Pro Ser Ser Ser Ser Ala
250             255             260             265

ggt tca ggg act atg gag aca tta gat ccg agg caa atg tag
923
Gly Ser Gly Thr Met Glu Thr Leu Asp Pro Arg Gln Met
                270             275

caacaatggt ggtagagaca ttgataatcg gatgtcgtcg gtccaattca accgaactaa
983

tagcactaca acggctaaca tgtcgaggca tctaggctcg gagcgttgta caagtagagg
1043

aagtgatcac catatgtgaa gttagattat tgaaacgata taattgttgt ttgatgtgtt
1103

cagaaataag gggacac
1120
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<210> 284 <211> 278 <212> PRT <213> Arabidopsis thaliana <400>
284

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Met Asn Ile Val Ser Trp Lys Asp Ala Asn Asp Glu Val Ala Gly Gly
1               5               10              15

Ala Thr Thr Arg Arg Glu Arg Glu Val Lys Glu Asp Gln Glu Glu Thr
                20              25              30

Glu Val Arg Ala Thr Ser Gly Lys Thr Val Ile Lys Lys Gln Pro Thr
        35              40              45

Ser Ile Ser Ser Ser Ser Ser Ser Trp Met Lys Ser Lys Asp Pro Arg
    50              55              60
```

503

Ile Val Arg Val Ser Arg Ala Phe Gly Gly Lys Asp Arg His Ser Lys
65   70   75   80

Val Cys Thr Leu Arg Gly Leu Arg Asp Arg Arg Val Arg Leu Ser Val
                85   90   95

Pro Thr Ala Ile Gln Leu Tyr Asp Leu Gln Glu Arg Leu Gly Val Asp
                100   105   110

Gln Pro Ser Lys Ala Val Asp Trp Leu Leu Asp Ala Ala Lys Glu Glu
            115   120   125

Ile Asp Glu Leu Pro Pro Leu Pro Ile Ser Pro Glu Asn Phe Ser Ile
    130   135   140

Phe Asn His His Gln Ser Phe Leu Asn Leu Gly Gln Arg Pro Gly Gln
145   150   155   160

Asp Pro Thr Gln Leu Gly Phe Lys Ile Asn Gly Cys Val Gln Lys Ser
                165   170   175

Thr Thr Thr Ser Arg Glu Glu Asn Asp Arg Glu Lys Gly Glu Asn Asp
            180   185   190

Val Val Tyr Thr Asn Asn His His Val Gly Ser Tyr Gly Thr Tyr His
        195   200   205

Asn Leu Glu His His His His His Gln His Leu Ser Leu Gln Ala
    210   215   220

Asp Tyr His Ser His Gln Leu His Ser Leu Val Pro Phe Pro Ser Gln
225   230   235   240

Ile Leu Val Cys Pro Met Thr Thr Ser Pro Thr Thr Thr Thr Ile Gln
                245   250   255

Ser Leu Phe Pro Ser Ser Ser Ser Ala Gly Ser Gly Thr Met Glu Thr
            260   265   270

Leu Asp Pro Arg Gln Met
        275

<210> 285 <211> 1024 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (89)..(784) <223> G2143

<400> 285

tcttcttctt cctccatacc ttatctcacc agcttctcca tatctctcaa agaaaaaaca
60

aaccctataa attccacaaa aaaggagg atg gat aac tcc gac att cta atg
112
                                   Met Asp Asn Ser Asp Ile Leu Met
                                   1   5

aac atg atg atg cag cag atg gag aag ctt. cct gaa cac ttc tct aac
160
Asn Met Met Met Gln Gln Met Glu Lys Leu Pro Glu His Phe Ser Asn
    10   15   20

tca aac cct aac cct aat ccc cat aac att atg atg ctt tct gaa tcc
208
Ser Asn Pro Asn Pro Asn Pro His Asn Ile Met Met Leu Ser Glu Ser
25   30   35   40

aac acc cac ccg ttc ttc ttc aac ccc act cat tct cat ctc cca ttt
256
Asn Thr His Pro Phe Phe Phe Asn Pro Thr His Ser His Leu Pro Phe
             45   50   55

gac caa acc atg cct cac cac caa ccc ggt tta aat ttc cgg tac gcc
304
Asp Gln Thr Met Pro His His Gln Pro Gly Leu Asn Phe Arg Tyr Ala
             60   65   70

ccc tcc ccg tca tca tct ctc ccg gag aag aga gga ggc tgc agc gac
352
Pro Ser Pro Ser Ser Ser Leu Pro Glu Lys Arg Gly Gly Cys Ser Asp
             75   80   85

aac gcc aac atg gcg gcg atg aga gag atg atc ttt cga ata gcc gtg
400
Asn Ala Asn Met Ala Ala Met Arg Glu Met Ile Phe Arg Ile Ala Val
    90   95   100

atg cag cct ata cat att gat ccg gaa tcc gta aag cca cca aag aga
448
Met Gln Pro Ile His Ile Asp Pro Glu Ser Val Lys Pro Pro Lys Arg
105   110   115   120

aag aac gtg agg atc tct aag gat cca cag agc gtg gca gct cgg cat
496
Lys Asn Val Arg Ile Ser Lys Asp Pro Gln Ser Val Ala Ala Arg His
             125   130   135

cga agg gag agg ata agc gag cgg att cgg att ctt cag cgg ctt gtt
544
Arg Arg Glu Arg Ile Ser Glu Arg Ile Arg Ile Leu Gln Arg Leu Val
             140   145   150

ccc ggt ggg act aag atg gat acg gcg tcg atg ctc gat gag gct atc
592
Pro Gly Gly Thr Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile
             155   160   165

cat tac gtt aag ttt ctc aag aag caa gtg cag tcg ctg gag gaa cat
640
His Tyr Val Lys Phe Leu Lys Lys Gln Val Gln Ser Leu Glu Glu His

505

```
      170                    175                    180

gcg gtg gtt aac ggc gga gga atg acg gcg gtg gcc gga gga gca ctt
688
Ala Val Val Asn Gly Gly Gly Met Thr Ala Val Ala Gly Gly Ala Leu
185                190                195                200

gcg ggt act gtt ggt gga gga tat gga gga aaa ggg tgt ggc att atg
736
Ala Gly Thr Val Gly Gly Gly Tyr Gly Gly Lys Gly Cys Gly Ile Met
                   205                210                215

cgg tct gat cat cac cag atg ctt gga aat gca cag att ctt aga tga
784
Arg Ser Asp His His Gln Met Leu Gly Asn Ala Gln Ile Leu Arg
               220                225                230

tgatgatgtt gatttttaaa tatatatcat atgtttatta atatgacggg aaaaaatatt
844

atcgagggag ttgaatttag tatcatgaaa ctatgagagc attttttttta aatgtttttta
904

tctttccggg tttcgataat gtttgggatg gttaattaac aatttaaaag tcagacaact
964

tggttgtaaa gactaaagaa taagcatagt ttatcaattt atcattacta aatgaaatag
1024


<210> 286 <211> 231 <212> PRT <213> Arabidopsis thaliana <400>
286

Met Asp Asn Ser Asp Ile Leu Met Asn Met Met Met Gln Gln Met Glu
1              5                10                15


Lys Leu Pro Glu His Phe Ser Asn Ser Asn Pro Asn Pro Asn Pro His
             20                25                30


Asn Ile Met Met Leu Ser Glu Ser Asn Thr His Pro Phe Phe Phe Asn
          35                40                45


Pro Thr His Ser His Leu Pro Phe Asp Gln Thr Met Pro His His Gln
       50                55                60


Pro Gly Leu Asn Phe Arg Tyr Ala Pro Ser Pro Ser Ser Ser Leu Pro
65                70                75                80


Glu Lys Arg Gly Gly Cys Ser Asp Asn Ala Asn Met Ala Ala Met Arg
                85                90                95


Glu Met Ile Phe Arg Ile Ala Val Met Gln Pro Ile His Ile Asp Pro
                100                105                110
```

```
Glu Ser Val Lys Pro Pro Lys Arg Lys Asn Val Arg Ile Ser Lys Asp
        115              120              125

Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile Ser Glu Arg
        130              135              140

Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys Met Asp Thr
145              150              155              160

Ala Ser Met Leu Asp Glu Ala Ile His Tyr Val Lys Phe Leu Lys Lys
                165              170              175

Gln Val Gln Ser Leu Glu Glu His Ala Val Val Asn Gly Gly Gly Met
                180              185              190

Thr Ala Val Ala Gly Gly Ala Leu Ala Gly Thr Val Gly Gly Gly Tyr
        195              200              205

Gly Gly Lys Gly Cys Gly Ile Met Arg Ser Asp His His Gln Met Leu
    210              215              220

Gly Asn Ala Gln Ile Leu Arg
225              230
```

<210> 287 <211> 1000 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (143)..(934) <223> G2509

<400> 287

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atatattccc tctttcattc tccttcttcg tcttttctttt gtttctcata ttcaagacat
60

cctcaattcc aaatcttaaa ccctaaattt acagacacaa tcgagatcac ctgaaaaaag
120

aggtttaaag attttagcaa ag atg gcg aat tca gga aat tat gga aag agg
172
                       Met Ala Asn Ser Gly Asn Tyr Gly Lys Arg
                       1               5                 10

ccc ttt cga ggc gat gaa tcg gat gaa aag aaa gaa gcc gat gat gat
220
Pro Phe Arg Gly Asp Glu Ser Asp Glu Lys Lys Glu Ala Asp Asp Asp
            15              20              25

gag aac ata ttc cct ttc ttc tct gcc cga tcc caa tat gac atg cgt
268
Glu Asn Ile Phe Pro Phe Phe Ser Ala Arg Ser Gln Tyr Asp Met Arg
            30              35              40

gcc atg gtc tca gcc ttg act caa gtc att gga aac caa agc agc tct
316
Ala Met Val Ser Ala Leu Thr Gln Val Ile Gly Asn Gln Ser Ser Ser
        45              50              55
```

507

```
cat gat aat aac caa cat caa cct gtt gtg tat aat caa caa gat cct
364
His Asp Asn Asn Gln His Gln Pro Val Val Tyr Asn Gln Gln Asp Pro
    60              65              70


aac cca ccg gct cct cca act caa gat caa ggg cta ttg agg aag agg
412
Asn Pro Pro Ala Pro Pro Thr Gln Asp Gln Gly Leu Leu Arg Lys Arg
75              80              85              90


cac tat aga ggg gta aga caa cga cca tgg gga aag tgg gca gct gaa
460
His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
                95              100             105


att cgg gat ccg caa aag gca gca cgg gtg tgg ctc ggg aca ttt gag
508
Ile Arg Asp Pro Gln Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu
            110             115             120


act gct gaa gct gcg gct tta gct tat gat aac gca gct ctt aag ttc
556
Thr Ala Glu Ala Ala Ala Leu Ala Tyr Asp Asn Ala Ala Leu Lys Phe
            125             130             135


aaa gga agc aaa gcc aaa ctc aat ttc cct gag aga gct caa cta gca
604
Lys Gly Ser Lys Ala Lys Leu Asn Phe Pro Glu Arg Ala Gln Leu Ala
        140             145             150


agt aac act agt aca act acc ggt cca cca aac tat tat tct tct aat
652
Ser Asn Thr Ser Thr Thr Thr Gly Pro Pro Asn Tyr Tyr Ser Ser Asn
155             160             165             170


aat caa att tac tac tca aat ccg cag act aat ccg caa acc ata cct
700
Asn Gln Ile Tyr Tyr Ser Asn Pro Gln Thr Asn Pro Gln Thr Ile Pro
                175             180             185


tat ttt aac caa tac tac tat aac caa tat ctt cat caa ggg ggg aat
748
Tyr Phe Asn Gln Tyr Tyr Tyr Asn Gln Tyr Leu His Gln Gly Gly Asn
                190             195             200


agt aac gat gca tta agt tat agc ttg gcc ggt gga gaa acc gga ggc
796
Ser Asn Asp Ala Leu Ser Tyr Ser Leu Ala Gly Gly Glu Thr Gly Gly
        205             210             215


tca atg tat aat cat cag acg tta tct act aca aat tct tca tct tct
844
Ser Met Tyr Asn His Gln Thr Leu Ser Thr Thr Asn Ser Ser Ser Ser
    220             225             230


ggt gga tct tca agg caa caa gat gat gaa caa gat tac gcc aga tat
892
Gly Gly Ser Ser Arg Gln Gln Asp Asp Glu Gln Asp Tyr Ala Arg Tyr
235             240             245             250
```

ttg cgt ttt ggg gat tct tca cct cct aat tct ggt ttt tga
934
Leu Arg Phe Gly Asp Ser Ser Pro Pro Asn Ser Gly Phe
                    255   260

gatcttcaat aaactgataa taaaggattt gggtcacttg ttatgagggg atcatatgtt
994

ttctaa
1000

<210> 288 <211> 263 <212> PRT <213> Arabidopsis thaliana <400>
288

Met Ala Asn Ser Gly Asn Tyr Gly Lys Arg Pro Phe Arg Gly Asp Glu
1   5   10   15

Ser Asp Glu Lys Lys Glu Ala Asp Asp Asp Glu Asn Ile Phe Pro Phe
            20   25   30

Phe Ser Ala Arg Ser Gln Tyr Asp Met Arg Ala Met Val Ser Ala Leu
            35   40   45

Thr Gln Val Ile Gly Asn Gln Ser Ser Ser His Asp Asn Asn Gln His
    50   55   60

Gln Pro Val Val Tyr Asn Gln Gln Asp Pro Asn Pro Pro Ala Pro Pro
65   70   75   80

Thr Gln Asp Gln Gly Leu Leu Arg Lys Arg His Tyr Arg Gly Val Arg
                85   90   95

Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Gln Lys
            100   105   110

Ala Ala Arg Val Trp Leu Gly Thr Phe Glu Thr Ala Glu Ala Ala Ala
            115   120   125

Leu Ala Tyr Asp Asn Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys
    130   135   140

Leu Asn Phe Pro Glu Arg Ala Gln Leu Ala Ser Asn Thr Ser Thr Thr
145   150   155   160

Thr Gly Pro Pro Asn Tyr Tyr Ser Ser Asn Asn Gln Ile Tyr Tyr Ser
                165   170   175

Asn Pro Gln Thr Asn Pro Gln Thr Ile Pro Tyr Phe Asn Gln Tyr Tyr
                180   185   190

```
Tyr Asn Gln Tyr Leu His Gln Gly Gly Asn Ser Asn Asp Ala Leu Ser
        195                 200                 205


Tyr Ser Leu Ala Gly Gly Glu Thr Gly Gly Ser Met Tyr Asn His Gln
    210                 215                 220
                                                  ı

Thr Leu Ser Thr Thr Asn Ser Ser Ser Ser Gly Gly Ser Ser Arg Gln
225                 230                 235                 240


Gln Asp Asp Glu Gln Asp Tyr Ala Arg Tyr Leu Arg Phe Gly Asp Ser
            245                 250                 255


Ser Pro Pro Asn Ser Gly Phe
            260
```

<210> 289 <211> 1502 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (94)..(1215) <223>- G2557

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<400> 289
tcgacttcct gtgaactcat ctgtttgttc tcttcttccg gtttcacttt ttcatgtcct
60

gccgttatta caacgaggat tgtgtttgat ccg atg gaa gga ttg gaa tct gtg
114
                                  Met Glu Gly Leu Glu Ser Val
                                  1               5

tac gct caa gct atg tat gga atg aca cga gag agc aaa atc atg gag
162
Tyr Ala Gln Ala Met Tyr Gly Met Thr Arg Glu Ser Lys Ile Met Glu
        10                  15                  20

cat caa gga tca gat ttg att tgg gga gga aat gag cta atg gct cga
210
His Gln Gly Ser Asp Leu Ile Trp Gly Gly Asn Glu Leu Met Ala Arg
    25                  30                  35

gaa ctc tgt tct tct tct tct tat cac cac caa ctc att aat ccg aat
258
Glu Leu Cys Ser Ser Ser Ser Tyr His His Gln Leu Ile Asn Pro Asn
40                  45                  50                  55

ctt agc agc tgt ttc atg tct gat ctt gga gtc tta ggt gag att caa
306
Leu Ser Ser Cys Phe Met Ser Asp Leu Gly Val Leu Gly Glu Ile Gln
                60                  65                  70

cag cag caa cat gtt ggc aac aga gct agc tcg ata gat cca tca tca
354
Gln Gln Gln His Val Gly Asn Arg Ala Ser Ser Ile Asp Pro Ser Ser
            75                  80                  85

ctc gat tgt ttg tta tct gcg acg tcg aat agc aac aac acc tcg acg
402
```

510

```
Leu Asp Cys Leu Leu Ser Ala Thr Ser Asn Ser Asn Asn Thr Ser Thr
        90                  95              100

gag gac gat gaa gga ata tct gtg ctt ttc tca gat tgt cag act ctt
450
Glu Asp Asp Glu Gly Ile Ser Val Leu Phe Ser Asp Cys Gln Thr Leu
        105             110                 115

tgg agc ttt ggt gga gtc tca tct gca gag tct gag aac aga gag atc
498
Trp Ser Phe Gly Gly Val Ser Ser Ala Glu Ser Glu Asn Arg Glu Ile
120                 125                 130                 135

act act gag acg aca aca acg ata aag cct aag cct ttg aag aga aac
546
Thr Thr Glu Thr Thr Thr Thr Ile Lys Pro Lys Pro Leu Lys Arg Asn
                140                 145                 150

aga gga gga gat gga gga act act gag act aca aca aca aca aca aaa
594
Arg Gly Gly Asp Gly Gly Thr Thr Glu Thr Thr Thr Thr Thr Thr Lys
                155                 160                 165

cct aag tct ttg aag aga aac aga gga gac gag aca gga agt cac ttt
642
Pro Lys Ser Leu Lys Arg Asn Arg Gly Asp Glu Thr Gly Ser His Phe
        170                 175                 180

agt ctt gtt cat cct caa gat gat tcg gag aaa gga ggt ttc aag ctt
690
Ser Leu Val His Pro Gln Asp Asp Ser Glu Lys Gly Gly Phe Lys Leu
        185                 190                 195

ata tac gat gag aat caa tcg aaa tca aag aaa cca aga aca gag aaa
738
Ile Tyr Asp Glu Asn Gln Ser Lys Ser Lys Lys Pro Arg Thr Glu Lys
200                 205                 210                 215

gaa cga ggc ggt tct tcg aac att agt ttc caa cat tca act tgt ttg
786
Glu Arg Gly Gly Ser Ser Asn Ile Ser Phe Gln His Ser Thr Cys Leu
                220                 225                 230

tct gac aat gtc gag ccc gat gct gag gcg att gca caa atg aag gag
834
Ser Asp Asn Val Glu Pro Asp Ala Glu Ala Ile Ala Gln Met Lys Glu
                235                 240                 245

atg ata tac aga gcg gct gca ttt aga ccg gtg aat ttc ggg tta gag
882
Met Ile Tyr Arg Ala Ala Ala Phe Arg Pro Val Asn Phe Gly Leu Glu
            250                 255                 260

att gtg gag aag cct aag agg aag aac gtc aag ata tcg acg gat cct
930
Ile Val Glu Lys Pro Lys Arg Lys Asn Val Lys Ile Ser Thr Asp Pro
        265                 270                 275

caa acg gtt gca gcg aga cag aga agg gag agg ata agt gag aag att
978
Gln Thr Val Ala Ala Arg Gln Arg Arg Glu Arg Ile Ser Glu Lys Ile
```

511

```
            280                 285                 290                 295

agg gtt tta caa aca ttg gtt cca ggt ggg acg aag atg gat act gca
1026
Arg Val Leu Gln Thr Leu Val Pro Gly Gly Thr Lys Met Asp Thr Ala
                300                 305                 310

tca atg ctt gat gaa gct gct aat tat ctc aag ttc ctt aga gca caa
1074
Ser Met Leu Asp Glu Ala Ala Asn Tyr Leu Lys Phe Leu Arg Ala Gln
                315                 320                 325

gta aaa gct tta gaa aac ttg aga ccc aag ctt gac caa acc aat ctc
1122
Val Lys Ala Leu Glu Asn Leu Arg Pro Lys Leu Asp Gln Thr Asn Leu
                330                 335                 340

tct ttc tct tct gct cct aca tcg ttt cca tta ttc cac cca tct ttt
1170
Ser Phe Ser Ser Ala Pro Thr Ser Phe Pro Leu Phe His Pro Ser Phe
         345                 350                 355

ctt cca ttg caa aat cct aat caa atc cat cat cca gag tgt tga
1215
Leu Pro Leu Gln Asn Pro Asn Gln Ile His His Pro Glu Cys
360                 365                 370

cagattataa actttgagt ttcatcatca tcaacagaat catggcgtct tgattgtttt
1275

agcagttctc aagaaaggca acttctgtga caagggtggt gtcgggcagt gttgtttaca
1335

ctttccagtc tttgttttgc atttcttttt atataaagtt tgtattttat atagaatctg
1395

tggaattcga gggttgaaat attgtgaaaa acagagccgc aagaggttaa ttacagtctc
1455

tgcaatattt tcaacctttt attactttat tagagtaaag atagcgt
1502


<210> 290 <211> 373 <212> PRT <213> Arabidopsis thaliana <400>
290

Met Glu Gly Leu Glu Ser Val Tyr Ala Gln Ala Met Tyr Gly Met Thr
1               5                   10                  15


Arg Glu Ser Lys Ile Met Glu His Gln Gly Ser Asp Leu Ile Trp Gly
                20                  25                  30


Gly Asn Glu Leu Met Ala Arg Glu Leu Cys Ser Ser Ser Ser Tyr His
         35                  40                  45


His Gln Leu Ile Asn Pro Asn Leu Ser Ser Cys Phe Met Ser Asp Leu
    50                  55                  60
```

512

Gly Val Leu Gly Glu Ile Gln Gln Gln Gln His Val Gly Asn Arg Ala
65   70   75   80

Ser Ser Ile Asp Pro Ser Ser Leu Asp Cys Leu Leu Ser Ala Thr Ser
                85   90   95

Asn Ser Asn Asn Thr Ser Thr Glu Asp Asp Glu Gly Ile Ser Val Leu
            100   105   110

Phe Ser Asp Cys Gln Thr Leu Trp Ser Phe Gly Gly Val Ser Ser Ala
            115   120   125

Glu Ser Glu Asn Arg Glu Ile Thr Thr Glu Thr Thr Thr Thr Ile Lys
    130   135   140

Pro Lys Pro Leu Lys Arg Asn Arg Gly Gly Asp Gly Gly Thr Thr Glu
145   150   155   160

Thr Thr Thr Thr Thr Thr Lys Pro Lys Ser Leu Lys Arg Asn Arg Gly
            165   170   175

Asp Glu Thr Gly Ser His Phe Ser Leu Val His Pro Gln Asp Asp Ser
            180   185   190

Glu Lys Gly Gly Phe Lys Leu Ile Tyr Asp Glu Asn Gln Ser Lys Ser
        195   200   205

Lys Lys Pro Arg Thr Glu Lys Glu Arg Gly Gly Ser Ser Asn Ile Ser
    210   215   220

Phe Gln His Ser Thr Cys Leu Ser Asp Asn Val Glu Pro Asp Ala Glu
225   230   235   240

Ala Ile Ala Gln Met Lys Glu Met Ile Tyr Arg Ala Ala Ala Phe Arg
            245   250   255

Pro Val Asn Phe Gly Leu Glu Ile Val Glu Lys Pro Lys Arg Lys Asn
            260   265   270

Val Lys Ile Ser Thr Asp Pro Gln Thr Val Ala Ala Arg Gln Arg Arg
    275   280   285

Glu Arg Ile Ser Glu Lys Ile Arg Val Leu Gln Thr Leu Val Pro Gly
    290   295   300

513

```
Gly Thr Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ala Asn Tyr
305                 310             315                 320


Leu Lys Phe Leu Arg Ala Gln Val Lys Ala Leu Glu Asn Leu Arg Pro
            325             330                 335


Lys Leu Asp Gln Thr Asn Leu Ser Phe Ser Ser Ala Pro Thr Ser Phe
            340             345                 350


Pro Leu Phe His Pro Ser Phe Leu Pro Leu Gln Asn Pro Asn Gln Ile
            355             360                 365


His His Pro Glu Cys
    370
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<210> 291 <211> 1023 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (14)..(682) <223> G6

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tatctatccg aga atg gcc aag atg ggc ttg aaa ccc gac ccg gct act
49
                Met Ala Lys Met Gly Leu Lys Pro Asp Pro Ala Thr
                1               5                   10

act aac cag acc cac aat aat gcc aag gag att cgt tac aga ggc gtt
97
Thr Asn Gln Thr His Asn Asn Ala Lys Glu Ile Arg Tyr Arg Gly Val
        15                  20                  25

agg aag cgt cct tgg ggc cgt tat gcc gcc gag atc cga gat ccg ggc
145
Arg Lys Arg Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Gly
    30              35                  40

aag aaa acc cgc gtc tgg ctt ggc act ttc gat acg gct gaa gag gcg
193
Lys Lys Thr Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala
45              50              55                  60

gcg cgt gct tac gat acg gcg gcg cgt gat ttt cgt ggt gct aag gct
241
Ala Arg Ala Tyr Asp Thr Ala Ala Arg Asp Phe Arg Gly Ala Lys Ala
                65                  70                  75

aag acc aat ttc cca act ttt ctc gag ctg agt gac cag aag gtc cct
289
Lys Thr Asn Phe Pro Thr Phe Leu Glu Leu Ser Asp Gln Lys Val Pro
                80              85                  90

acc ggt ttc gcg cgt agc cct agc cag agc agc acg ctc gac tgt gct
337
Thr Gly Phe Ala Arg Ser Pro Ser Gln Ser Ser Thr Leu Asp Cys Ala
        95                  100                 105

tct cct ccg acg tta gtt gtg cct tca gcg acg gct ggg aat gtt ccc
385
```

514

```
Ser Pro Pro Thr Leu Val Val Pro Ser Ala Thr Ala Gly Asn Val Pro
    110                     115                 120

ccg cag ctc gag ctt agt ctc ggc gga gga ggc ggc ggc tcg tgt tat
433
Pro Gln Leu Glu Leu Ser Leu Gly Gly Gly Gly Gly Gly Ser Cys Tyr
125                 130                 135                 140

cag atc ccg atg tcg cgt cct gtc tac ttt ttg gac ctg atg ggg atc
481
Gln Ile Pro Met Ser Arg Pro Val Tyr Phe Leu Asp Leu Met Gly Ile
                145                 150                 155

ggt aac gta ggt cgt ggt cag cct cct cct gtg aca tcg gcg ttt aga
529
Gly Asn Val Gly Arg Gly Gln Pro Pro Pro Val Thr Ser Ala Phe Arg
                160                 165                 170

tcg ccg gtg gtg cat gtt gcg acg aag atg gct tgt ggt gcc caa agc
577
Ser Pro Val Val His Val Ala Thr Lys Met Ala Cys Gly Ala Gln Ser
            175                 180                 185

gac tct gat tcg tca tcg gtc gtt gat ttc gaa ggt ggg atg gag aag
625
Asp Ser Asp Ser Ser Ser Val Val Asp Phe Glu Gly Gly Met Glu Lys
        190                 195                 200

aga tct cag ctg tta gat cta gat ctt aat ttg cct cct cca tcg gaa
673
Arg Ser Gln Leu Leu Asp Leu Asp Leu Asn Leu Pro Pro Pro Ser Glu
205                 210                 215                 220

cag gcc tga gctttaacg gtgtcgtttc aattcgaagc gcatgcgttt
722
Gln Ala

cttcttcttt ttgagctgtg aaaattcgtt ttctcatagt ttttcctctc tctctctctc
782

agtctaaatt tattaccagt ttttagaaag aaaaaacaga ttaaatctga gagagaaaaa
842

tataatttta gctgacatgg atcgttatgt acatattatt acataaccgg agatctgaac
902

ttttgttgtg tgcttttaat tttttgcgac ttggtttcac cccatgttgt ttctctattt
962

tttttactac tttttttttt tttgttcttc caaattttca atcaataatt tggtaatctt
1022

c
1023


<210> 292 <211> 222 <212> PRT <213> Arabidopsis thaliana <400>
292

Met Ala Lys Met Gly Leu Lys Pro Asp Pro Ala Thr Thr Asn Gln Thr
```

```
1               5                    10                   15


His Asn Asn Ala Lys Glu Ile Arg Tyr Arg Gly Val Arg Lys Arg Pro
        20                      25              30


Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Gly Lys Lys Thr Arg
        35                  40                  45


Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr
    50                  55                  60


Asp Thr Ala Ala Arg Asp Phe Arg Gly Ala Lys Ala Lys Thr Asn Phe
65              70·                  75                  80


Pro Thr Phe Leu Glu Leu Ser Asp Gln Lys·Val Pro Thr Gly Phe Ala
            85                  90                  95


Arg Ser Pro Ser Gln Ser Ser·Thr Leu Asp Cys Ala Ser Pro Pro Thr
            100                 105                 110


Leu Val Val Pro Ser Ala Thr Ala Gly Asn Val Pro Pro Gln Leu Glu
        115                 120                 125


Leu Ser Leu Gly Gly Gly Gly Gly Ser Cys Tyr Gln Ile Pro Met
    130                 135                 140


Ser Arg Pro Val Tyr Phe Leu Asp Leu Met Gly Ile Gly Asn Val Gly
145                 150                 155                 160


Arg Gly Gln Pro Pro Pro Val Thr Ser Ala Phe Arg Ser Pro Val Val
            165                 170                 175


His Val Ala Thr Lys Met Ala Cys Gly Ala Gln Ser Asp Ser Asp Ser
            180                 185                 190


Ser Ser Val Val Asp Phe Glu Gly Gly Met Glu Lys Arg Ser Gln Leu
        195                 200                 205


Leu Asp Leu Asp Leu Asn Leu Pro Pro Pro Ser Glu Gln Ala
    210                 215                 220
```

<210> 293 <211> 1246 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (81)..(1139) <223> G9

<400> 293
gtgtttcttc tttctgctaa aaggttataa tttttgtttc ttggtttggt gagaatcttc
60

516

```
aagaaactga aacaaagaaa atg gat tct agt tgc ata gac gag ata agt tcc
113
                         Met Asp Ser Ser Cys Ile Asp Glu Ile Ser Ser
                         1               5                   10

tcc act tca gaa tct ttc tcc gcc acc acc gcc aag aag ctc tct cct
161
Ser Thr Ser Glu Ser Phe Ser Ala Thr Thr Ala Lys Lys Leu Ser Pro
            15              20              25

cct ccc gcg gcg gcg tta cgc ctc tac cgg atg gga agc ggc ggg agc
209
Pro Pro Ala Ala Ala Leu Arg Leu Tyr Arg Met Gly Ser Gly Gly Ser
            30              35              40

agc gtc gtg ttg gat ccc gag aac ggc cta gag acg gag tca cga aag
257
Ser Val Val Leu Asp Pro Glu Asn Gly Leu Glu Thr Glu Ser Arg Lys
        45              50              55

cta cca tct tca aaa tac aaa ggt gtt gtt cct cag cct aac gga aga
305
Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg
60              65              70                      75

tgg gga gct cag atc tac gag aag cac caa cga gta tgg ctc ggg act
353
Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr
                80              85              90

ttc aac gag caa gaa gaa gct gct cgt tcc tac gac atc gca gct tgt
401
Phe Asn Glu Gln Glu Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys
                95              100             105

aga ttc cgt ggc cgc gac gcc gtc gtc aac ttc aag aac gtt ctg gaa
449
Arg Phe Arg Gly Arg Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu
            110             115             120

gac ggc gat tta gct ttt ctt gaa gct cac tca aag gcc gag atc gtc
497
Asp Gly Asp Leu Ala Phe Leu Glu Ala His Ser Lys Ala Glu Ile Val
            125             130             135

gac atg ttg aga aaa cac act tac gcc gac gag ctt gaa cag aac aat
545
Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Leu Glu Gln Asn Asn
140             145             150                     155

aaa cgg cag ttg ttt ctc tcc gtc gac gct aac gga aaa cgt aac gga
593
Lys Arg Gln Leu Phe Leu Ser Val Asp Ala Asn Gly Lys Arg Asn Gly
                160             165             170

tcg agt act act caa aac gac aaa gtt tta aag acg tgt gaa gtt ctt
641
Ser Ser Thr Thr Gln Asn Asp Lys Val Leu Lys Thr Cys Glu Val Leu
                175             180             185
```

517

```
ttc gag aag gct gtt aca cct agc gac gtt ggg aag cta aac cgt ctc
689
Phe Glu Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
        190             195             200

gtg ata cct aaa caa cac gcc gag aaa cac ttt ccg tta ccg tca ccg
737
Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro Ser Pro
    205             210             215

tca ccg gca gtg act aaa gga gtt ttg atc aac ttc gaa gac gtt aac
785
Ser Pro Ala Val Thr Lys Gly Val Leu Ile Asn Phe Glu Asp Val Asn
220             225             230             235

ggt aaa gtg tgg agg ttc cgt tac tca tac tgg aac agt agt caa agt
833
Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
            240             245             250

tac gtg ttg acc aag gga tgg agt cga ttc gtc aag gag aag aat ctt
881
Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu
            255             260             265

cga gcc ggt gat gtt gtt act ttc gag aga tcg acc gga cta gag cgg
929
Arg Ala Gly Asp Val Val Thr Phe Glu Arg Ser Thr Gly Leu Glu Arg
        270             275             280

cag tta tat att gat tgg aaa gtt cgg tct ggt ccg aga gaa aac ccg
977
Gln Leu Tyr Ile Asp Trp Lys Val Arg Ser Gly Pro Arg Glu Asn Pro
    285             290             295

gtt cag gtg gtg gtt cgg ctt ttc gga gtt gat atc ttt aat gtg acc
1025
Val Gln Val Val Val Arg Leu Phe Gly Val Asp Ile Phe Asn Val Thr
300             305             310             315

acc gtg aag cca aac gac gtc gtg gcc gtt tgc ggt gga aag aga tct
1073
Thr Val Lys Pro Asn Asp Val Val Ala Val Cys Gly Gly Lys Arg Ser
            320             325             330

cga gat gtt gat gat atg ttt gcg tta cgg tgt tcc aag aag cag gcg
1121
Arg Asp Val Asp Asp Met Phe Ala Leu Arg Cys Ser Lys Lys Gln Ala
        335             340             345

ata atc aat gct ttg tga catatttcct tttccgattt tatgctttcg
1169
Ile Ile Asn Ala Leu
        350


tttttttaatt tttttttttg tcaagttgtg taggttgtga ttcatgctag gttgtattta
1229

ggaaaagaga taagacc
1246
```

<210> 294 <211> 352 <212> PRT <213> Arabidopsis thaliana <400>
294

Met Asp Ser Ser Cys Ile Asp Glu Ile Ser Ser Ser Thr Ser·Glu Ser
1   5   10   15

Phe Ser Ala Thr Thr Ala Lys Lys Leu Ser Pro Pro Pro Ala Ala Ala
            20   25   30

Leu Arg Leu Tyr Arg Met Gly Ser Gly Gly Ser Ser Val Val Leu Asp
        35   40   45

Pro Glu Asn Gly Leu Glu Thr Glu Ser Arg Lys Leu Pro Ser Ser Lys
    50   55   60

Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile
65   70   75   80

Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Gln Glu
            85   90   95

Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys Arg Phe Arg Gly Arg
            100   105   110

Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu Asp Gly Asp Leu Ala
        115   120   125

Phe Leu Glu Ala His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys
    130   135   140

His Thr Tyr Ala Asp Glu Leu Glu Gln Asn Asn Lys Arg Gln Leu Phe
145   150   155   160

Leu Ser Val Asp Ala Asn Gly Lys Arg Asn Gly Ser Ser Thr·Thr Gln
            165   170   175

Asn Asp Lys Val Leu Lys Thr Cys Glu Val Leu Phe Glu Lys Ala Val
        180   185   190

Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
    195   200   205

His Ala Glu Lys His Phe Pro Leu Pro Ser Pro Ser Pro Ala Val Thr
    210   215   220

Lys Gly Val Leu Ile Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg

519

225   230   235   240

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
                245   250   255

Gly Trp Ser Arg Phe Val Lys·Glu Lys Asn Leu Arg Ala Gly Asp Val
                260   265   270

Val Thr Phe Glu Arg Ser Thr Gly Leu Glu Arg Gln Leu Tyr Ile Asp
            275   280   285

Trp Lys Val Arg Ser Gly Pro Arg Glu Asn Pro Val Gln Val Val Val
    290   ·   295   300

Arg Leu Phe Gly Val Asp Ile Phe Asn Val Thr Thr Val Lys Pro Asn
305   310   315   320

Asp Val Val Ala Val Cys Gly Gly Lys Arg Ser Arg Asp Val Asp Asp
            325   330   335

Met Phe Ala Leu Arg Cys Ser Lys Lys Gln Ala Ile Ile Asn Ala Leu
            340   345   350

<210> 295 <211> 553 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (41)..(442) <223> G30

<400> 295
ctcttctgac gcacaacagt atatacacat acacagatat atg gat caa gga ggt
55
                                            Met Asp Gln Gly Gly
                                            1   5

cgt agc agt ggt agt gga gga gga gga gcc gag caa ggg aag tac cgt
103
Arg Ser Ser Gly Ser Gly Gly Gly Gly Ala Glu Gln Gly Lys Tyr Arg
            10   15   20

gga gta agg aga cga cct tgg ggt aaa tac gcc gcg gaa ata aga gat
151
Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile Arg Asp
            25   30   35

tcg agg aag cac gga gag cgt gtg tgg cta ggg aca ttc gac act gcg
199
Ser Arg Lys His Gly Glu Arg Val Trp Leu Gly Thr Phe Asp Thr Ala
            40   45   50

gaa gac gcg gct cga gcc tat gac cga gcc gcc tat tca atg aga ggc
247
Glu Asp Ala Ala Arg Ala Tyr Asp Arg Ala Ala Tyr Ser Met Arg Gly
            55   60   65

520

aaa gct gcc att ctc aac ttc cct cac gag tat aac atg gga acc gga
295
Lys Ala Ala Ile Leu Asn Phe Pro His Glu Tyr Asn Met Gly Thr Gly
70   75   80   85

tcc tca tcc act gcg gct aat tct tct tcc tcg tcg cag caa gtt ttt
343
Ser Ser Ser Thr Ala Ala Asn Ser Ser Ser Ser Ser Gln Gln Val Phe
                90   95   100

gag ttt gag tac ttg gac gat agc gtt ttg gat gaa ctt ctt gaa tat
391
Glu Phe Glu Tyr Leu Asp Asp Ser Val Leu Asp Glu Leu Leu Glu Tyr
                105   110   115

gga gag aac tat aac aag act cat aat atc aac atg ggc aag agg caa
439
Gly Glu Asn Tyr Asn Lys Thr His Asn Ile Asn Met Gly Lys Arg Gln
        120   125   130

taa agggaataca atcggtatta actgaaagtt atgtgaaaga ccattttcag
492

ttataacaaa taaaataaaa tcccaagcgt acaaagctgt ttctaaaaaa aaaaaaaaaa
552

a
553

<210> 296 <211> 133 <212> PRT <213> Arabidopsis thaliana <400>
296

Met Asp Gln Gly Gly Arg Ser Ser Gly Ser Gly Gly Gly Gly Ala Glu
1   5   10   15

Gln Gly Lys Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala
            20   25   30

Ala Glu Ile Arg Asp Ser Arg Lys His Gly Glu Arg Val Trp Leu Gly
        35   40   45

Thr Phe Asp Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp Arg Ala Ala
    50   55   60

Tyr Ser Met Arg Gly Lys Ala Ala Ile Leu Asn Phe Pro His Glu Tyr
65   70   75   80

Asn Met Gly Thr Gly Ser Ser Ser Thr Ala Ala Asn Ser Ser Ser Ser
                85   90   95

Ser Gln Gln Val Phe Glu Phe Glu Tyr Leu Asp Asp Ser Val Leu Asp
            100   105   110

```
Glu Leu Leu Glu Tyr Gly Glu Asn Tyr Asn Lys Thr His Asn Ile Asn
        115                 120                 125


Met Gly Lys Arg Gln
    130
```

<210> 297 <211> 929 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (164)..(805) <223> G40

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<400> 297
cttgaaaaag aatctacctg aaaagaaaaa aaagagagag agatataaat agctttacca
·60

agacagatat actatctttt attaatccaa aaagactgag aactctagta actacgtact
120

acttaaacct tatccagttt cttgaaacag agtactctga tca atg aac tca ttt
175
                                                     Met Asn Ser Phe
                                 -                    1

tca gct ttt tct gaa atg ttt ggc tcc gat tac gag cct caa ggc gga
223
Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu Pro Gln Gly Gly
5               10                  15                  20

gat tat tgt ccg acg ttg gcc acg agt tgt ccg aag aaa ccg gcg ggc
·271
Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly
            25                  30                  35

cgt aag aag ttt cgt gag act cgt cac cca att tac aga gga gtt cgt
319
Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg
            40                  45                  50

caa aga aac tcc ggt aag tgg gtt tct gaa gtg aga gag cca aac aag
367
Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg Glu Pro Asn Lys
        55                  60                  65

aaa acc agg att tgg ctc ggg act ttc caa acc gct gag atg gca gct
415
Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala
    70                  75                  80

cgt gct cac gac gtc gct gca tta gcc ctc cgt ggc cga tca gca tgt
463
Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys
85                  90                  95                  100

ctc aac ttc gct gac tcg gct tgg cgg cta cga atc ccg gag tca aca
511
Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr
            105                 110                 115

tgc gcc aag gat atc caa aaa gcg gct gct gaa gcg gcg ttg gct ttt
559
Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Ala Phe
```

<center>522</center>

```
                 120                  125                  130

caa gat gag acg tgt gat acg acg acc acg aat cat ggc ctg gac atg
607
Gln Asp Glu Thr Cys Asp Thr Thr Thr Thr Asn His Gly Leu Asp Met
        135                  140                  145

gag gag acg atg gtg gaa gct att tat aca ccg gaa cag agc gaa ggt
655
Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Glu Gly
     150                  155                  160

gcg ttt tat atg gat gag gag aca atg ttt ggg atg ccg act ttg ttg
703
Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met Pro Thr Leu Leu
165                  170                  175                  180

gat aat atg gct gaa ggc atg ctt tta ccg ccg ccg tct gtt caa tgg
751
Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro Ser Val Gln Trp
                185                  190                  195

aat cat aat tat gac ggc gaa gga gat ggt gac gtg tcg ctt tgg agt
799
Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val Ser Leu Trp Ser
            200                  205                  210

tac taa tattcgatag tcgtttccat ttttgtacta tagtttgaaa atattctagt
855
Tyr

tccttttttt agaatggttc cttcatttta ttttatttta ttgttgtaga aacgagtgga
915

aaataattca atac
929
```

`<210> 298 <211> 213 <212> PRT <213> Arabidopsis thaliana <400> 298`

```
Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
1               5                   10                  15

Pro Gln Gly Gly Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys
            20                  25                  30

Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr
        35                  40                  45

Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg
     50                  55                  60

Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala
65                  70                  75                  80
```

523

```
Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly
                 85              90              95
```

```
Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile
             100             105             110
```

```
Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala
         115             120             125
```

```
Ala Leu Ala Phe Gln Asp Glu Thr Cys Asp Thr Thr Thr Asn His
    130             135             140
```

```
Gly Leu Asp Met Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu
145             150             155             160
```

```
Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met
             165             170             175
```

```
Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro
             180             185      .      190
```

```
Ser Val Gln Trp Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val
             195             200             205
```

```
Ser Leu Trp Ser Tyr
    210
```

```
<210>  299 <211>  803 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (35)..(658) <223>  G41
```

```
 <400>  299
ctgatcaatg aactcatttt ctgccttttc tgaa atg ttt ggc tcc gat tac gag
55
                                    Met Phe Gly Ser Asp Tyr Glu
                                  .  1               5
```

```
tct ccg gtt tcc tca ggc ggt gat tac agt ccg aag ctt gcc acg agc
103
Ser Pro Val Ser Ser Gly Gly Asp Tyr Ser Pro Lys Leu Ala Thr Ser
         10              15              20
```

```
tgc ccc aag aaa cca gcg gga agg aag aag ttt cgt gag act cgt cac
151
Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
     25              30              35
```

```
cca att tac aga gga gtt cgt caa aga aac tcc ggt aag tgg gtg tgt
199
Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Cys
40              45              50              55
```

524

```
gag ttg aga gag cca aac aag aaa acg agg att tgg ctc ggg act ttc
247
Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
            60              65              70


caa acc gct gag atg gca gct cgt gct cac gac gtc gcc gcc ata gct
295
Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Ile Ala
            75              80              85


ctc cgt ggc aga tct gcc tgt ctc aat ttc gct gac tcg gct tgg cgg
343
Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
            90              95              100


cta cga atc ccg gaa tca acc tgt gcc aag gaa atc caa aag gcg gcg
391
Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile Gln Lys Ala Ala
    105             110             115


gct gaa gcc gcg ttg aat ttt caa gat gag atg tgt cat atg acg acg
439
Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys His Met Thr Thr
120             125             130             135


gat gct cat ggt ctt gac atg gag gag acc ttg gtg gag gct att tat
487
Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr
            140             145             150


acg ccg gaa cag agc caa gat gcg ttt tat atg gat gaa gag gcg atg
535
Thr Pro Glu Gln Ser Gln Asp Ala Phe Tyr Met Asp Glu Glu Ala Met
            155             160             165


ttg ggg atg tct agt ttg ttg gat aac atg gcc gaa ggg atg ctt tta
583
Leu Gly Met Ser Ser Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu
            170             175             180


ccg tcg ccg tcg gtt caa tgg aac tat aat ttt gat gtc gag gga gat
631
Pro Ser Pro Ser Val Gln Trp Asn Tyr Asn Phe Asp Val Glu Gly Asp
    185             190             195


gat gac gtg tcc tta tgg agc tat taa aattcgattt ttatttccat
678
Asp Asp Val Ser Leu Trp Ser Tyr
200             205


ttttggtatt atagcttttt atacatttga tcctttttta gaatggatct tcttcttttt
738


ttggttgtga gaaacgaatg taaatggtaa aagttgttgt caaatgcaaa tgttttgag
798


tgcag
803
```

<210> 300 <211> 207 <212> PRT <213> Arabidopsis thaliana <400>
300

```
Met Phe Gly Ser Asp Tyr Glu Ser Pro Val Ser Ser Gly Gly Asp Tyr
1               5               10                  15


Ser Pro Lys Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly Arg Lys
            20              25                  30


Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg
        35                  40                  45


Asn Ser Gly Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr
    50              55                  60


Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala Arg Ala
65              70                  75                  80


His Asp Val Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn
                85                  90                  95


Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala
            100                 105                 110


Lys Glu Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp
        115                 120                 125


Glu Met Cys His Met Thr Thr Asp Ala His Gly Leu Asp Met Glu Glu
    130                 135                 140


Thr Leu Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Gln Asp Ala Phe
145                 150                 155                 160


Tyr Met Asp Glu Glu Ala Met Leu Gly Met Ser Ser Leu Leu Asp Asn
                165                 170                 175


Met Ala Glu Gly Met Leu Leu Pro Ser Pro Ser Val Gln Trp Asn Tyr
                180                 185                 190


Asn Phe Asp Val Glu Gly Asp Asp Asp Val Ser Leu Trp Ser Tyr
            195                 200                 205
```

<210> 301 <211> 908 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (119)..(769) <223> G42

<400> 301
cctgaactag aacagaaaga gagagaaact attatttcag caaaccatac caacaaaaaa
60

gacagagatc ttttagttac cttatccagt ttcttgaaac agagtactct tctgatca
118

atg aac tca ttt tct gct ttt tct gaa atg ttt ggc tcc gat tac gag
166
Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
1   5   10   15

tct tcg gtt tcc tca ggc ggt gat tat att ccg acg ctt gcg agc agc
214
Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
                20   25   30

tgc ccc aag aaa ccg gcg ggt cgt aag aag ttt cgt gag act cgt cac
262
Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
            35   40   45

cca ata tac aga gga gtt cgt cgg aga aac tcc ggt aag tgg gtt tgt
310
Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys
        50   55   60

gag gtt aga gaa cca aac aag aaa aca agg att tgg ctc gga aca ttt
358
Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
65   70   75   80

caa acc gct gag atg gca gct cga gct cac gac gtt gcc gct tta gcc
406
Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
                85   90   95

ctt cgt ggc cga tca gcc tgt ctc aat ttc gct gac tcg gct tgg aga
454
Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
            100   105   110

ctc cga atc ccg gaa tca act tgc gct aag gac atc caa aag gcg gcg
502
Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala
        115   120   125

gct gaa gct gcg ttg gcg ttt cag gat gag atg tgt gat gcg acg acg
550
Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr
    130   135   140

gat cat ggc ttc gac atg gag gag acg ttg gtg gag gct att tac acg
598
Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr
145   150   155   160

gcg gaa cag agc gaa aat gcg ttt tat atg cac gat gag gcg atg ttt
646
Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe
                165   170   175

gag atg ccg agt ttg ttg gct aat atg gca gaa ggg atg ctt ttg ccg
694

527

```
Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro
        180                 185                 190

ctt ccg tcc gta cag tgg aat cat aat cat gaa gtc gac ggc gat gat
742
Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp
        195                 200                 205

gac gac gta tcg tta tgg agt tat taa aactcagatt attatttcca
789
Asp Asp Val Ser Leu Trp Ser Tyr
        210                 215


ttttttagtac gatacttttt attttattat tatttttaga tcctttttta gaatggaatc
849

tacattatgt ttgtaaaact gagaaacgag tgtaaattaa attgattcag tttcagtat
908


<210> 302 <211> 216 <212> PRT <213> Arabidopsis thaliana <400>
302

Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
1               5                   10                  15


Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
        20                  25                  30


Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
        35                  40                  45


Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys
    50                  55                  60


Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
65                  70                  75                  80


Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
                85                  90                  95


Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
            100                 105                 110


Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala
            115                 120                 125


Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr
        130                 135                 140


Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr
145                 150                 155                 160
```

```
Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe
            165                 170                 175


Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro
            180                 185                 190


Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp
        195                 200                 205


Asp Asp Val Ser Leu Trp Ser Tyr
    210                 215
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<210> 303 <211> 959 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (50)..(733) <223> G152

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<400> 303
cctagaacgc accaagatct aaaggaagat caaaataggg tttaaatta atg ggg aga
58
                                                        Met Gly Arg
                                                        1


ggg aag att gtg atc cag aag atc gat gat tcc acg agt aga caa gtc
106
Gly Lys Ile Val Ile Gln Lys Ile Asp Asp Ser Thr Ser Arg Gln Val
    5                 10                  15


act ttc tcc aaa aga aga aag ggt ctc atc aag aaa gct aaa gaa ctt
154
Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Lys Lys Ala Lys Glu Leu
20                  25                  30                  35


gct att ctc tgc gac gcc gag gtc tgt ctc atc att ttc tcc aac act
202
Ala Ile Leu Cys Asp Ala Glu Val Cys Leu Ile Ile Phe Ser Asn Thr
                40                  45                  50


gac aag ctc tat gac ttt gcc agc tcc agt gtg aaa tct act att gaa
250
Asp Lys Leu Tyr Asp Phe Ala Ser Ser Ser Val Lys Ser Thr Ile Glu
            55                  60                  65


cga ttc aat acg gct aag atg gag gag caa gaa cta atg aac cct gca
298
Arg Phe Asn Thr Ala Lys Met Glu Glu Gln Glu Leu Met Asn Pro Ala
        70                  75                  80


tca gaa gtt aag ttt tgg cag aga gag gct gaa act cta agg caa gaa
346
Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Glu Thr Leu Arg Gln Glu
        85                  90                  95


ttg cac tca ttg caa gaa aat tat cgg caa cta acg gga gtg gaa tta
394
Leu His Ser Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly Val Glu Leu
100                 105                 110                 115
```

529

aat ggt ttg agc gtt aag gag tta caa aac ata gag agt caa ctt gaa
442
Asn Gly Leu Ser Val Lys Glu Leu Gln Asn Ile Glu Ser Gln Leu Glu
            120   125   130

atg agt tta cgt gga att cgt atg aaa agg gaa caa att ttg acc aat
490
Met Ser Leu Arg Gly Ile Arg Met Lys Arg Glu Gln Ile Leu Thr Asn
            135   140   145

gaa att aaa gag cta acc aga aag agg aat ctt gtt cat cat gaa aac
538
Glu Ile Lys Glu Leu Thr Arg Lys Arg Asn Leu Val His His Glu Asn
        150   155   160

ctc gaa ttg tcg aga aaa gta caa agg att cat caa gaa aat gtc gaa
586
Leu Glu Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu Asn Val Glu
        165   170   175

cta tac aag aag gct tat gga acg tcg aac aca aat gga ttg gga cat
634
Leu Tyr Lys Lys Ala Tyr Gly Thr Ser Asn Thr Asn Gly Leu Gly His
180   185   190   195

cat gag cta gta gat gca gtt tat gaa tcc cat gaa cag gtt agg ctg
682
His Glu Leu Val Asp Ala Val Tyr Glu Ser His Ala Gln Val Arg Leu
            200   205   210

cag cta agc cag cct gag cag tcc cat tat aag aca tct tca aac agc
730
Gln Leu Ser Gln Pro Glu Gln Ser His Tyr Lys Thr Ser Ser Asn Ser
            215   220   225

taa gatcatataa gagatatata acaaattgtt cgttcttgat tatctcaaaa
783

ccctttcaaa tatatatacg tgcatattat atatgaagac tcgtttgact atgtcaatat
843

atatgttttc atgcaggagt aagtgtgagt gtaatcatgt cggagagcaa accaaaggtt
903

tgatttgtac gatatatact tatatatggt ctcaagtgaa agcaatggaa cagctt
959

<210> 304 <211> 227 <212> PRT <213> Arabidopsis thaliana <400>
304

Met Gly Arg Gly Lys Ile Val Ile Gln Lys Ile Asp Asp Ser Thr Ser
1   5   10   15

Arg Gln Val Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Lys Lys Ala
            20   25   30

Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Cys Leu Ile Ile Phe

```
            35                    40                    45

Ser Asn Thr Asp Lys Leu Tyr Asp Phe Ala Ser Ser Ser Val Lys Ser
    50                    55          .           60


Thr Ile Glu Arg Phe Asn Thr Ala Lys Met Glu Glu Gln Glu Leu Met
65                    70              75                    80
                                .

Asn Pro Ala Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Glu Thr Leu
                85                  90              95


Arg Gln Glu Leu His Ser Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly
            100                 105                 110
                                                        .

Val Glu Leu Asn Gly Leu Ser Val Lys Glu Leu Gln Asn Ile Glu Ser
            115                 120     ι       125


Gln Leu Glu Met Ser Leu Arg Gly Ile Arg Met Lys Arg Glu Gln Ile
    130             .135       .       140


Leu Thr Asn Glu Ile Lys Glu Leu Thr Arg Lys Arg Asn Leu Val His
145                 150             155                 .160
            .

His Glu Asn Leu Glu Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu
    .           .165             170                 175
                    .                                       .

Asn Val Glu Leu Tyr Lys Lys Ala Tyr Gly Thr Ser Asn Thr Asn Gly
            180                 185                 190


Leu Gly His His Glu Leu Val Asp Ala Val Tyr Glu Ser His Ala Gln
    195                 200                 205


Val Arg Leu Gln Leu Ser Gln Pro Glu Gln Ser His Tyr Lys Thr Ser
    210                 215                 220


Ser Asn Ser
225


<210>  305 <211>  1098 <212>   DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>   (97)..(801) <223>  G153

  <400>  305                           ;              .
aaaaaaaaga agcttctcct cttcctctgc cttcttcttt ccatttattg caaaccctga
60

tcaattggtt ttggtgttag tcttttgggg agagag atg ggg aga ggg aag ata
114
                                    Met Gly Arg Gly Lys Ile
```

                                                  1   5

gtt ata cga agg atc gat aac tct aca agt aga caa gtg act ttc tcc
162
Val Ile Arg Arg Ile Asp Asn Ser Thr Ser Arg Gln Val Thr Phe Ser
            10   15   20

aag aga agg agt ggt ttg ctt aag aag gct aaa gag tta tcg atc ctt
210
Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala Lys Glu Leu Ser Ile Leu
        25   30   35

tgt gat gca gaa gtt ggt gtt atc ata ttc tct agc acc gga aag ctc
258
Cys Asp Ala Glu Val Gly Val Ile Ile Phe Ser Ser Thr Gly Lys Leu
    40   45   50

tac gac tac gca agc aat tca agt atg aaa aca atc att gag cgg tac
306
Tyr Asp Tyr Ala Ser Asn Ser Ser Met Lys Thr Ile Ile Glu Arg Tyr
55   60   65   70

aac aga gta aaa gag gag cag cat caa ctt ctg aat cat gcc tca gag
354
Asn Arg Val Lys Glu Glu Gln His Gln Leu Leu Asn His Ala Ser Glu
            75   80   85

ata aag ttt tgg caa aga gag gtt gca agt ttg cag cag cag ctc caa
402
Ile Lys Phe Trp Gln Arg Glu Val Ala Ser Leu Gln Gln Gln Leu Gln
            90   95   100

cat cta caa gaa tgc cac agg aaa cta gtg gga gag gaa ctt tct gga
450
His Leu Gln Glu Cys His Arg Lys Leu Val Gly Glu Glu Leu Ser Gly
        105   110   115

atg aat gct aac gac cta caa aat ctt gaa gac cag cta gta aca agt
498
Met Asn Ala Asn Asp Leu Gln Asn Leu Glu Asp Gln Leu Val Thr Ser
    120   125   130

cta aaa ggt gtt cgt ctc aaa aag gat caa ctt atg aca aat gaa atc
546
Leu Lys Gly Val Arg Leu Lys Lys Asp Gln Leu Met Thr Asn Glu Ile
135   140   145   150

aga gaa ctt aat cgt aag gga caa atc atc caa aaa gag aat cac gag
594
Arg Glu Leu Asn Arg Lys Gly Gln Ile Ile Gln Lys Glu Asn His Glu
            155   160   165

cta caa aat att gta gat ata atg cgt aag gaa aat att aaa ttg caa
642
Leu Gln Asn Ile Val Asp Ile Met Arg Lys Glu Asn Ile Lys Leu Gln
            170   175   180

aag aag gtt cat gga aga aca aat gtg att gaa ggc aat tca agt gta
690
Lys Lys Val His Gly Arg Thr Asn Val Ile Glu Gly Asn Ser Ser Val
            185   190   195

                                532

```
gat cca ata agc aat gga acc aca aca tat gca cca ccg caa ctt caa
738
Asp Pro Ile Ser Asn Gly Thr Thr Thr Tyr Ala Pro Pro Gln Leu Gln
    200             205         210

ctc ata caa cta caa cca gct cct aga gaa aaa tca atc aga cta ggg
786
Leu Ile Gln Leu Gln Pro Ala Pro Arg Glu Lys Ser Ile Arg Leu Gly
215             220         225                 230

cta caa ctt tcc tag caaaacatgt gggacatcga acaatatacg aaaagagttt
841
Leu Gln Leu Ser
```

```
gtatgtcatc ttcagtaaca accaagctgg atcatttcat tcttggttat gtaattctgt
901

ttactacttt ggagtttaat atgttatatg acaagtttct ctttgtcaag ttacttgtgt
961

atgtacatca taaaataatg atgtgatgtg agtgccgaac atactagaca tcattttacc
1021

gtgtgttttt ttcgggtaca ttaaatgtac aaaatccagt ctaattggca tttttataca
1081

aaaaaaaaaa aaaaaaa
1098
```

<210> 306 <211> 234 <212> PRT <213> Arabidopsis thaliana <400>
306

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Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser
1               5               10              15

Arg Gln Val Thr Phe Ser Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala
            20              25              30

Lys Glu Leu Ser Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe
        35              40              45

Ser Ser Thr Gly Lys Leu Tyr Asp Tyr Ala Ser Asn Ser Ser Met Lys
    50              55              60

Thr Ile Ile Glu Arg Tyr Asn Arg Val Lys Glu Glu Gln His Gln Leu
65              70              75              80

Leu Asn His Ala Ser Glu Ile Lys Phe Trp Gln Arg Glu Val Ala Ser
            85              90              95

Leu Gln Gln Gln Leu Gln His Leu Gln Glu Cys His Arg Lys Leu Val
            100             105             110
```

533

```
Gly Glu Glu Leu Ser Gly Met Asn Ala Asn Asp Leu Gln Asn Leu Glu
    115                 120             125


Asp Gln Leu Val Thr Ser Leu Lys Gly Val Arg Leu Lys Lys Asp Gln
    130                 135              140


Leu Met Thr Asn Glu Ile Arg Glu Leu Asn Arg Lys Gly Gln Ile Ile
145                 150             155                 160


Gln Lys Glu Asn His Glu Leu Gln Asn Ile Val Asp Ile Met Arg Lys
                165             170                 175


Glu Asn Ile Lys Leu Gln Lys Lys Val His Gly Arg Thr Asn Val Ile
            180             185             190


Glu Gly Asn Ser Ser Val Asp Pro Ile Ser Asn Gly Thr Thr Thr Tyr
    195                 200     -           205


Ala Pro Pro Gln Leu Gln Leu Ile Gln Leu Gln Pro Ala Pro Arg Glu
    210                 215             220


Lys Ser Ile Arg Leu Gly Leu Gln Leu Ser
225                 230
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<210> 307 <211> 1952 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (100)..(1761) <223> G186

 <400> 307
ctttcaacca aaccccctaaa caaaaaaaaa atacattttc tgatctctct aaaaatcttt
60

ctccttcgtt aatctcgtga tctctttctt tttctatat atg gac aga gga tgg
114
```
                                          Met Asp Arg Gly Trp
                                          1               5
```

```
tct ggt ctc act ctt gat tca tct tct ctt gat ctt tta aac cct aat
162
Ser Gly Leu Thr Leu Asp Ser Ser Ser Leu Asp Leu Leu Asn Pro Asn
              10              15                  20
```

```
cgt att tct cat aag aat cac cga cgt ttc tca aat cct ttg gcg atg
210
Arg Ile Ser His Lys Asn His Arg Arg Phe Ser Asn Pro Leu Ala Met
              25              30                  35
```

```
tct aga att gac gaa gaa gat gat cag aag acg aga ata tca acc aac
258
Ser Arg Ile Asp Glu Glu Asp Asp Gln Lys Thr Arg Ile Ser Thr Asn
          40              45                  50
```

534

ggt agt gaa ttt agg ttt ccg gtg agt ctc tca ggt att cgt gat cgt
306
Gly Ser Glu Phe Arg Phe Pro Val Ser Leu Ser Gly Ile Arg Asp Arg
    55   60   65

gaa gat gaa gat ttt tca tct ggc gtt gct gga gat aat gac cgt gaa
354
Glu Asp Glu Asp Phe Ser Ser Gly Val Ala Gly Asp Asn Asp Arg Glu
70   75   80   85

gtt ccc ggc gaa gtg gat ttc ttc tcc gac aag aaa tct agg gtt tgt
402
Val Pro Gly Glu Val Asp Phe Phe Ser Asp Lys Lys Ser Arg Val Cys
            90   95   100

cgt gaa gac gac gaa gga ttt cgt gtg aag aag gaa gaa caa gat gat
450
Arg Glu Asp Asp Glu Gly Phe Arg Val Lys Lys Glu Glu Gln Asp Asp
            105   110   115

cga acg gac gta aat acc ggt ttg aat ctt cga aca act ggt aat aca
498
Arg Thr Asp Val Asn Thr Gly Leu Asn Leu Arg Thr Thr Gly Asn Thr
        ·120   125   130

aag agt gat gag tca atg atc gat gat gga gaa tct tcc gaa atg gaa
546
Lys Ser Asp Glu Ser Met Ile Asp Asp Gly Glu Ser Ser Glu Met Glu
    135   140   145

gat aag cgt gcg aaa aat gag ttg gtg aaa tta caa gat gag ttg aag
594
Asp Lys Arg Ala Lys Asn Glu Leu Val Lys Leu Gln Asp Glu Leu Lys
150   155   160   165

aaa atg aca atg gat aat caa aag ctt aga gaa ttg ctt aca caa gtt
642
Lys Met Thr Met Asp Asn Gln Lys Leu Arg Glu Leu Leu Thr Gln Val
            170   175   180

agc aac agt tac act tca ctt cag atg cat ctt gtt tca cta atg cag
690
Ser Asn Ser Tyr Thr Ser Leu Gln Met His Leu Val Ser Leu Met Gln
            185   190   195

caa cag caa caa cag aac aat aag gta ata gaa gct gct gag aag cct
738
Gln Gln Gln Gln Gln Asn Asn Lys Val Ile Glu Ala Ala Glu Lys Pro
            200   205   210

gag gag acg ata gta cca agg caa ttt att gat tta ggc cct acg aga
786
Glu Glu Thr Ile Val Pro Arg Gln Phe Ile Asp Leu Gly Pro Thr Arg
    · 215   220   ·   225

gca gta ggt gag gcc gag gat gtg tca aat tct tca tcc gaa gat aga ·
834
Ala Val Gly Glu Ala Glu Asp Val Ser Asn Ser Ser Ser Glu Asp Arg
230   235   240   245

535

act cgt tcg ggg ggt tct tct gca gcc gag agg cgt agt aac ggg aag
882
Thr Arg Ser Gly Gly Ser Ser Ala Ala Glu Arg Arg Ser Asn Gly Lys
              250   255   260

aga ctt ggg cgt gaa gaa agc ccc gaa act gag tcc aac aaa att cag
930
Arg Leu Gly Arg Glu Glu Ser Pro Glu Thr Glu Ser Asn Lys Ile Gln
              265   270   275

aag gtg aat tct act acc ccg acg aca ttt gat caa acc gct gaa gct
978
Lys Val Asn Ser Thr Thr Pro Thr Thr Phe Asp Gln Thr Ala Glu Ala
              280   285   290

acg atg agg aaa gcc cgt gtc tcc gtt cgt gcc cga tcg gaa gct ccg
1026
Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala Arg Ser Glu Ala Pro
    295   300   305

atg ata agc gat gga tgt caa tgg aga aaa tat ggc cag aag atg gcc
1074
Met Ile Ser Asp Gly Cys Gln Trp Arg Lys Tyr Gly Gln Lys Met Ala
310   315   320   325

aaa ggg aat cct tgt ccg cgg gca tat tac cgc tgc acg atg gcc acg
1122
Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg Cys Thr Met Ala Thr
              330   335   340

ggc tgt ccc gtt cgc aaa caa gtt caa cgt tgc gcg gaa gac aga tca
1170
Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala Glu Asp Arg Ser
              345   350   355

att ctg att aca acc tac gag gga aac cat aac cat ccg ttg ccg cca
1218
Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His Pro Leu Pro Pro
              360   365   370

gcc gcg gta gcc atg gct tct acc acc acg gcg gcg gct aac atg ttg
1266
Ala Ala Val Ala Met Ala Ser Thr Thr Thr Ala Ala Ala Asn Met Leu
    375   380   385

cta tcc ggg tca atg tct agt cac gac ggg atg atg aac cct aca aat
1314
Leu Ser Gly Ser Met Ser Ser His Asp Gly Met Met Asn Pro Thr Asn
390   395   400   405

tta cta gct agg gct gtt ctt cct tgc tcc aca agc atg gca aca atc
1362
Leu Leu Ala Arg Ala Val Leu Pro Cys Ser Thr Ser Met Ala Thr Ile
              410   415   420

tca gcc tcc gcg ccg ttt cca acc gtc aca tta gac ctc acc cac tca
1410
Ser Ala Ser Ala Pro Phe Pro Thr Val Thr Leu Asp Leu Thr His Ser
              425   430   435

```
cct ccg cct cct aat ggt tcc aat cct tcc tct tcc gcg gct acc aac
1458
Pro Pro Pro Pro Asn Gly Ser Asn Pro Ser Ser Ser Ala Ala Thr Asn
        440                 445                 450

aac aac cac aac tca ctg atg cag cgg ccg caa caa caa caa cag caa
1506
Asn Asn His Asn Ser Leu Met Gln Arg Pro Gln Gln Gln Gln Gln Gln
    455                 460                 465

atg acg aac tta cct ccg gga atg cta cct cat gta ata ggc cag gca
1554
Met Thr Asn Leu Pro Pro Gly Met Leu Pro His Val Ile Gly Gln Ala
470                 475                 480                 485

ttg tat aac caa tcc aag ttc tcg ggg ctg cag ttc tct ggt ggc tct
1602
Leu Tyr Asn Gln Ser Lys Phe Ser Gly Leu Gln Phe Ser Gly Gly Ser
                490                 495                 500

ccc tcg acg gca gcg ttt tct cag tca cac gcg gtg gct gat aca ata
1650
Pro Ser Thr Ala Ala Phe Ser Gln Ser His Ala Val Ala Asp Thr Ile
            505                 510                 515

acg gca ctc aca gct gac ccg aat ttc acg gcg gct ctt gca gcc gtt
1698
Thr Ala Leu Thr Ala Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala Val
            520                 525                 530

att tct tct atg atc aat ggt acg aac cac cac gac ggc gaa gga aac
1746
Ile Ser Ser Met Ile Asn Gly Thr Asn His His Asp Gly Glu Gly Asn
    535                 540                 545

aac aaa aat caa tag aaaaatatta catttttttt ttgggtatct acattttttt
1801
Asn Lys Asn Gln
550

tccaactggg ttataggaaa cagagagttt atttcattga ttcacatttg ttctgtttcg
1861

taccaaaatc ccagtaaata tacaaaagca aactatactc aagttcatat tcgtaaacac
1921

tataaatagt acgttactta ataaaaaaaa a
1952


<210> 308 <211> 553 <212> PRT <213> Arabidopsis thaliana <400>
308

Met Asp Arg Gly Trp Ser Gly Leu Thr Leu Asp Ser Ser Ser Leu Asp
1               5               10              15

Leu Leu Asn Pro Asn Arg Ile Ser His Lys Asn His Arg Arg Phe Ser
            20              25              30
```

Asn Pro Leu Ala Met Ser Arg Ile Asp Glu Glu Asp Asp Gln Lys Thr
        35   40   45

Arg Ile Ser Thr Asn Gly Ser Glu Phe Arg Phe Pro Val Ser Leu Ser
        50   55   60

Gly Ile Arg Asp Arg Glu Asp Glu Asp Phe Ser Ser Gly Val Ala Gly
65   70   75   80

Asp Asn Asp Arg Glu Val Pro Gly Glu Val Asp Phe Phe Ser Asp Lys
                85   90   95

Lys Ser Arg Val Cys Arg Glu Asp Asp Glu Gly Phe Arg Val Lys Lys
            100   105   110

Glu Glu Gln Asp Asp Arg Thr Asp Val Asn Thr Gly Leu Asn Leu Arg
            115   120   125

Thr Thr Gly Asn Thr Lys Ser Asp Glu Ser Met Ile Asp Asp Gly Glu
        130   135   140

Ser Ser Glu Met Glu Asp Lys Arg Ala Lys Asn Glu Leu Val Lys Leu
145   150   155   160

Gln Asp Glu Leu Lys Lys Met Thr Met Asp Asn Gln Lys Leu Arg Glu
                165   170   175

Leu Leu Thr Gln Val Ser Asn Ser Tyr Thr Ser Leu Gln Met His Leu
            180   185   190

Val Ser Leu Met Gln Gln Gln Gln Gln Gln Asn Asn Lys Val Ile Glu
            195   200   205

Ala Ala Glu Lys Pro Glu Glu Thr Ile Val Pro Arg Gln Phe Ile Asp
        210   215   220

Leu Gly Pro Thr Arg Ala Val Gly Glu Ala Glu Asp Val Ser Asn Ser
225   230   235   240

Ser Ser Glu Asp Arg Thr Arg Ser Gly Gly Ser Ser Ala Ala Glu Arg
                245   250   255

Arg Ser Asn Gly Lys Arg Leu Gly Arg Glu Glu Ser Pro Glu Thr Glu
            260   265   270

Ser Asn Lys Ile Gln Lys Val Asn Ser Thr Thr Pro Thr Thr Phe Asp

538

          275   280   285

Gln Thr Ala Glu Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala
    290   295   300

Arg Ser Glu Ala Pro Met Ile Ser Asp Gly Cys Gln Trp Arg Lys Tyr
305   ·   310   315   320

Gly Gln Lys Met Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg
                325   330   335

Cys Thr Met Ala Thr Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys
            340   345   350

Ala Glu Asp Arg Ser Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn
        355   360   365

His Pro Leu Pro Pro Ala Ala Val Ala Met Ala Ser Thr Thr Thr Ala
    370   .   375   380

Ala Ala Asn Met Leu Leu Ser Gly Ser Met Ser Ser His Asp Gly Met
385   390   395   400

Met Asn Pro Thr Asn Leu Leu Ala Arg Ala Val Leu Pro Cys Ser Thr
                405   410   415

Ser Met Ala Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Val Thr Leu
            420   425   430

Asp Leu Thr His Ser Pro Pro Pro Asn Gly Ser Asn Pro Ser Ser
            435   440   445

Ser Ala Ala Thr Asn Asn Asn His Asn Ser Leu Met Gln Arg Pro Gln
    450   455   460

Gln Gln Gln Gln Gln Met Thr Asn Leu Pro Pro Gly Met Leu Pro His
465   470   475   480

Val Ile Gly Gln Ala Leu Tyr Asn Gln Ser Lys Phe Ser Gly Leu Gln
                485   490   495

Phe Ser Gly Gly Ser Pro Ser Thr Ala Ala Phe Ser Gln Ser His Ala
            500   505   510

Val Ala Asp Thr Ile Thr Ala Leu Thr Ala Asp Pro Asn Phe Thr Ala
            515   520   525

                              539

Ala Leu Ala Ala Val Ile Ser Ser Met Ile Asn Gly Thr Asn His His
    530   535   540

Asp Gly Glu Gly Asn Asn Lys Asn Gln
545   550

<210> 309 <211> 1136 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (118)..(1074) <223> G187

<400> 309
tagacctctt aggaaaaaaa cctaaaaacc taatccccaa acctaaaagg cttatctcat
60

ctcttcttct ttgtcttctt tactcttttt ttacctctct cttcattgtt cttcacc
117

atg tct aat gaa acc aga gat ctc tac aac tac caa tac cct tca tcg
165
Met Ser Asn Glu Thr Arg Asp Leu Tyr Asn Tyr Gln Tyr Pro Ser Ser
1   5   10   15

ttt tcg ttg cac gaa atg atg aat ctg cct act tca aat cca tct tct
213
Phe Ser Leu His Glu Met Met Asn Leu Pro Thr Ser Asn Pro Ser Ser
            20   25   30

tat gga aac ctc cca tca caa aac ggt ttt aat cca tct act tat tcc
261
Tyr Gly Asn Leu Pro Ser Gln Asn Gly Phe Asn Pro Ser Thr Tyr Ser
        35   40   45

ttc acc gat tgt ctc caa agt tct cca gca gcg tat gaa tct cta ctt
309
Phe Thr Asp Cys Leu Gln Ser Ser Pro Ala Ala Tyr Glu Ser Leu Leu
    50   55   60

cag aaa act ttt ggt ctt tct ccc tct tcc tca gag gtt ttc aat tct
357
Gln Lys Thr Phe Gly Leu Ser Pro Ser Ser Ser Glu Val Phe Asn Ser
65   70   75   80

tcg atc gat caa gaa ccg aac cgt gat gtt act aat gac gta atc aat
405
Ser Ile Asp Gln Glu Pro Asn Arg Asp Val Thr Asn Asp Val Ile Asn
                85   90   95

ggt ggt gca tgc aac gag act gaa act agg gtt tct cct tct aat tct
453
Gly Gly Ala Cys Asn Glu Thr Glu Thr Arg Val Ser Pro Ser Asn Ser
            100   105   110

tcc tct agt gag gct gat cac ccc ggt gaa gat tcc ggt aag agc cgg
501
Ser Ser Ser Glu Ala Asp His Pro Gly Glu Asp Ser Gly Lys Ser Arg
        115   120   125

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agg aaa cga gag tta gtc ggt gaa gaa gat caa att tcc aaa aaa gtt
549
Arg Lys Arg Glu Leu Val Gly Glu Glu Asp Gln Ile Ser Lys Lys Val
    130             135             140

ggg aaa acg aaa aag act gag gtg aag aaa caa aga gag cca cga gtc
597
Gly Lys Thr Lys Lys Thr Glu Val Lys Lys Gln Arg Glu Pro Arg Val
145             150             155             160

tcg ttt atg act aaa agt gaa gtt gat cat ctt gaa gat ggt tat aga
645
Ser Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg
            165             170             175

tgg aga aaa tac ggc caa aag gct gta aaa aat agc cct tat cca agg
693
Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Tyr Pro Arg
            180             185             190

agt tac tat aga tgt aca aca caa aag tgc aac gtg aag aaa cga gtg
741
Ser Tyr Tyr Arg Cys Thr Thr Gln Lys Cys Asn Val Lys Lys Arg Val
            195             200             205

gag aga tcg ttc caa gat cca acg gtt gtg att aca act tac gag ggt
789
Glu Arg Ser Phe Gln Asp Pro Thr Val Val Ile Thr Thr Tyr Glu Gly
    210             215             220

caa cac aac cac ccg att ccg act aat ctt cga gga agt tct gcc gcg
837
Gln His Asn His Pro Ile Pro Thr Asn Leu Arg Gly Ser Ser Ala Ala
225             230             235             240

gct gct atg ttc tcc gca gac ctc atg act cca aga agc ttt gca cat
885
Ala Ala Met Phe Ser Ala Asp Leu Met Thr Pro Arg Ser Phe Ala His
            245             250             255

gat atg ttt agg acg gca gct tat act aac ggc ggt tct gtg gcg gcg
933
Asp Met Phe Arg Thr Ala Ala Tyr Thr Asn Gly Gly Ser Val Ala Ala
            260             265             270

gct ttg gat tat gga tat gga caa agt ggt tat ggt agt gtg aat tca
981
Ala Leu Asp Tyr Gly Tyr Gly Gln Ser Gly Tyr Gly Ser Val Asn Ser
            275             280             285

aac cct agt tct cac caa gtg tat cat caa ggg ggt gag tat gag ctc
1029
Asn Pro Ser Ser His Gln Val Tyr His Gln Gly Gly Glu Tyr Glu Leu
            290             295             300

ttg agg gag att ttt cct tca att ttc ttt aag caa gag cct tga
1074
Leu Arg Glu Ile Phe Pro Ser Ile Phe Phe Lys Gln Glu Pro
305             310             315
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tcgatcattg ttataactac atatattata tatattgaga gagagaggta gagaaaaaaa
1134

aa
1136

<210> 310 <211> 318 <212> PRT <213> Arabidopsis thaliana <400> 310

Met Ser Asn Glu Thr Arg Asp Leu Tyr Asn Tyr Gln Tyr Pro Ser Ser
1   5   10   15

Phe Ser Leu His Glu Met Met Asn Leu Pro Thr Ser Asn Pro Ser Ser
            20   25   30

Tyr Gly Asn Leu Pro Ser Gln Asn Gly Phe Asn Pro Ser Thr Tyr Ser
        35   40   45

Phe Thr Asp Cys Leu Gln Ser Ser Pro Ala Ala Tyr Glu Ser Leu Leu
    50   55   60

Gln Lys Thr Phe Gly Leu Ser Pro Ser Ser Ser Glu Val Phe Asn Ser
65   70   75   80

Ser Ile Asp Gln Glu Pro Asn Arg Asp Val Thr Asn Asp Val Ile Asn
                85   90   95

Gly Gly Ala Cys Asn Glu Thr Glu Thr Arg Val Ser Pro Ser Asn Ser
            100   105   110

Ser Ser Ser Glu Ala Asp His Pro Gly Glu Asp Ser Gly Lys Ser Arg
        115   120   125

Arg Lys Arg Glu Leu Val Gly Glu Glu Asp Gln Ile Ser Lys Lys Val
    130   135   140

Gly Lys Thr Lys Lys Thr Glu Val Lys Lys Gln Arg Glu Pro Arg Val
145   150   155   160

Ser Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg
                165   170   175

Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Tyr Pro Arg
                180   185   190

Ser Tyr Tyr Arg Cys Thr Thr Gln Lys Cys Asn Val Lys Lys Arg Val
        195   200   205

542

```
Glu Arg Ser Phe Gln Asp Pro Thr Val Val Ile Thr Thr Tyr Glu Gly
    210             215             220

Gln His Asn His Pro Ile Pro Thr Asn Leu Arg Gly Ser Ser Ala Ala
225             230             235             240

Ala Ala Met Phe Ser Ala Asp Leu Met Thr Pro Arg Ser Phe Ala His
            245             250             255

Asp Met Phe Arg Thr Ala Ala Tyr Thr Asn Gly Gly Ser Val Ala Ala
        260             265             270

Ala Leu Asp Tyr Gly Tyr Gly Gln Ser Gly Tyr Gly Ser Val Asn Ser
    275             280             285

Asn Pro Ser Ser His Gln Val Tyr His Gln Gly Gly Glu Tyr Glu Leu
    290             295             300

Leu Arg Glu Ile Phe Pro Ser Ile Phe Phe Lys Gln Glu Pro
305             310             315
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<210>  311 <211>  1252 <212>   DNA <213>   Arabidopsis thaliana  <220>
<221>  CDS <222>   (145)..(1125) <223>   G210
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<400>  311
tcagaacaca aaagtttggc tacagttgtg ttctgatagt gatgatcatg atcatcacat
60

gaataagtag aagatatctc ttaccttctc cttcttctaa taagatcaga gttttggttc
120

ttatttcttt gacctctcaa aaca atg ggt aga tca ccg tgt tgt gac aaa
171
                          Met Gly Arg Ser Pro Cys Cys Asp Lys
                          1               5

ttg ggt ttg aag aaa gga cct tgg aca cca gag gag gat cag aaa ctt
219
Leu Gly Leu Lys Lys Gly Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu
10              15              20              25

tta gct tat att gaa gaa cat ggt cat gga agt tgg cgt tca ttg cct
267
Leu Ala Tyr Ile Glu Glu His Gly His Gly Ser Trp Arg Ser Leu Pro
            30              35              40

gag aaa gct ggt ctc cat cga tgc gga aag agt tgt aga cta aga tgg
315
Glu Lys Ala Gly Leu His Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp
        45              50              55

act aac tac cta aga cct gac atc aaa aga ggc aaa ttc aac tta caa
363
```

543

```
Thr Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Lys Phe Asn Leu Gln
        60                  65                  70

gaa gaa caa acc att atc caa ctc cat gct ctg tta gga aac aga tgg
411
Glu Glu Gln Thr Ile Ile Gln Leu His Ala Leu Leu Gly Asn Arg Trp
      75                  80                  85

tca gcg att gct act cat ttg cca aag aga aca gac aac gag atc aag
459
Ser Ala Ile Ala Thr His Leu Pro Lys Arg Thr Asp Asn Glu Ile Lys
90                  95                  100                 105

aac tat tgg aac act cat ttg aag aaa cgg tta gtg aaa atg ggg att
507
Asn Tyr Trp Asn Thr His Leu Lys Lys Arg Leu Val Lys Met Gly Ile
              110                 115                 120

gat cca gtg act cat aaa ccc aaa aac gag act cct tta tct tct ctt
555
Asp Pro Val Thr His Lys Pro Lys Asn Glu Thr Pro Leu Ser Ser Leu
              125                 130                 135

ggt cta tcc aag aac gca gct ata ctt agc cac act gct caa tgg gaa
603
Gly Leu Ser Lys Asn Ala Ala Ile Leu Ser His Thr Ala Gln Trp Glu
          140                 145                 150

agt gca agg ctt gaa gct gaa gca aga cta gct aga gaa tca aag ctt
651
Ser Ala Arg Leu Glu Ala Glu Ala Arg Leu Ala Arg Glu Ser Lys Leu
        155                 160                 165

ctt cat tta caa cat tac caa acc aaa aca tca tct caa cct cat cat
699
Leu His Leu Gln His Tyr Gln Thr Lys Thr Ser Ser Gln Pro His His
170                 175                 180                 185

cat cat gga ttc act cac aag tca ttg tta cct aat tgg aca aca aaa
747
His His Gly Phe Thr His Lys Ser Leu Leu Pro Asn Trp Thr Thr Lys
              190                 195                 200

cca cac gaa gat caa caa cag ctt gaa tct ccg aca tct aca gtg tca
795
Pro His Glu Asp Gln Gln Gln Leu Glu Ser Pro Thr Ser Thr Val Ser
              205                 210                 215

ttc tct gag atg aag gaa tca atc ccg gcg aag ata gag ttt gtc gga
843
Phe Ser Glu Met Lys Glu Ser Ile Pro Ala Lys Ile Glu Phe Val Gly
          220                 225                 230

tca tca act ggt gtg act ctg atg aaa gaa cct gaa cac gat tgg atc
891
Ser Ser Thr Gly Val Thr Leu Met Lys Glu Pro Glu His Asp Trp Ile
        235                 240                 245

aat tca acg atg cac gag ttt gaa act acg cag atg gga gaa gga atc
939
Asn Ser Thr Met His Glu Phe Glu Thr Thr Gln Met Gly Glu Gly Ile
```

544

250   255   260   265

gaa gaa ggg ttc acg ggt ctc ttg ctc ggt ggt gat tca atc gac cgg
987
Glu Glu Gly Phe Thr Gly Leu Leu Leu Gly Gly Asp Ser Ile Asp Arg
                    270   275   280

agt ttt tcc ggc gat aaa aac gag acg gcc ggc gag agt agt ggt ggt
1035
Ser Phe Ser Gly Asp Lys Asn Glu Thr Ala Gly Glu Ser Ser Gly Gly
                    285   290   295

gac tgc aac tac tat gag gac aac aag aac tac ttg gac agc att ttc
1083
Asp Cys Asn Tyr Tyr Glu Asp Asn Lys Asn Tyr Leu Asp Ser Ile Phe
            300   305   310

aac ttt gta gat cct tca ccg tcg gat tca ccg atg ttc tga
1125
Asn Phe Val Asp Pro Ser Pro Ser Asp Ser Pro Met Phe
        315   320   325

atctaagggt tgatatttgt tgggaatgtt tttgattctt tttttagttt ctagtttttg
1185

tgcttaaact ctgattagac aattttttaaa ctaatccaat ttttgcgcta aaaaaaaaaa
1245

aaaaaaa
1252

<210> 312 <211> 326 <212> PRT <213> Arabidopsis thaliana <400>
312

Met Gly Arg Ser Pro Cys Cys Asp Lys Leu Gly Leu Lys Lys Gly Pro
1   5   10   15

Trp Thr Pro Glu Glu Asp Gln Lys Leu Leu Ala Tyr Ile Glu Glu His
            20   25   30

Gly His Gly Ser Trp Arg Ser Leu Pro Glu Lys Ala Gly Leu His Arg
        35   40   45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
    50   55   60

Ile Lys Arg Gly Lys Phe Asn Leu Gln Glu Glu Gln Thr Ile Ile Gln
65   70   75   80

Leu His Ala Leu Leu Gly Asn Arg Trp Ser Ala Ile Ala Thr His Leu
                85   90   95

Pro Lys Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Leu
            100   105   110

545

Lys Lys Arg Leu Val Lys Met Gly Ile Asp Pro Val Thr His Lys Pro
        115   120   125

Lys Asn Glu Thr Pro Leu Ser Ser Leu Gly Leu Ser Lys Asn Ala Ala
        130   135   140

Ile Leu Ser His Thr Ala Gln Trp Glu Ser Ala Arg Leu Glu Ala Glu
145   150   155   160

Ala Arg Leu Ala Arg Glu Ser Lys Leu Leu His Leu Gln His Tyr Gln
            165   170   175

Thr Lys Thr Ser Ser Gln Pro His His His His Gly Phe Thr His Lys
            180   185   190

Ser Leu Leu Pro Asn Trp Thr Thr Lys Pro His Glu Asp Gln Gln Gln
        195   200   –   205

Leu Glu Ser Pro Thr Ser Thr Val Ser Phe Ser Glu Met Lys Glu Ser
        210   215   220

Ile Pro Ala Lys Ile Glu Phe Val Gly Ser Ser Thr Gly Val Thr Leu
225   230   235   240

Met Lys Glu Pro Glu His Asp Trp Ile Asn Ser Thr Met His Glu Phe
            245   250   255

Glu Thr Thr Gln Met Gly Glu Gly Ile Glu Glu Gly Phe Thr Gly Leu
            260   265   270

Leu Leu Gly Gly Asp Ser Ile Asp Arg Ser Phe Ser Gly Asp Lys Asn
        275   280   285

Glu Thr Ala Gly Glu Ser Ser Gly Gly Asp Cys Asn Tyr Tyr Glu Asp
        290   295   300

Asn Lys Asn Tyr Leu Asp Ser Ile Phe Asn Phe Val Asp Pro Ser Pro
305   310   315   320

Ser Asp Ser Pro Met Phe
            325

<210> 313 <211> 989 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (21)..(983) <223> G227

<400> 313
gtaccgtcga cgatccggcg atg tca aac ccg acc cgt aag aat atg gag agg
53
                        Met Ser Asn Pro Thr Arg Lys Asn Met Glu Arg
                        1   5   10

att aaa ggt cca tgg agt cca gaa gaa gat gat ctg ttg cag agg ctt
101
Ile Lys Gly Pro Trp Ser Pro Glu Glu Asp Asp Leu Leu Gln Arg Leu
        15   20   25

gtt cag aaa cat ggt ccg agg aac tgg tct ttg att agc aaa tca atc
149
Val Gln Lys His Gly Pro Arg Asn Trp Ser Leu Ile Ser Lys Ser Ile
        30   35   40

cct gga cgt tcc ggc aaa tct tgt cgt ctc cgg tgg tgt aac cag cta
197
Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Cys Asn Gln Leu
        45   50   55

tct ccg gag gta gag cac cgt gct ttt tcg cag gaa gaa gac gag acg
245
Ser Pro Glu Val Glu His Arg Ala Phe Ser Gln Glu Glu Asp Glu Thr
60   65   70   75

att att cga gct cac gct cgg ttt ggt aac aag tgg gct acg atc tct
293
Ile Ile Arg Ala His Ala Arg Phe Gly Asn Lys Trp Ala Thr Ile Ser
                80   85   90

cgt ctt ctc aat gga cga acc gat aac gct atc aag aat cat tgg aac
341
Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Ile Lys Asn His Trp Asn
                95   100   105

tcg acg ctg aag cga aaa tgc agc gtc gaa ggg caa agt tgt gat ttt
389
Ser Thr Leu Lys Arg Lys Cys Ser Val Glu Gly Gln Ser Cys Asp Phe
            110   115   120

ggt ggt aat gga ggg tat gat ggt aat tta gga gaa gag caa ccg ttg
437
Gly Gly Asn Gly Gly Tyr Asp Gly Asn Leu Gly Glu Glu Gln Pro Leu
        125   130   135

aaa cgt acg gcg agt ggt ggt ggt ggt gtc tcg act ggc ttg tat atg
485
Lys Arg Thr Ala Ser Gly Gly Gly Gly Val Ser Thr Gly Leu Tyr Met
140   145   150   155

agt ccc gga agt cca tcg gga tct gac gtc agc gag caa tct agt ggt
533
Ser Pro Gly Ser Pro Ser Gly Ser Asp Val Ser Glu Gln Ser Ser Gly
                160   165   170

ggt gca cac gtg ttt aaa cca acg gtt aga tct gag gtt aca gcg tca
581
Gly Ala His Val Phe Lys Pro Thr Val Arg Ser Glu Val Thr Ala Ser
            175   180   185

547

```
tcg tct ggt gaa gat cct cca act tat ctt agt ttg tct ctt cct tgg
629
Ser Ser Gly Glu Asp Pro Pro Thr Tyr Leu Ser Leu Ser Leu Pro Trp
        190                 195                 200

act gac gag acg gtt cga gtc aac gag ccg gtt caa ctt aac cag aat
677
Thr Asp Glu Thr Val Arg Val Asn Glu Pro Val Gln Leu Asn Gln Asn
        205                 210                 215

acg gtt atg gac ggt ggt tat acg gcg gag ctg ttt ccg gtt aga aag
725
Thr Val Met Asp Gly Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg Lys
220                 225                 230                 235

gaa gag caa gtg gaa gta gaa gaa gaa gaa gcg aag ggg ata tct ggt
773
Glu Glu Gln Val Glu Val Glu Glu Glu Glu Ala Lys Gly Ile Ser Gly
            240                 245                 250

gga ttc ggt ggt gag ttc atg acg gtg gtt cag gag atg ata agg acg
821
Gly Phe Gly Gly Glu Phe Met Thr Val Val Gln Glu Met Ile Arg Thr
        255                 260                 265

gag gtg agg agt tac atg gcg gat tta cag cga gga aac gtc ggt ggt
869
Glu Val Arg Ser Tyr Met Ala Asp Leu Gln Arg Gly Asn Val Gly Gly
        270                 275                 280

agt agt tct ggc ggc gga ggt ggc ggt tcg tgt atg cca caa agt gta
917
Ser Ser Ser Gly Gly Gly Gly Gly Gly Ser Cys Met Pro Gln Ser Val
        285                 290                 295

aac agc cgt cgt gtt ggg ttt aga gag ttt ata gtg aac caa atc gga
965
Asn Ser Arg Arg Val Gly Phe Arg Glu Phe Ile Val Asn Gln Ile Gly
300                 305                 310                 315

att ggg aag atg gag tag gcggcc
989
Ile Gly Lys Met Glu
                320


<210> 314 <211> 320 <212> PRT <213> Arabidopsis thaliana <400>
314

Met Ser Asn Pro Thr Arg Lys Asn Met Glu Arg Ile Lys Gly Pro Trp
1               5                   10                  15


Ser Pro Glu Glu Asp Asp Leu Leu Gln Arg Leu Val Gln Lys His Gly
            20                  25                  30


Pro Arg Asn Trp Ser Leu Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly
            35                  40                  45
```

548

Lys Ser Cys Arg Leu Arg Trp Cys Asn Gln Leu Ser Pro Glu Val Glu
    50   55   60

His Arg Ala Phe Ser Gln Glu Glu Asp Glu Thr Ile Ile Arg Ala His
65   70   75   80

Ala Arg Phe Gly Asn Lys Trp Ala Thr Ile Ser Arg Leu Leu Asn Gly
                85   90   95

Arg Thr Asp Asn Ala Ile Lys Asn His Trp Asn Ser Thr Leu Lys Arg
                100   105   110

Lys Cys Ser Val Glu Gly Gln Ser Cys Asp Phe Gly Gly Asn Gly Gly
            115   120   125

Tyr Asp Gly Asn Leu Gly Glu Glu Gln Pro Leu Lys Arg Thr Ala Ser
    130   135   140

Gly Gly Gly Gly Val Ser Thr Gly Leu Tyr Met Ser Pro Gly Ser Pro
145   150   155   160

Ser Gly Ser Asp Val Ser Glu Gln Ser Ser Gly Gly Ala His Val Phe
                165   170   175

Lys Pro Thr Val Arg Ser Glu Val Thr Ala Ser Ser Ser Gly Glu Asp
                180   185   190

Pro Pro Thr Tyr Leu Ser Leu Ser Leu Pro Trp Thr Asp Glu Thr Val
            195   200   205

Arg Val Asn Glu Pro Val Gln Leu Asn Gln Asn Thr Val Met Asp Gly
    210   215   220

Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg Lys Glu Glu Gln Val Glu
225   230   235   240

Val Glu Glu Glu Glu Ala Lys Gly Ile Ser Gly Gly Phe Gly Gly Glu
                245   250   255

Phe Met Thr Val Val Gln Glu Met Ile Arg Thr Glu Val Arg Ser Tyr
            260   265   270

Met Ala Asp Leu Gln Arg Gly Asn Val Gly Gly Ser Ser Ser Gly Gly
        275   280   285

Gly Gly Gly Gly Ser Cys Met Pro Gln Ser Val Asn Ser Arg Arg Val

                                  549

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          290                    295                    300
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```
Gly Phe Arg Glu Phe Ile Val Asn Gln Ile Gly Ile Gly Lys Met Glu
305                 310                315                320
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<210> 315 <211> 920 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(852) <223> G237

<400> 315
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atg gcg aag acg aaa tat gga gag aga cat agg aaa ggg tta tgg tca       48
Met Ala Lys Thr Lys Tyr Gly Glu Arg His Arg Lys Gly Leu Trp Ser
1               5                   10                  15

cct gaa gaa gac gag aag cta agg agc ttc atc ctc tct tat ggc cat       96
Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His
            20                  25                  30

tct tgc tgg acc act gtt ccc atc aaa gct ggg tta caa agg aat ggg      144
Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly
        35                  40                  45

aag agc tgc aga tta aga tgg att aat tac cta aga cca ggg tta aag      192
Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys
    50                  55                  60

agg gat atg att agt gca gaa gaa gaa gag act atc ttg acg ttt cat      240
Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His
65                  70                  75                  80

tct ccc ttg ggt aac aag tgg tcg caa ata gct aaa ttc tta ccg gga      288
Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly
                85                  90                  95

aga aca gac aat gag ata aag aac tat tgg cac tct cat ttg aaa aag      336
Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys
            100                 105                 110

aaa tgg ctc aag tct cag agc tta caa gat gca aaa tct att tcc cct      384
Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro
        115                 120                 125

cct tcg tct tca tca tca tca ctt gtt gct tgt gga gaa aga aat ccg      432
Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro
    130                 135                 140

gaa acc ttg atc tcg aat cac gtg ttc tcc ctc cag aga ctt cta gag      480
Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu
145                 150                 155                 160
```

```
aac aaa tct tca tct ccc tca caa gaa agc aac gga aat aac agc cat
528
Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His
                165               170               175

caa tgt tct tct gct cct gag att cca agg ctt ttc ttc tct gaa tgg
576
Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp
            180               185               190

ctt tct tct tca tat ccc cac acc gat tat tcc tct gag ttt acc gac
624
Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp
            195               200               205

tct aag cac agt caa gct cca aat gtc gaa gag act ctc tca gct tat
672
Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr
        210               215               220

gaa gaa atg ggt gat gtt gat cag ttc cat tac aac gaa atg atg atc
720
Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile
225               230               235               240

aac aac agc aac tgg act ctt aac gac att gtg ttt ggt tcc aaa tgt
768
Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys
                245               250               255

aag aag cag gag cat cat att tat aga gag gct tca gat tgt aat tct
816
Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser
            260               265               270

tct gct gaa ttc ttt tct cca cca aca acg acg taa attgcgttta
862
Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr
            275               280

ttgtaatgta aatcaaattt ctaaggcaaa accggaaaaa aaaaaaaaaa aaaaaaa
920
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<210> 316 <211> 283 <212> PRT <213> Arabidopsis thaliana <400>
316

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Met Ala Lys Thr Lys Tyr Gly Glu Arg His Arg Lys Gly Leu Trp Ser
1                5                10               15

Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His
            20               25               30

Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly
        35               40               45

Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys
    50               55               60
```

551

```
Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His
65              70              75              80


Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly
            85              90          .       95


Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys
            100             105             110


Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro
        115             120             125


Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro
    130             135             140


Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu  .
145             150             -   155             160


Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His
            165             170             175


Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp
        180             185             190


Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp
    . 195             200             205


Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr
    210             215             220


Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile
225             230             235             240


Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys
            245             250             255


Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser
            260             265             270


Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr
            275             280
```

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<210> 317 <211> 723 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(723) <223> G342
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<400> 317

atg gac gtc tac ggc atg tct tca ccg gac ttg ctt cgt atc gac gac
48
Met Asp Val Tyr Gly Met Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp
1   5   10   15

ctt ctc gat ttc tcc aac gac gaa atc ttc tct tcc tct tcc acc gtc
96
Leu Leu Asp Phe Ser Asn Asp Glu Ile Phe Ser Ser Ser Ser Thr Val
                20   25   30

act tcc tcc gcc gct tcc tcc gcc gct tct tcc gaa aac cct ttc agc
144
Thr Ser Ser Ala Ala Ser Ser Ala Ala Ser Ser Glu Asn Pro Phe Ser
            35   40   45

ttt cct tct tcc acc tac act tct cct act ctc ctc acc gac ttc act
192
Phe Pro Ser Ser Thr Tyr Thr Ser Pro Thr Leu Leu Thr Asp Phe Thr
        50   55   60

cac gat ctc tgc gtt ccc agt gac gac gca gct cat ctc gaa tgg tta
240
His Asp Leu Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu Trp Leu
65   70   75   80

tcg cga ttc gtt gac gat tca ttc tcc gat ttc cca gca aat cct tta
288
Ser Arg Phe Val Asp Asp Ser Phe Ser Asp Phe Pro Ala Asn Pro Leu
                85   90   95

acc atg acc gtt aga ccc gag att tca ttc acc gga aaa cct aga agt
336
Thr Met Thr Val Arg Pro Glu Ile Ser Phe Thr Gly Lys Pro Arg Ser
                100   105   110

cgc cga tca aga gca cca gca cct tcc gta gct gga act tgg gct ccg
384
Arg Arg Ser Arg Ala Pro Ala Pro Ser Val Ala Gly Thr Trp Ala Pro
            115   120   125

atg tct gaa tca gag ctt tgt cac tcc gtc gct aaa cct aaa ccg aag
432
Met Ser Glu Ser Glu Leu Cys His Ser Val Ala Lys Pro Lys Pro Lys
        130   135   140

aaa gtc tac aac gct gaa tcg gtt acg gcg gat gga gcg agg cgg tgc
480
Lys Val Tyr Asn Ala Glu Ser Val Thr Ala Asp Gly Ala Arg Arg Cys
145   150   155   160

acg cac tgt gcc tcg gag aaa acg cca cag tgg aga act gga ccg ctt
528
Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp Arg Thr Gly Pro Leu
                165   170   175

gga cct aaa aca ctt tgt aac gct tgt gga gtt cgt tac aaa tca ggg
576
Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val Arg Tyr Lys Ser Gly
                180   185   190

553

```
agg ctt gta ccg gaa tac aga ccg gcg tcg agt ccg acg ttt gta ttg
624
Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser Pro Thr Phe Val Leu
        195             200             205

act cag cat tcg aac tct cat cgg aaa gtt atg gag ctc cgg cga cag
672
Thr Gln His Ser Asn Ser His Arg Lys Val Met Glu Leu Arg Arg Gln
    210             215             220

aag gaa caa caa gaa tct tgc gtt cga att ccg ccg ttt cag ccg cag
720
Lys Glu Gln Gln Glu Ser Cys Val Arg Ile Pro Pro Phe Gln Pro Gln
225             230             235             240

taa
723
```

<210> 318 <211> 240 <212> PRT <213> Arabidopsis thaliana <400>
318

```
Met Asp Val Tyr Gly Met Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp
1               5               10              15

Leu Leu Asp Phe Ser Asn Asp Glu Ile Phe Ser Ser Ser Ser Thr Val
            20              25              30

Thr Ser Ser Ala Ala Ser Ser Ala Ala Ser Ser Glu Asn Pro Phe Ser
        35              40              45

Phe Pro Ser Ser Thr Tyr Thr Ser Pro Thr Leu Leu Thr Asp Phe Thr
    50              55              60

His Asp Leu Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu Trp Leu
65              70              75              80

Ser Arg Phe Val Asp Asp Ser Phe Ser Asp Phe Pro Ala Asn Pro Leu
            85              90              95

Thr Met Thr Val Arg Pro Glu Ile Ser Phe Thr Gly Lys Pro Arg Ser
            100             105             110

Arg Arg Ser Arg Ala Pro Ala Pro Ser Val Ala Gly Thr Trp Ala Pro
        115             120             125

Met Ser Glu Ser Glu Leu Cys His Ser Val Ala Lys Pro Lys Pro Lys
    130             135             140

Lys Val Tyr Asn Ala Glu Ser Val Thr Ala Asp Gly Ala Arg Arg Cys
145             150             155             160
```

```
Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp Arg Thr Gly Pro Leu
                165              170                  175


Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val Arg Tyr Lys Ser Gly
            180              185              190


Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser Pro Thr Phe Val Leu
            195              200              205


Thr Gln His Ser Asn Ser His Arg Lys Val Met Glu Leu Arg Arg Gln
        210              215              220


Lys Glu Gln Gln Glu Ser Cys Val Arg Ile Pro Pro Phe Gln Pro Gln
225              230              235              240
```

<210> 319 <211> 932 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (43)..(759) <223> G350

<400> 319

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54
                                            Met Ala Leu Glu
                                              1

act ctt act tct cca aga tta tct tct ccg atg ccg act ctg ttt caa
102
Thr Leu Thr Ser Pro Arg Leu Ser Ser Pro Met Pro Thr Leu Phe Gln
5                   10              15                  20

gat tca gca cta ggg ttt cat gga agc aaa ggc aaa cga tct aag cga
150
Asp Ser Ala Leu Gly Phe His Gly Ser Lys Gly Lys Arg Ser Lys Arg
                25              30                  35

tca aga tct gaa ttc gac cgt cag agt ctc acg gag gat gaa tat atc
198
Ser Arg Ser Glu Phe Asp Arg Gln Ser Leu Thr Glu Asp Glu Tyr Ile
            40              45                  50

gct tta tgt ctc atg ctt ctt gct cgc gac gga gat aga aac cgt gac
246
Ala Leu Cys Leu Met Leu Leu Ala Arg Asp Gly Asp Arg Asn Arg Asp
        55              60                  65

ctt gac ctg cct tct tct tcg tct tca cct cct ctg ctt cct cct ctt
294
Leu Asp Leu Pro Ser Ser Ser Ser Ser Pro Pro Leu Leu Pro Pro Leu
        70              75                  80

cct act ccg atc tac aag tgt agc gtc tgt gac aag gcg ttt tcg tct
342
Pro Thr Pro Ile Tyr Lys Cys Ser Val Cys Asp Lys Ala Phe Ser Ser
85                  90                  95                  100
```

```
tac cag gct ctt ggt gga cac aag gca agt cac cgg aaa agc ttt tcg
390
Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Lys Ser Phe Ser
                105                 110                 115

ctt act caa tct gcc gga gga gat gag ctg tcg aca tcg tcg gcg ata
438
Leu Thr Gln Ser Ala Gly Gly Asp Glu Leu Ser Thr Ser Ser Ala Ile
            120                 125                 130

acc acg tct ggt ata tcc ggt ggc ggg gga gga agt gtg aag tcg cac
486
Thr Thr Ser Gly Ile Ser Gly Gly Gly Gly Gly Ser Val Lys Ser His
            135                 140                 145

gtt tgc tct atc tgt cat aaa tcg ttc gcc acc ggt caa gct ctc ggc
534
Val Cys Ser Ile Cys His Lys Ser Phe Ala Thr Gly Gln Ala Leu Gly
        150                 155                 160

ggc cac aaa cgg tgc cac tac gaa gga aag aac gga ggc ggt gtg agt
582
Gly His Lys Arg Cys His Tyr Glu Gly Lys Asn Gly Gly Gly Val Ser
165                 170                 175                 180

agt agc gtg tcg aat tct gaa gat gtg ggg tct aca agc cac gtc agc
630
Ser Ser Val Ser Asn Ser Glu Asp Val Gly Ser Thr Ser His Val Ser
                185                 190                 195

agt ggc cac cgt ggg ttt gac ctc aac ata ccg ccg ata ccg gaa ttc
678
Ser Gly His Arg Gly Phe Asp Leu Asn Ile Pro Pro Ile Pro Glu Phe
            200                 205                 210

tcg atg gtc aac gga gac gaa gag gtg atg agt cct atg ccg gcg aag
726
Ser Met Val Asn Gly Asp Glu Glu Val Met Ser Pro Met Pro Ala Lys
            215                 220                 225

aaa ctc cgg ttt gac ttc ccg gag aaa ccc taa acataaacct aggaaaaact
779
Lys Leu Arg Phe Asp Phe Pro Glu Lys Pro
        230                 235

ttacagaatt cattttatag gaaattgttt tactgtatat acaaatatcg attttgattg
839

atgttcttct tcactgaaaa attatgattc tttgttgtat aattgatgtt tctgaaaaag
899

atataacttt ttattaaaaa aaaaaaaaaa aaa
932


<210> 320 <211> 238 <212> PRT <213> Arabidopsis thaliana <400>
320


Met Ala Leu Glu Thr Leu Thr Ser Pro Arg Leu Ser Ser Pro Met Pro
1               5                   10                  15
```

Thr Leu Phe Gln Asp Ser Ala Leu Gly Phe His Gly Ser Lys Gly Lys
              20   25   30

Arg Ser Lys Arg Ser Arg Ser Glu Phe Asp Arg Gln Ser Leu Thr Glu
              35   40   45

Asp Glu Tyr Ile Ala Leu Cys Leu Met Leu Leu Ala Arg Asp Gly Asp
       50   55   60

Arg Asn Arg Asp Leu Asp Leu Pro Ser Ser Ser Ser Ser Pro Pro Leu
65   70   75   80

Leu Pro Pro Leu Pro Thr Pro Ile Tyr Lys Cys Ser Val Cys Asp Lys
              85   90   95

Ala Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg
              100   105   110

Lys Ser Phe Ser Leu Thr Gln Ser Ala Gly Gly Asp Glu Leu Ser Thr
        115   120   125

Ser Ser Ala Ile Thr Thr Ser Gly Ile Ser Gly Gly Gly Gly Gly Ser
    130   135   140

Val Lys Ser His Val Cys Ser Ile Cys His Lys Ser Phe Ala Thr Gly
145   150   155   160

Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly Lys Asn Gly
              165   170   175

Gly Gly Val Ser Ser Ser Val Ser Asn Ser Glu Asp Val Gly Ser Thr
              180   185   190

Ser His Val Ser Ser Gly His Arg Gly Phe Asp Leu Asn Ile Pro Pro
        195   200   205

Ile Pro Glu Phe Ser Met Val Asn Gly Asp Glu Glu Val Met Ser Pro
    210   215   220

Met Pro Ala Lys Lys Leu Arg Phe Asp Phe Pro Glu Lys Pro
225   230   235

<210> 321 <211> 2940 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (336)..(2492) <223> G384

<400> 321

557

gttttttctt ctgaagagtg atatatattc taccttctc tggttaaaga aactccctga
60

atccaccggt tatgtcttga ccggctttaa gcctataaac tgatgcccta agacaccttt
120

ttaggtttct caataattct ccgcatctat cttttcttct ccacaagtaa gggaaccaga
180

aaaccaggga agaatccgag caagctaggg tttcattgtg tgcacaaaat gggatataca
240

ggcagaagaa aatcgagata aatcaactaa atgatttgga taatcatctt gaagatttga
300

aggatttcga gactaagtcc ggcgcagaag tcacc atg gag aat cct tta gaa
353
                                      Met Glu Asn Pro Leu Glu
                                      1   5

gaa gag ctt caa gat cct aat cag cgt ccc aac aaa aag aag cgt tac
401
Glu Glu Leu Gln Asp Pro Asn Gln Arg Pro Asn Lys Lys Lys Arg Tyr
            10   15 --   20

cac cgt cac aca caa cgc cag att caa gag cta gag tcg ttc ttc aag
449
His Arg His Thr Gln Arg Gln Ile Gln Glu Leu Glu Ser Phe Phe Lys
        25   30   35

gaa tgt cct cat cca gac gat aag caa aga aag gag ctg agt cgc gag
497
Glu Cys Pro His Pro Asp Asp Lys Gln Arg Lys Glu Leu Ser Arg Glu
    40   45   50

cta agc tta gaa cct ctt caa gtc aag ttc tgg ttc caa aac aaa cgc
545
Leu Ser Leu Glu Pro Leu Gln Val Lys Phe Trp Phe Gln Asn Lys Arg
55   60   65   70

act caa atg aag gca caa cat gag agg cac gag aac cag ata ctg aag
593
Thr Gln Met Lys Ala Gln His Glu Arg His Glu Asn Gln Ile Leu Lys
            75   80   85

tca gaa aat gac aag ctc cga gca gag aac aat agg tac aag gat gct
641
Ser Glu Asn Asp Lys Leu Arg Ala Glu Asn Asn Arg Tyr Lys Asp Ala
            90   95   100

cta agc aac gca aca tgc cca aac tgt ggt ggt ccg gca gct ata gga
689
Leu Ser Asn Ala Thr Cys Pro Asn Cys Gly Gly Pro Ala Ala Ile Gly
        105   110   115

gaa atg tcc ttc gac gaa cag cat tta agg atc gaa aat gct cgt tta
737
Glu Met Ser Phe Asp Glu Gln His Leu Arg Ile Glu Asn Ala Arg Leu
    120   125   130

```
cgc gaa gag att gac aga atc tct gcc ata gct gct aaa tac gta ggg
785
Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala Lys Tyr Val Gly
135             140             145             150

aag cct tta atg gct aat tcc tct tct ttc cct cag ctc tct tct tca
833
Lys Pro Leu Met Ala Asn Ser Ser Ser Phe Pro Gln Leu Ser Ser Ser
                155             160             165

cac cac att ccc tcg cgc tcg ctt gat ctt gaa gtt ggg aac ttt ggg
881
His His Ile Pro Ser Arg Ser Leu Asp Leu Glu Val Gly Asn Phe Gly
            170             175             180

aac aat aac aat agc cac act ggt ttc gtt ggg gaa atg ttt gga agc
929
Asn Asn Asn Asn Ser His Thr Gly Phe Val Gly Glu Met Phe Gly Ser
        185             190             195

agc gac att ttg agg tcg gtt tcg ata cct tct gag gct gat aag cct
977
Ser Asp Ile Leu Arg Ser Val Ser Ile Pro Ser Glu Ala Asp Lys Pro
    200             205             210

atg att gtt gag tta gct gtt gca gca atg gaa gag ctt gtg aga atg
1025
Met Ile Val Glu Leu Ala Val Ala Ala Met Glu Glu Leu Val Arg Met
215             220             225             230

gct caa act ggt gat ccc tta tgg gtt tca agc gat aat tct gtt gag
1073
Ala Gln Thr Gly Asp Pro Leu Trp Val Ser Ser Asp Asn Ser Val Glu
                235             240             245

att ctc aat gaa gaa gag tat ttt agg acg ttt cct aga gga att gga
1121
Ile Leu Asn Glu Glu Glu Tyr Phe Arg Thr Phe Pro Arg Gly Ile Gly
            250             255             260

ccg aaa cct atc ggt ttg aga tca gaa gct tca aga gag tct act gtt
1169
Pro Lys Pro Ile Gly Leu Arg Ser Glu Ala Ser Arg Glu Ser Thr Val
            265             270             275

gtt atc atg aat cat atc aat ctc att gag att cta atg gat gtg aat
1217
Val Ile Met Asn His Ile Asn Leu Ile Glu Ile Leu Met Asp Val Asn
        280             285             290

caa tgg tct agt gtg ttc tgc ggg att gta tca aga gca ttg act cta
1265
Gln Trp Ser Ser Val Phe Cys Gly Ile Val Ser Arg Ala Leu Thr Leu
295             300             305             310

gaa gtt ctc tca act ggc gta cga ggg aac tac aat ggg gca ttg caa
1313
Glu Val Leu Ser Thr Gly Val Arg Gly Asn Tyr Asn Gly Ala Leu Gln
                315             320             325
```

559

```
gtg atg aca gca gag ttc caa gtc cca tcg ccg ctt gtc cct act cgt
1361
Val Met Thr Ala Glu Phe Gln Val Pro Ser Pro Leu Val Pro Thr Arg
        330                 335                 340

gag aac tac ttt gta agg tac tgt aaa cag cac agt gac ggt att tgg
1409
Glu Asn Tyr Phe Val Arg Tyr Cys Lys Gln His Ser Asp Gly Ile Trp
        345                 350                 355

gcg gtt gtg gat gtc tct ttg gac agc cta aga cca agt ccg atc act
1457
Ala Val Val Asp Val Ser Leu Asp Ser Leu Arg Pro Ser Pro Ile Thr
    360                 365                 370

aga agc aga aga aga ccc tct ggt tgt ctg att caa gaa ttg cag aat
1505
Arg Ser Arg Arg Arg Pro Ser Gly Cys Leu Ile Gln Glu Leu Gln Asn
375                 380                 385                 390

ggt tac tcc aag gtg aca tgg gta gag cat att gag gtg gat gat aga
1553
Gly Tyr Ser Lys Val Thr Trp Val Glu His Ile Glu Val Asp Asp Arg
                395                 400                 405

tcg gtt cac aac atg tat aaa ccg ttg gtt aat acc ggt tta gct ttc
1601
Ser Val His Asn Met Tyr Lys Pro Leu Val Asn Thr Gly Leu Ala Phe
            410                 415                 420

ggt gca aaa cgt tgg gtg gct aca ctt gac cgc caa tgt gag cgg ctc
1649
Gly Ala Lys Arg Trp Val Ala Thr Leu Asp Arg Gln Cys Glu Arg Leu
        425                 430                 435

gcc agt tcc atg gcc agc aac att ccg gct tgt gat ctt tcc gtg ata
1697
Ala Ser Ser Met Ala Ser Asn Ile Pro Ala Cys Asp Leu Ser Val Ile
    440                 445                 450

acg agt cct gag ggg aga aag agc atg ctg aaa cta gcg gag aga atg
1745
Thr Ser Pro Glu Gly Arg Lys Ser Met Leu Lys Leu Ala Glu Arg Met
455                 460                 465                 470

gtg atg agc ttc tgt acc gga gtc ggc gcg tca acc gcc gat gcc tgg
1793
Val Met Ser Phe Cys Thr Gly Val Gly Ala Ser Thr Ala Asp Ala Trp
                475                 480                 485

act aca ttg tcg acc aca gga tcc gac gac gtt cgg gtc atg acc cga
1841
Thr Thr Leu Ser Thr Thr Gly Ser Asp Asp Val Arg Val Met Thr Arg
            490                 495                 500

aag agc atg gat gat ccg gga aga cct cca ggc atc gtt ctc agc gcc
1889
Lys Ser Met Asp Asp Pro Gly Arg Pro Pro Gly Ile Val Leu Ser Ala
        505                 510                 515
```

560

```
gct act tct ttc tgg atc cct gta gct cca aaa cga gtg ttc gat ttt
1937
Ala Thr Ser Phe Trp Ile Pro Val Ala Pro Lys Arg Val Phe Asp Phe
    520             525           .       530

ctc aga gat gaa aac tca aga agc gag tgg gat ata ctt tcc aat gga
1985
Leu Arg Asp Glu Asn Ser Arg Ser Glu Trp Asp Ile Leu Ser Asn Gly
535             540             545             550

ggc ttg gtt caa gaa atg gct cat atc gca aat ggt cgt gat cct ggg
2033
Gly Leu Val Gln Glu Met Ala His Ile Ala Asn Gly Arg Asp Pro Gly
            555             560             565

aat agt gtc tcc ttg ctt cga gtc aat agt ggg aac tca ggg cag agc
2081
Asn Ser Val Ser Leu Leu Arg Val Asn Ser Gly Asn Ser Gly Gln Ser
            570             575             580      .

aac atg ttg atc tta caa gaa agt tgt acg gac gca tca ggg tcc tat
2129
Asn Met Leu Ile Leu Gln Glu Ser Cys Thr Asp Ala Ser Gly Ser Tyr
            585             590             595

gtg ata tac gca cca gtt gat ata ata gct atg aac gtt gtc ctg agt
2177
Val Ile Tyr Ala Pro Val Asp Ile Ile Ala Met Asn Val Val Leu Ser
    600             605             610

ggt ggt gat ccg gat tat gtc gct ttg tta cca tcc gga ttc gct att
2225
Gly Gly Asp Pro Asp Tyr Val Ala Leu Leu Pro Ser Gly Phe Ala Ile
615             620             625             630

ttg ccg gat ggc tct gct aga gga gga gga ggt agt gct aat gcc agt
2273
Leu Pro Asp Gly Ser Ala Arg Gly Gly Gly Gly Ser Ala Asn Ala Ser
            635             640             645

gct gga gcc gga gtt gaa gga gga gga gag ggg aat aat ctt gaa gtg
2321
Ala Gly Ala Gly Val Glu Gly Gly Gly Glu Gly Asn Asn Leu Glu Val
            650             655             660

gtt act act act ggg agt tgt ggc ggt tca cta ctc aca gtt gcg ttt
2369
Val Thr Thr Thr Gly Ser Cys Gly Gly Ser Leu Leu Thr Val Ala Phe
        665             670             675

cag ata ctt gtt gac tct gtt cct acc gct aaa ctc tct ctc ggt tca
2417
Gln Ile Leu Val Asp Ser Val Pro Thr Ala Lys Leu Ser Leu Gly Ser
    680             685             690

gtt gct aca gtc aat agt ctg atc aaa tgc act gtc gag cgg att aaa
2465
Val Ala Thr Val Asn Ser Leu Ile Lys Cys Thr Val Glu Arg Ile Lys
695             700             705             710
```

561

gcc gct ctg gcc tgc gac gga gcc taa tcgatgtttt cggaaggtaa
2512
Ala Ala Leu Ala Cys Asp Gly Ala
                  715

gagtgaaagg ggaggtttag ggagtttatg ataatgtttg tgttcttttg gttttttaaag
2572

tcttttgaga ttctccaaag gaagtcaaga acgctccttt ttgcgtttaa tctcatttcc
2632

gcgtttgtta gcggacgggc caaagaaaga ggcttgagaa agaaaaggta aagaggttcg
2692

ggtattgact tctgctggaa ccaaaaaaaa aggaatcggg tttgttgtgt ttcggcggtt
2752

tagcattttg cgtttctttt gttattattt atcattgact agtgaacagt ttagcgttct
2812

gcttttcgcg tctactgtga aactccttgt tattaagcca ctctagtggt actgtcatta
2872

tatattatga atctatgaaa ctgtgtttat tagtttgttt ctttaatcca aacttgagat
2932

tctcttct
2940

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322

Met Glu Asn Pro Leu Glu Glu Glu Leu Gln Asp Pro Asn Gln Arg Pro
1   5   10   15

Asn Lys Lys Lys Arg Tyr His Arg His Thr Gln Arg Gln Ile Gln Glu
            20   25   30

Leu Glu Ser Phe Phe Lys Glu Cys Pro His Pro Asp Asp Lys Gln Arg
        35   40   45

Lys Glu Leu Ser Arg Glu Leu Ser Leu Glu Pro Leu Gln Val Lys Phe
    50   55   60

Trp Phe Gln Asn Lys Arg Thr Gln Met Lys Ala Gln His Glu Arg His
65   70   75   80

Glu Asn Gln Ile Leu Lys Ser Glu Asn Asp Lys Leu Arg Ala Glu Asn
                85   90   95

Asn Arg Tyr Lys Asp Ala Leu Ser Asn Ala Thr Cys Pro Asn Cys Gly
            100   105   110

562

Gly Pro Ala Ala Ile Gly Glu Met Ser Phe Asp Glu Gln His Leu Arg
        115   120   125

Ile Glu Asn Ala Arg Leu Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile
    130   135   140

Ala Ala Lys Tyr Val Gly Lys Pro Leu Met Ala Asn Ser Ser Ser Phe
145   150   155   160

Pro Gln Leu Ser Ser Ser His His Ile Pro Ser Arg Ser Leu Asp Leu
                165   170   175

Glu Val Gly Asn Phe Gly Asn Asn Asn Ser His Thr Gly Phe Val
                180   185   190

Gly Glu Met Phe Gly Ser Ser Asp Ile Leu Arg Ser Val Ser Ile Pro
        195   200   205

Ser Glu Ala Asp Lys Pro Met Ile Val Glu Leu Ala Val Ala Ala Met
    210   215   220

Glu Glu Leu Val Arg Met Ala Gln Thr Gly Asp Pro Leu Trp Val Ser
225   230   235   240

Ser Asp Asn Ser Val Glu Ile Leu Asn Glu Glu Glu Tyr Phe Arg Thr
                245   250   255

Phe Pro Arg Gly Ile Gly Pro Lys Pro Ile Gly Leu Arg Ser Glu Ala
            260   265   270

Ser Arg Glu Ser Thr Val Val Ile Met Asn His Ile Asn Leu Ile Glu
        275   280   285

Ile Leu Met Asp Val Asn Gln Trp Ser Ser Val Phe Cys Gly Ile Val
    290   295   300

Ser Arg Ala Leu Thr Leu Glu Val Leu Ser Thr Gly Val Arg Gly Asn
305   310   315   320

Tyr Asn Gly Ala Leu Gln Val Met Thr Ala Glu Phe Gln Val Pro Ser
            325   330   335

Pro Leu Val Pro Thr Arg Glu Asn Tyr Phe Val Arg Tyr Cys Lys Gln
            340   345   350

His Ser Asp Gly Ile Trp Ala Val Val Asp Val Ser Leu Asp Ser Leu

563

```
           355                    360'                    365


Arg Pro Ser Pro Ile Thr Arg Ser Arg Arg Arg Pro Ser Gly Cys Leu
    370             375                 380


Ile Gln Glu Leu Gln Asn Gly Tyr Ser Lys Val Thr Trp Val Glu His
385             390                 395                 400


Ile Glu Val Asp Asp Arg Ser Val His Asn Met Tyr Lys Pro Leu Val
            405                 410                 415


Asn Thr Gly Leu Ala Phe Gly Ala Lys Arg Trp Val Ala Thr Leu Asp
            420                 425                 430


Arg Gln Cys Glu Arg Leu Ala Ser Ser Met Ala Ser Asn Ile Pro Ala
        435                 440                 445


Cys Asp Leu Ser Val Ile Thr Ser Pro Glu Gly Arg Lys Ser Met Leu
    450                 455                 460


Lys Leu Ala Glu Arg Met Val Met Ser Phe Cys Thr Gly Val Gly Ala
465                 470                 475                 480


Ser Thr Ala Asp Ala Trp Thr Thr Leu Ser Thr Thr Gly Ser Asp Asp
            485                 490                 495


Val Arg Val Met Thr Arg Lys Ser Met Asp Asp Pro Gly Arg Pro Pro
            500                 505                 510


Gly Ile Val Leu Ser Ala Ala Thr Ser Phe Trp Ile Pro Val Ala'Pro
            515                 520                 525


Lys Arg Val Phe Asp Phe Leu Arg Asp Glu Asn Ser Arg Ser Glu Trp
    530                 535                 540


Asp Ile Leu Ser Asn Gly Gly Leu Val Gln Glu Met Ala His Ile Ala
545                 550                 555                 560


Asn Gly Arg Asp Pro Gly Asn Ser Val Ser Leu Leu Arg Val Asn Ser
            565                 570                 575


Gly Asn Ser Gly Gln Ser Asn Met Leu Ile Leu Gln Glu Ser Cys Thr
            580                 585                 590


Asp Ala Ser Gly Ser Tyr Val Ile Tyr Ala Pro Val Asp Ile Ile Ala
            595                 600                 605
```

```
Met Asn Val Val Leu Ser Gly Gly Asp Pro Asp Tyr Val Ala Leu Leu
    610               615               620

Pro Ser Gly Phe Ala Ile Leu Pro Asp Gly Ser Ala Arg Gly Gly Gly
625               630               635               640

Gly Ser Ala Asn Ala Ser Ala Gly Ala Gly Val Glu Gly Gly Gly Glu
              645               650               655

Gly Asn Asn Leu Glu Val Val Thr Thr Thr Gly Ser Cys Gly Gly Ser
              660               665               670

Leu Leu Thr Val Ala Phe Gln Ile Leu Val Asp Ser Val Pro Thr Ala
          675               680               685

Lys Leu Ser Leu Gly Ser Val Ala Thr Val Asn Ser Leu Ile Lys Cys
    690               695               700

Thr Val Glu Arg Ile Lys Ala Ala Leu Ala Cys Asp Gly Ala
705               710               715
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<221> CDS <222> (217)..(957) <223> G463

<400> 323
ctcgagctac gtcaggggtc tctttctgtt tgtttgtttt cttgtttcct tctctctctc
60

tctttctttc tttgtcttcc tttcccaggt tgttttttttt tgctctctct gccttcttga
120

ctttcaaaag actctttctt tcttttggat tgattttgga ttctagggct ctctttcttt
180

tagtgggttt ttgttgttgt tgttgtggtc tctctg atg att act gaa ctt gag
234
                                        Met Ile Thr Glu Leu Glu
                                        1   5

atg ggg aaa ggt gag agt gag ctt gag ctt ggt cta ggg ctg agt ctt
282
Met Gly Lys Gly Glu Ser Glu Leu Glu Leu Gly Leu Gly Leu Ser Leu
             10   15   20

ggc ggt gga acg gcg gcc aag att ggt aaa tca ggt ggt ggt ggc gcg
330
Gly Gly Gly Thr Ala Ala Lys Ile Gly Lys Ser Gly Gly Gly Gly Ala
          25   30   35

tgg gga gag cgt gga agg ctt ttg acg gct aag gat ttt cct tct gtt
378
Trp Gly Glu Arg Gly Arg Leu Leu Thr Ala Lys Asp Phe Pro Ser Val

565

```
            40                      45                      50

ggt tct aaa cgt gct gct gat tct gct tct cat gct ggt tca tct cct
426
Gly Ser Lys Arg Ala Ala Asp Ser Ala Ser His Ala Gly Ser Ser Pro
55                  60              65                      70


cct cgt tca agt caa gtt gtt gga tgg cct cct ata ggg tca cac agg
474
Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Ser His Arg
                75              80                  85


atg aac agt ttg gtt aat aac caa gct aca aag tca gca aga gaa gaa
522
Met Asn Ser Leu Val Asn Asn Gln Ala Thr Lys Ser Ala Arg Glu Glu
            90                  95              100


gaa gaa gct ggt aag aag aaa gtg aaa gat gat gaa cct aaa gat gtg
570
Glu Glu Ala Gly Lys Lys Lys Val Lys Asp Asp Glu Pro Lys Asp Val
            105                 110                 115


aca aag aaa gtg aat ggg aaa gta caa gtt gga ttt att aag gtg aac
618
Thr Lys Lys Val Asn Gly Lys Val Gln Val Gly Phe Ile Lys Val Asn
    120                 125                 130


atg gat gga gtt gct ata gga aga aaa gtg gat ttg aat gct cat tct
666
Met Asp Gly Val Ala Ile Gly Arg Lys Val Asp Leu Asn Ala His Ser
135                 140                 145                 150


tct tac gag aat ttg gcg caa aca ttg gaa gat atg ttc ttt cgc act
714
Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Asp Met Phe Phe Arg Thr
                155                 160                 165


aat ccg ggt act gtc ggg tta acc agt cag ttc act aaa ccg ttg agg
762
Asn Pro Gly Thr Val Gly Leu Thr Ser Gln Phe Thr Lys Pro Leu Arg
                170                 175                 180


ctt tta gat gga tcg tct gag ttt gta ctt act tat gaa gat aag gaa
810
Leu·Leu Asp Gly Ser Ser Glu Phe Val Leu Thr Tyr Glu Asp Lys Glu
                185                 190                 195


gga gat tgg atg ctt gtt ggt gat gtt cca tgg aga atg ttc atc aac
858
Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Arg Met Phe Ile Asn
        200                 205                 210


tcg gtg aaa agg cta cgt gtg atg aaa acc tct gaa gct aat gga ctc
906
Ser Val Lys Arg Leu Arg Val Met Lys Thr Ser Glu Ala Asn Gly Leu
215                 220                 225                 230


gct gca cga aat caa gaa cca aac gag aga cag cga aag cag ccg gtt
954
Ala Ala Arg Asn Gln Glu Pro Asn Glu Arg Gln Arg Lys Gln Pro Val
                235                 240                 245
```

566

tag atctcttttc gacgttacgg tgttacaggt tttatatttt ggggtttttgc
1007

aagtctgaga tacttctgaa gcaagcataa gctagattga tcttatatcc agtttgtgta
1067

ttttcttggt tcttataatg gttttttactg gttttcttta gtttttttttt ttgctgtctt
1127

ttaattttcg gttgcgattt cactatatac tatggatgga agagaatgct ctttatatct
1187

tttactacac tgtaaatatt tgaagcttat ctaatatcgt ttttaagggt taaaaaaccc
1247

tgacgtagcc tcgag
1262

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324

Met Ile Thr Glu Leu Glu Met Gly Lys Gly Glu Ser Glu Leu Glu Leu
1   5   10   15

Gly Leu Gly Leu Ser Leu Gly Gly Gly Thr Ala Ala Lys Ile Gly Lys
            20   25   30

Ser Gly Gly Gly Gly Ala Trp Gly Glu Arg Gly Arg Leu Leu Thr Ala
        35   ·   40   45

Lys Asp Phe Pro Ser Val Gly Ser Lys Arg Ala Ala Asp Ser Ala Ser
    50   55   60

His Ala Gly Ser Ser Pro Pro Arg Ser Ser Gln Val Val Gly Trp Pro
65   70   75   80

Pro Ile Gly Ser His Arg Met Asn Ser Leu Val Asn Asn Gln Ala Thr
                85   90   ·95

Lys Ser Ala Arg Glu Glu Glu Glu Ala Gly Lys Lys Lys Val Lys Asp
                100   105   110

Asp Glu Pro Lys Asp Val Thr Lys Lys Val Asn Gly Lys Val Gln Val
                115   120   125

Gly Phe Ile Lys Val Asn Met Asp Gly Val Ala Ile Gly Arg Lys Val
            130   135   140

Asp Leu Asn Ala His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu
145   150   155   160

567

```
Asp Met Phe Phe Arg Thr Asn Pro Gly Thr Val Gly Leu Thr Ser Gln
            165                 170                 175


Phe Thr Lys Pro Leu Arg Leu Leu Asp Gly Ser Ser Glu Phe Val Leu
            180                 185                 190


Thr Tyr Glu Asp Lys Glu Gly Asp Trp Met Leu Val Gly Asp Val Pro
        195                 200                 205


Trp Arg Met Phe Ile Asn Ser Val Lys Arg Leu Arg Val Met Lys Thr
    210                 215                 220


Ser Glu Ala Asn Gly Leu Ala Ala Arg Asn Gln Glu Pro Asn Glu Arg
225                 230                 235                 240


Gln Arg Lys Gln Pro Val
                245
```


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<221> CDS <222> (1)..(2580) <223> G470

<400> 325
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48
Met Ala Ser Ser Glu Val Ser Met Lys Gly Asn Arg Gly Gly Asp Asn
1               5                   10                  15

ttc tcc tcc tct ggt ttt agt gac cct aag gag act aga aat gtc tcc
96
Phe Ser Ser Ser Gly Phe Ser Asp Pro Lys Glu Thr Arg Asn Val Ser
                20                  25                  30

gtc gcc ggc gag ggg caa aaa agt aat tct acc cga tcc gct gcg gct
144
Val Ala Gly Glu Gly Gln Lys Ser Asn Ser Thr Arg Ser Ala Ala Ala
            35                  40                  45

gag cgt gct ttg gac cct gag gct gct ctt tac aga gag cta tgg cac
192
Glu Arg Ala Leu Asp Pro Glu Ala Ala Leu Tyr Arg Glu Leu Trp His
        50                  55                  60

gct tgt gct ggt ccg ctt gtg acg gtt cct aga caa gac gac cga gtc
240
Ala Cys Ala Gly Pro Leu Val Thr Val Pro Arg Gln Asp Asp Arg Val
65                  70                  75                  80

ttc tat ttt cct caa gga cac atc gag cag gtg gag gct tcg acg aac
288
Phe Tyr Phe Pro Gln Gly His Ile Glu Gln Val Glu Ala Ser Thr Asn
                85                  90                  95
```

```
cag gcg gca gaa caa cag atg cct ctc tat gat ctt ccg tca aag ctt
336
Gln Ala Ala Glu Gln Gln Met Pro Leu Tyr Asp Leu Pro Ser Lys Leu
            100             105             110

ctc tgt cga gtt att aat gta gat tta aag gca gag gca gat aca gat
384
Leu Cys Arg Val Ile Asn Val Asp Leu Lys Ala Glu Ala Asp Thr Asp
            115             120             125

gaa gtt tat gcg cag att act ctt ctt cct gag gct aat caa gac gag
432
Glu Val Tyr Ala Gln Ile Thr Leu Leu Pro Glu Ala Asn Gln Asp Glu
        130             135             140

aat gca att gag aaa gaa gcg cct ctt cct cca cct ccg agg ttc cag
480
Asn Ala Ile Glu Lys Glu Ala Pro Leu Pro Pro Pro Pro Arg Phe Gln
145             150             155             160

gtg cat tcg ttc tgc aaa acc ttg act gca tcc gac aca agt aca cat
528
Val His Ser Phe Cys Lys Thr Leu Thr Ala Ser Asp Thr Ser Thr His
                165             170             175

ggt gga ttt tct gtt ctt agg cga cat gcg gat gaa tgt ctc cca cct
576
Gly Gly Phe Ser Val Leu Arg Arg His Ala Asp Glu Cys Leu Pro Pro
            180             185             190

ctg gat atg tct cga cag cct ccc act caa gag tta gtt gca aag gat
624
Leu Asp Met Ser Arg Gln Pro Pro Thr Gln Glu Leu Val Ala Lys Asp
            195             200             205

ttg cat gca aat gag tgg cga ttc aga cat ata ttc cgg ggt caa cca
672
Leu His Ala Asn Glu Trp Arg Phe Arg His Ile Phe Arg Gly Gln Pro
        210             215             220

cgg agg cat ttg cta cag agt ggg tgg agt gtg ttt gtt agc tcc aaa
720
Arg Arg His Leu Leu Gln Ser Gly Trp Ser Val Phe Val Ser Ser Lys
225             230             235             240

agg cta gtt gca ggc gat gcg ttt ata ttt cta agg ggc gag aat gga
768
Arg Leu Val Ala Gly Asp Ala Phe Ile Phe Leu Arg Gly Glu Asn Gly
            245             250             255

gaa tta aga gtt ggt gta agg cgt gcg atg cga caa caa gga aac gtg
816
Glu Leu Arg Val Gly Val Arg Arg Ala Met Arg Gln Gln Gly Asn Val
            260             265             270

ccg tct tct gtt ata tct agc cat agc atg cat ctt gga gta ctg gcc
864
Pro Ser Ser Val Ile Ser Ser His Ser Met His Leu Gly Val Leu Ala
            275             280             285
```

569

```
acc gca tgg cat gcc att tca aca ggg act atg ttt aca gtc tac tac
912
Thr Ala Trp His Ala Ile Ser Thr Gly Thr Met Phe Thr Val Tyr Tyr
    290                 295             300

aaa ccc agg acg agc cca tct gag ttt att gtt ccg ttc gat cag tat
960
Lys Pro Arg Thr Ser Pro Ser Glu Phe Ile Val Pro Phe Asp Gln Tyr
305                 310             315                 320

atg gag tct gtt aag aat aac tac tct att ggc atg aga ttc aaa atg
1008
Met Glu Ser Val Lys Asn Asn Tyr Ser Ile Gly Met Arg Phe Lys Met
                325             330             335

aga ttt gaa ggc gaa gag gct cct gag cag agg ttt act ggc aca atc
1056
Arg Phe Glu Gly Glu Glu Ala Pro Glu Gln Arg Phe Thr Gly Thr Ile
            340             345             350

gtt ggg att gaa gag tct gat cct act agg tgg cca aaa tca aag tgg
1104
Val Gly Ile Glu Glu Ser Asp Pro Thr Arg Trp Pro Lys Ser Lys Trp
        355             360     -       365

aga tcc ctc aag gtg aga tgg gat gag act tct agt att cct cga cct
1152
Arg Ser Leu Lys Val Arg Trp Asp Glu Thr Ser Ser Ile Pro Arg Pro
    370             375             380

gat aga gta tct ccg tgg aaa gta gag cca gct ctt gct cct cct gct
1200
Asp Arg Val Ser Pro Trp Lys Val Glu Pro Ala Leu Ala Pro Pro Ala
385             390             395                 400

ttg agt cct gtt cca atg cct agg cct aag agg ccc aga tca aat ata
1248
Leu Ser Pro Val Pro Met Pro Arg Pro Lys Arg Pro Arg Ser Asn Ile
            405             410             415

gca cct tca tct cct gac tct tcg atg ctt acc aga gaa ggt aca act
1296
Ala Pro Ser Ser Pro Asp Ser Ser Met Leu Thr Arg Glu Gly Thr Thr
            420             425             430

aag gca aac atg gac cct tta cca gca agc gga ctt tca agg gtc ttg
1344
Lys Ala Asn Met Asp Pro Leu Pro Ala Ser Gly Leu Ser Arg Val Leu
    435                 440             445

caa ggt caa gaa tac tcg acc ttg agg acg aaa cat act gag agt gta
1392
Gln Gly Gln Glu Tyr Ser Thr Leu Arg Thr Lys His Thr Glu Ser Val
    450             455             460

gag tgt gat gct cct gag aat tct gtt gtc tgg caa tct tca gcg gat
1440
Glu Cys Asp Ala Pro Glu Asn Ser Val Val Trp Gln Ser Ser Ala Asp
465             470             475                 480
```

570

```
gat gat aag gtt gac gtg gtt tcg ggt tct aga aga tat gga tct gag
1488
Asp Asp Lys Val Asp Val Val Ser Gly Ser Arg Arg Tyr Gly Ser Glu
            485             490             495


aac tgg atg tcc tca gcc agg cat gaa cct act tac aca gat ttg ctc
1536
Asn Trp Met Ser Ser Ala Arg His Glu Pro Thr Tyr Thr Asp Leu Leu
        500             505             510


tcc ggc ttt ggg act aac ata gat cca tcc cat ggt cag cgg ata cct
1584
Ser Gly Phe Gly Thr Asn Ile Asp Pro Ser His Gly Gln Arg Ile Pro
        515             520             525


ttt tat gac cat tca tca tca cct tct atg cct gca aag aga atc ttg
1632
Phe Tyr Asp His Ser Ser Ser Pro Ser Met Pro Ala Lys Arg Ile Leu
    530             535             540


agt gat tca gaa ggc aag ttc gat tat ctt gct aac cag tgg cag atg
1680
Ser Asp Ser Glu Gly Lys Phe Asp Tyr Leu Ala Asn Gln Trp Gln Met
545             550             555             560


ata cac tct ggt ctc tcc ctg aag tta cat gaa tct cct aag gta cct
1728
Ile His Ser Gly Leu Ser Leu Lys Leu His Glu Ser Pro Lys Val Pro
            565             570             575


gca gca act gat gcg tct ctc caa ggg cga tgc aat gtt aaa tac agc
1776
Ala Ala Thr Asp Ala Ser Leu Gln Gly Arg Cys Asn Val Lys Tyr Ser
            580             585             590


gaa tat cct gtt ctt aat ggt cta tcg act gag aat gct ggt ggt aac
1824
Glu Tyr Pro Val Leu Asn Gly Leu Ser Thr Glu Asn Ala Gly Gly Asn
        595             600             605


tgg cca ata cgt cca cgt gct ttg aat tat tat gag gaa gtg gtc aat
1872
Trp Pro Ile Arg Pro Arg Ala Leu Asn Tyr Tyr Glu Glu Val Val Asn
    610             615             620


gct caa gcg caa gct cag gct agg gag caa gta aca aaa caa ccc ttc
1920
Ala Gln Ala Gln Ala Gln Ala Arg Glu Gln Val Thr Lys Gln Pro Phe
625             630             635             640


acg ata caa gag gag aca gca aag tca aga gaa ggg aac tgc agg ctc
1968
Thr Ile Gln Glu Glu Thr Ala Lys Ser Arg Glu Gly Asn Cys Arg Leu
            645             650             655


ttt ggc att cct ctg acc aac aac atg aat ggg aca gac tca acc atg
2016
Phe Gly Ile Pro Leu Thr Asn Asn Met Asn Gly Thr Asp Ser Thr Met
            660             665             670
```

571

```
tct cag aga aac aac ttg aat gat gct gcg ggg ctt aca cag ata gca
2064
Ser Gln Arg Asn Asn Leu Asn Asp Ala Ala Gly Leu Thr Gln Ile Ala
        675                 680                 685


tca cca aag gtt cag gac ctt tca gat cag tca aaa ggg tca aaa tca
2112
Ser Pro Lys Val Gln Asp Leu Ser Asp Gln Ser Lys Gly Ser Lys Ser
    690                 695                 700


aca aac gat cat cgt gaa cag gga aga cca ttc cag act aat aat cct
2160
Thr Asn Asp His Arg Glu Gln Gly Arg Pro Phe Gln Thr Asn Asn Pro
705                 710                 715                 720


cat ccg aag gat gct caa acg aaa acc aac tca agt agg agt tgc aca
2208
His Pro Lys Asp Ala Gln Thr Lys Thr Asn Ser Ser Arg Ser Cys Thr
                725                 730                 735


aag gtt cac aag cag gga att gca ctt ggc cgt tca gtg gat ctt tca
2256
Lys Val His Lys Gln Gly Ile Ala Leu Gly Arg Ser Val Asp Leu Ser
            740                 745                 750


aag ttc caa aac tat gag gag tta gtc gct gag ctg gac agg ctg ttt
2304
Lys Phe Gln Asn Tyr Glu Glu Leu Val Ala Glu Leu Asp Arg Leu Phe
        755                 760                 765


gag ttc aat gga gag ttg atg gct cct aag aaa gat tgg ttg ata gtt
2352
Glu Phe Asn Gly Glu Leu Met Ala Pro Lys Lys Asp Trp Leu Ile Val
    770                 775                 780


tac aca gat gaa gag aat gat atg atg ctt gtt ggt gac gat cct tgg
2400
Tyr Thr Asp Glu Glu Asn Asp Met Met Leu Val Gly Asp Asp Pro Trp
785                 790                 795                 800


cag gag ttt tgt tgc atg gtt cgc aaa atc ttc ata tac acg aaa gag
2448
Gln Glu Phe Cys Cys Met Val Arg Lys Ile Phe Ile Tyr Thr Lys Glu
                805                 810                 815


gaa gtg agg aag atg aac ccg ggg act tta agc tgt agg agc gag gaa
2496
Glu Val Arg Lys Met Asn Pro Gly Thr Leu Ser Cys Arg Ser Glu Glu
                820                 825                 830


gaa gca gtt gtt ggg gaa gga tca gat gca aag gac gcc aag tct gca
2544
Glu Ala Val Val Gly Glu Gly Ser Asp Ala Lys Asp Ala Lys Ser Ala
            835                 840                 845


tca aat cct tca ttg tcc agc gct ggg aac tct taa
2580
Ser Asn Pro Ser Leu Ser Ser Ala Gly Asn Ser
    850                 855
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572

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326

Met Ala Ser Ser Glu Val Ser Met Lys Gly Asn Arg Gly Gly Asp Asn
1   5   10   15

Phe Ser Ser Ser Gly Phe Ser Asp Pro Lys Glu Thr Arg Asn Val Ser
            20   25   30

Val Ala Gly Glu Gly Gln Lys Ser Asn Ser Thr Arg Ser Ala Ala Ala
        35   40   45

Glu Arg Ala Leu Asp Pro Glu Ala Ala Leu Tyr Arg Glu Leu Trp His
    50   55   60

Ala Cys Ala Gly Pro Leu Val Thr Val Pro Arg Gln Asp Asp Arg Val
65   70   75   80

Phe Tyr Phe Pro Gln Gly His Ile Glu Gln Val Glu Ala Ser Thr Asn
                85   90   95

Gln Ala Ala Glu Gln Gln Met Pro Leu Tyr Asp Leu Pro Ser Lys Leu
            100   105   110

Leu Cys Arg Val Ile Asn Val Asp Leu Lys Ala Glu Ala Asp Thr Asp
        115   120   125

Glu Val Tyr Ala Gln Ile Thr Leu Leu Pro Glu Ala Asn Gln Asp Glu
    130   135   140

Asn Ala Ile Glu Lys Glu Ala Pro Leu Pro Pro Pro Pro Arg Phe Gln
145   150   155   160

Val His Ser Phe Cys Lys Thr Leu Thr Ala Ser Asp Thr Ser Thr His
                165   170   175

Gly Gly Phe Ser Val Leu Arg Arg His Ala Asp Glu Cys Leu Pro Pro
            180   185   190

Leu Asp Met Ser Arg Gln Pro Pro Thr Gln Glu Leu Val Ala Lys Asp
            195   200   205

Leu His Ala Asn Glu Trp Arg Phe Arg His Ile Phe Arg Gly Gln Pro
    210   215   220

Arg Arg His Leu Leu Gln Ser Gly Trp Ser Val Phe Val Ser Ser Lys
225   230   235   240

573

```
Arg Leu Val Ala Gly Asp Ala Phe Ile Phe Leu Arg Gly Glu Asn Gly
            245             250             255

Glu Leu Arg Val Gly Val Arg Arg Ala Met Arg Gln Gln Gly Asn Val
            260             265             270

Pro Ser Ser Val Ile Ser Ser His Ser Met His Leu Gly Val Leu Ala
            275             280             285

Thr Ala Trp His Ala Ile Ser Thr Gly Thr Met Phe Thr Val Tyr Tyr
    290             295             300

Lys Pro Arg Thr Ser Pro Ser Glu Phe Ile Val Pro Phe Asp Gln Tyr
305             310             315             320

Met Glu Ser Val Lys Asn Asn Tyr Ser Ile Gly Met Arg Phe Lys Met
            325             330             335

Arg Phe Glu Gly Glu Glu Ala Pro Glu Gln Arg Phe Thr Gly Thr Ile
            340             345             350

Val Gly Ile Glu Glu Ser Asp Pro Thr Arg Trp Pro Lys Ser Lys Trp
            355             360             365

Arg Ser Leu Lys Val Arg Trp Asp Glu Thr Ser Ser Ile Pro Arg Pro
    370             375             380

Asp Arg Val Ser Pro Trp Lys Val Glu Pro Ala Leu Ala Pro Pro Ala
385             390             395             400

Leu Ser Pro Val Pro Met Pro Arg Pro Lys Arg Pro Arg Ser Asn Ile
            405             410             415

Ala Pro Ser Ser Pro Asp Ser Ser Met Leu Thr Arg Glu Gly Thr Thr
            420             425             430

Lys Ala Asn Met Asp Pro Leu Pro Ala Ser Gly Leu Ser Arg Val Leu
            435             440             445

Gln Gly Gln Glu Tyr Ser Thr Leu Arg Thr Lys His Thr Glu Ser Val
    450             455             460

Glu Cys Asp Ala Pro Glu Asn Ser Val Val Trp Gln Ser Ser Ala Asp
465             470             475             480
```

```
Asp Asp Lys Val Asp Val Val Ser Gly Ser Arg Arg Tyr Gly Ser Glu
            485             490             495


Asn Trp Met Ser Ser Ala Arg His Glu Pro Thr Tyr Thr Asp Leu Leu
            500             505             510


Ser Gly Phe Gly Thr Asn Ile Asp Pro Ser His Gly Gln Arg Ile Pro
            515             520             525


Phe Tyr Asp His Ser Ser Ser Pro Ser Met Pro Ala Lys Arg Ile Leu
    530             535             540


Ser Asp Ser Glu Gly Lys Phe Asp Tyr Leu Ala Asn Gln Trp Gln Met
545             550             555             560


Ile His Ser Gly Leu Ser Leu Lys Leu His Glu Ser Pro Lys Val Pro
            565             570             575


Ala Ala Thr Asp Ala Ser Leu Gln Gly Arg Cys Asn Val Lys Tyr Ser
            580             585             590


Glu Tyr Pro Val Leu Asn Gly Leu Ser Thr Glu Asn Ala Gly Gly Asn
            595             600             605


Trp Pro Ile Arg Pro Arg Ala Leu Asn Tyr Tyr Glu Glu Val Val Asn
    610             615             620


Ala Gln Ala Gln Ala Gln Ala Arg Glu Gln Val Thr Lys Gln Pro Phe
625             630             635             640


Thr Ile Gln Glu Glu Thr Ala Lys Ser Arg Glu Gly Asn Cys Arg Leu
            645             650             655


Phe Gly Ile Pro Leu Thr Asn Asn Met Asn Gly Thr Asp Ser Thr Met
            660             665             670


Ser Gln Arg Asn Asn Leu Asn Asp Ala Ala Gly Leu Thr Gln Ile Ala
            675             680             685


Ser Pro Lys Val Gln Asp Leu Ser Asp Gln Ser Lys Gly Ser Lys Ser
            690             695             700


Thr Asn Asp His Arg Glu Gln Gly Arg Pro Phe Gln Thr Asn Asn Pro
705             710             715             720
```

                                          575

```
His Pro Lys Asp Ala Gln Thr Lys Thr Asn Ser Ser Arg Ser Cys Thr
            725                 730                 735

Lys Val His Lys Gln Gly Ile Ala Leu Gly Arg Ser Val Asp Leu Ser
            740                 745                 750

Lys Phe Gln Asn Tyr Glu Glu Leu Val Ala Glu Leu Asp Arg Leu Phe
        755                 760                 765

Glu Phe Asn Gly Glu Leu Met Ala Pro Lys Lys Asp Trp Leu Ile Val
    770                 775                 780

Tyr Thr Asp Glu Glu Asn Asp Met Met Leu Val Gly Asp Asp Pro Trp
785                 790                 795                 800

Gln Glu Phe Cys Cys Met Val Arg Lys Ile Phe Ile Tyr Thr Lys Glu
                805                 810                 815

Glu Val Arg Lys Met Asn Pro Gly Thr Leu Ser Cys Arg Ser Glu Glu
            820                 825                 830

Glu Ala Val Val Gly Glu Gly Ser Asp Ala Lys Asp Ala Lys Ser Ala
        835                 840                 845

Ser Asn Pro Ser Leu Ser Ser Ala Gly Asn Ser
    850                 855
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<221> CDS <222> (288)..(2204) <223> G472

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60

ggattgcgtt gcgttacgat tcagatctct ctcgatcgtt acttacatgc attagagaac
120

aagaaacgt ggagacggaa tccaagggac cttcttcttc aatttaattc ctcactttat
180

tacgcaccct tcttttattt tcgactgttt cagcttccgg ttcttcatcg gagagagata
240

gagagactgt gtgttttggt gtgactgata gaagatttaa tcagctg atg gca aat
296
                                               Met Ala Asn
                                               1

cgc gga ggt gaa tat ctg tac gat gag tta tgg aaa tta tgc gcg gga
344
Arg Gly Gly Glu Tyr Leu Tyr Asp Glu Leu Trp Lys Leu Cys Ala Gly
    5                 10                  15
```

```
cct ctt gtt gat gtt cct caa gct caa gaa aga gtt tat tat ttt cct
392
Pro Leu Val Asp Val Pro Gln Ala Gln Glu Arg Val Tyr Tyr Phe Pro
20              25          30              35

caa ggt cac atg gaa caa ctc gaa gcg tca acg caa caa gtc gac tta
440
Gln Gly His Met Glu Gln Leu Glu Ala Ser Thr Gln Gln Val Asp Leu
            40              45              50

aat acg atg aag cct ctt ttt gtt ctt cct cct aag att ctc tgc aat
488
Asn Thr Met Lys Pro Leu Phe Val Leu Pro Pro Lys Ile Leu Cys Asn
            55              60              65

gtt atg aac gtt agt ctt cag gcg gag aaa gat acg gat gag gtc tat
536
Val Met Asn Val Ser Leu Gln Ala Glu Lys Asp Thr Asp Glu Val Tyr
            70              75              80

gct cag att act ttg atc cct gtt gga act gaa gtt gat gaa cct atg
584
Ala Gln Ile Thr Leu Ile Pro Val Gly Thr Glu Val Asp Glu Pro Met
        85              90              95

agt cct gat ccc tct cct cct gag ttg caa agg ccg aaa gtt cac tct
632
Ser Pro Asp Pro Ser Pro Pro Glu Leu Gln Arg Pro Lys Val His Ser
100             105             110             115

ttc agc aag gtt ttg aca gcg tct gat aca agc acc cat ggt ggc ttt
680
Phe Ser Lys Val Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe
            120             125             130

tct gtt cta agg aaa cat gcc acg gaa tgt ctt cct ccg ctg gat atg
728
Ser Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Pro Leu Asp Met
            135             140             145

act cag caa acc ccg acc cag gag tta gta gcc gaa gat gtg cac ggt
776
Thr Gln Gln Thr Pro Thr Gln Glu Leu Val Ala Glu Asp Val His Gly
        150             155             160

tat cag tgg aaa ttc aag cat att ttt aga ggc caa cca cgg agg cat
824
Tyr Gln Trp Lys Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His
        165             170             175

cta ttg acg aca ggg tgg agc acc ttt gtt aca tca aag aga ttg gtt
872
Leu Leu Thr Thr Gly Trp Ser Thr Phe Val Thr Ser Lys Arg Leu Val
180             185             190             195

gct ggg gac acc ttt gta ttc ctg aga ggg gag aac gga gag ttg cga
920
Ala Gly Asp Thr Phe Val Phe Leu Arg Gly Glu Asn Gly Glu Leu Arg
            200             205             210
```

577

gtt gga gtc aga cgt gct aat ctt caa cag agc agt atg cct tca tcc
968
Val Gly Val Arg Arg Ala Asn Leu Gln Gln Ser Ser Met Pro Ser Ser
            215   220   225

gtt ata tca agt cat agt atg cat ctg gga gtg ctt gct act gca cgc
1016
Val Ile Ser Ser His Ser Met His Leu Gly Val Leu Ala Thr Ala Arg
        230   235   240

cat gct act caa acg aaa act atg ttc att gta tac tat aaa cca agg
1064
His Ala Thr Gln Thr Lys Thr Met Phe Ile Val Tyr Tyr Lys Pro Arg
    245   250   255

aca agc caa ttc atc att agc ttg aac aaa tat cta gaa gcc atg agc
1112
Thr Ser Gln Phe Ile Ile Ser Leu Asn Lys Tyr Leu Glu Ala Met Ser
260   265   270   275

aat aag ttc tct gta ggg atg aga ttt aag atg cgt ttt gag gga gag
1160
Asn Lys Phe Ser Val Gly Met Arg Phe Lys Met Arg Phe Glu Gly Glu
            280   285   290

gat tcc cct gaa aga aga tat tct ggc acg gtt att ggt gtg aaa gac
1208
Asp Ser Pro Glu Arg Arg Tyr Ser Gly Thr Val Ile Gly Val Lys Asp
            295   300   305

tgc tcc cct cac tgg aaa gac tca aaa tgg cga tgc tta gaa gtt cat
1256
Cys Ser Pro His Trp Lys Asp Ser Lys Trp Arg Cys Leu Glu Val His
            310   315   320

tgg gat gag cct gca tcg att tca aga ccc aat aag gtt tca cca tgg
1304
Trp Asp Glu Pro Ala Ser Ile Ser Arg Pro Asn Lys Val Ser Pro Trp
    325   330   335

gaa att gaa ccg ttt gta aat tca gaa aac gtt ccc aaa tca gtt atg
1352
Glu Ile Glu Pro Phe Val Asn Ser Glu Asn Val Pro Lys Ser Val Met
340   345   350   355

ctg aag aac aaa agg ccc cgt caa gtt agt gaa gta tct gca ctt gat
1400
Leu Lys Asn Lys Arg Pro Arg Gln Val Ser Glu Val Ser Ala Leu Asp
            360   365   370

gta ggc ata aca gct tca aac ctt tgg agc tct gtt ttg acg caa ccc
1448
Val Gly Ile Thr Ala Ser Asn Leu Trp Ser Ser Val Leu Thr Gln Pro
        375   380   385

cat gag ttt gca caa tcg tgc atc acc tca cag tgg agt tct cct cag
1496
His Glu Phe Ala Gln Ser Cys Ile Thr Ser Gln Trp Ser Ser Pro Gln
        390   395   400

caa tgt cat cgt gat gca aat gag gat gct aag aaa tct gac tgg cta
1544
Gln Cys His Arg Asp Ala Asn Glu Asp Ala Lys Lys Ser Asp Trp Leu
   405   410   415

aat aac tct tac tct gtg tca aat gta gca aaa gac tca aca ctg aac
1592
Asn Asn Ser Tyr Ser Val Ser Asn Val Ala Lys Asp Ser Thr Leu Asn
420   425   430   435

gac caa atg gtt tcc cca gtc gag cag aag aag cct gag aca acc gct
1640
Asp Gln Met Val Ser Pro Val Glu Gln Lys Lys Pro Glu Thr Thr Ala
              440   445   450

aat tat aga tta ttt gga att gat ctg atg agt tcc tcc cta gcg gtt
1688
Asn Tyr Arg Leu Phe Gly Ile Asp Leu Met Ser Ser Ser Leu Ala Val
           455   460   465

cct gag gag aaa act gca ccc atg cga cca atc aac ata tcc aaa ccg
1736
Pro Glu Glu Lys Thr Ala Pro Met Arg Pro Ile Asn Ile Ser Lys Pro
        470   475   480

act atg gac agc cac tca gac cca aaa tca gag att tca aaa gta tca
1784
Thr Met Asp Ser His Ser Asp Pro Lys Ser Glu Ile Ser Lys Val Ser
     485   490   495

gaa gag aaa aag cag gaa cct gcg gag gga tca cca aaa gag gtc caa
1832
Glu Glu Lys Lys Gln Glu Pro Ala Glu Gly Ser Pro Lys Glu Val Gln
500   505   510   515

agc aag caa agc agt tct aca aga agc cgt acc aag gtg cag atg caa
1880
Ser Lys Gln Ser Ser Ser Thr Arg Ser Arg Thr Lys Val Gln Met Gln
           520   525   530

ggc gta cct gtg ggc agg gct gtg gat tta aat gcg cta aag ggg tac
1928
Gly Val Pro Val Gly Arg Ala Val Asp Leu Asn Ala Leu Lys Gly Tyr
           535   540   545

aac gag ctc ata gat gac att gag aag ctg ttt gac ata aaa ggg gaa
1976
Asn Glu Leu Ile Asp Asp Ile Glu Lys Leu Phe Asp Ile Lys Gly Glu
        550   555   560

ctg cgg agt cgc aat caa tgg gaa ata gtg ttc aca gac gat gag gga
2024
Leu Arg Ser Arg Asn Gln Trp Glu Ile Val Phe Thr Asp Asp Glu Gly
     565   570   575

gat atg atg ctt gtc ggt gat gac cca tgg cct gag ttc tgc aac atg
2072
Asp Met Met Leu Val Gly Asp Asp Pro Trp Pro Glu Phe Cys Asn Met
580   585   590   595

```
gtg aag aga ata ttc ata tgg tcg aaa gag gaa gtg aag aaa atg acg
2120
Val Lys Arg Ile Phe Ile Trp Ser Lys Glu Glu Val Lys Lys Met Thr
            600             605             610


cct ggg aac caa ctc cgg atg ctg tta agg gaa gtt gaa aca aca cta
2168
Pro Gly Asn Gln Leu Arg Met Leu Leu Arg Glu Val Glu Thr Thr Leu
            615             620             625


aca aca act tcc aaa aca gat aat cat tcc aac taa tttttattct
2214
Thr Thr Thr Ser Lys Thr Asp Asn His Ser Asn
        630             635


attctctatc agtcttcgtc tccttcttat ttgctttgtc tttcggaatt atcttgtttg
2274


tgtctgtgtt ttgttgcg
2292
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Met Ala Asn Arg Gly Gly Glu Tyr Leu Tyr Asp Glu Leu Trp Lys Leu
1               5              10              15


Cys Ala Gly Pro Leu Val Asp Val Pro Gln Ala Gln Glu Arg Val Tyr
            20              25              30


Tyr Phe Pro Gln Gly His Met Glu Gln Leu Glu Ala Ser Thr Gln Gln
        35              40              45


Val Asp Leu Asn Thr Met Lys Pro Leu Phe Val Leu Pro Pro Lys Ile
    50              55              60


Leu Cys Asn Val Met Asn Val Ser Leu Gln Ala Glu Lys Asp Thr Asp
65              70              75              80


Glu Val Tyr Ala Gln Ile Thr Leu Ile Pro Val Gly Thr Glu Val Asp
            85              90              95


Glu Pro Met Ser Pro Asp Pro Ser Pro Pro Glu Leu Gln Arg Pro Lys
            100             105             110


Val His Ser Phe Ser Lys Val Leu Thr Ala Ser Asp Thr Ser Thr His
        115             120             125


Gly Gly Phe Ser Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Pro
        130             135             140
```

```
Leu Asp Met Thr Gln Gln Thr Pro Thr Gln Glu Leu Val Ala Glu Asp
145             150             155             160

Val His Gly Tyr Gln Trp Lys Phe Lys His Ile Phe Arg Gly Gln Pro
                165             170             175

Arg Arg His Leu Leu Thr Thr Gly Trp Ser Thr Phe Val Thr Ser Lys
        180             185             190

Arg Leu Val Ala Gly Asp Thr Phe Val Phe Leu Arg Gly Glu Asn Gly
        195             200             205

Glu Leu Arg Val Gly Val Arg Arg Ala Asn Leu Gln Gln Ser Ser Met
    210             215             220

Pro Ser Ser Val Ile Ser Ser His Ser Met His Leu Gly Val Leu Ala
225             230             235             240

Thr Ala Arg His Ala Thr Gln Thr Lys Thr Met Phe Ile Val Tyr Tyr
            245             250             255

Lys Pro Arg Thr Ser Gln Phe Ile Ile Ser Leu Asn Lys Tyr Leu Glu
        260             265             270

Ala Met Ser Asn Lys Phe Ser Val Gly Met Arg Phe Lys Met Arg Phe
        275             280             285

Glu Gly Glu Asp Ser Pro Glu Arg Arg Tyr Ser Gly Thr Val Ile Gly
    290             295             300

Val Lys Asp Cys Ser Pro His Trp Lys Asp Ser Lys Trp Arg Cys Leu
305             310             315             320

Glu Val His Trp Asp Glu Pro Ala Ser Ile Ser Arg Pro Asn Lys Val
            325             330             335

Ser Pro Trp Glu Ile Glu Pro Phe Val Asn Ser Glu Asn Val Pro Lys
        340             345             350

Ser Val Met Leu Lys Asn Lys Arg Pro Arg Gln Val Ser Glu Val Ser
        355             360             365

Ala Leu Asp Val Gly Ile Thr Ala Ser Asn Leu Trp Ser Ser Val Leu
    370             375             380

Thr Gln Pro His Glu Phe Ala Gln Ser Cys Ile Thr Ser Gln Trp Ser
```

581

```
385                    390                    395                    400
```

Ser Pro Gln Gln Cys His Arg Asp Ala Asn Glu Asp Ala Lys Lys Ser
             405   410   415

Asp Trp Leu Asn Asn Ser Tyr Ser Val Ser Asn Val Ala Lys Asp Ser
             420   425   430

Thr Leu Asn Asp Gln Met Val Ser Pro Val Glu Gln Lys Lys Pro Glu
             435   440   445

Thr Thr Ala Asn Tyr Arg Leu Phe Gly Ile Asp Leu Met Ser Ser Ser
     450   455   460

Leu Ala Val Pro Glu Glu Lys Thr Ala Pro Met Arg Pro Ile Asn Ile
465   470   475   480

Ser Lys Pro Thr Met Asp Ser His Ser Asp Pro Lys Ser Glu Ile Ser
             485   490   495

Lys Val Ser Glu Glu Lys Lys Gln Glu Pro Ala Glu Gly Ser Pro Lys
             500   505   510

Glu Val Gln Ser Lys Gln Ser Ser Ser Thr Arg Ser Arg Thr Lys Val
             515   520   525

Gln Met Gln Gly Val Pro Val Gly Arg Ala Val Asp Leu Asn Ala Leu
     530   535   540

Lys Gly Tyr Asn Glu Leu Ile Asp Asp Ile Glu Lys Leu Phe Asp Ile
545   550   555   560

Lys Gly Glu Leu Arg Ser Arg Asn Gln Trp Glu Ile Val Phe Thr Asp
             565   570   575

Asp Glu Gly Asp Met Met Leu Val Gly Asp Asp Pro Trp Pro Glu Phe
             580   585   590

Cys Asn Met Val Lys Arg Ile Phe Ile Trp Ser Lys Glu Glu Val Lys
     595   600   605

Lys Met Thr Pro Gly Asn Gln Leu Arg Met Leu Leu Arg Glu Val Glu
     610   615   620

Thr Thr Leu Thr Thr Thr Ser Lys Thr Asp Asn His Ser Asn
625   630   635

582

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60

cctcaagcta agattctggt tttgtgagtt gagtggatga aagaggaga gattaactaa
120

attagggttt caattgttta ctttttgttt gctttttata tcaagta atg gat cag
176
                                                     Met Asp Gln
                                                      1

gtc tct cgc tct ctt cct cca cct ttt ctc tca aga gat ctc cat ctt
224
Val Ser Arg Ser Leu Pro Pro Pro Phe Leu Ser Arg Asp Leu His Leu
     5   10   15

cac cca cac cat caa ttc cag cat cag cag cag cag cag caa cag aat
272
His Pro His His Gln Phe Gln His Gln Gln Gln Gln Gln Gln Gln Asn
20   25   30   35

cac ggc cac gat ata gac cag cac cga atc ggt ggg cta aaa cgt gac
320
His Gly His Asp Ile Asp Gln His Arg Ile Gly Gly Leu Lys Arg Asp
                40   45   50

cga gat gct gat atc gat ccc aac gag cac tct tca gcc gga aaa gat
368
Arg Asp Ala Asp Ile Asp Pro Asn Glu His Ser Ser Ala Gly Lys Asp
                55   60   65

caa agt act cct ggc tcc ggt gga gaa agc ggc ggc gga gga gga gga
416
Gln Ser Thr Pro Gly Ser Gly Gly Glu Ser Gly Gly Gly Gly Gly Gly
             70   75   80

gat aat cac atc acg aga agg cca cgt ggc aga cca gcg gga tct aag
464
Asp Asn His Ile Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys
         85   90   95

aac aaa cca aaa ccg cca atc atc atc act cga gac agc gca aac gct
512
Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala
100   105   110   115

ctc aaa tct cat gtc atg gaa gta gca aac gga tgt gac gtc atg gaa
560
Leu Lys Ser His Val Met Glu Val Ala Asn Gly Cys Asp Val Met Glu
                120   125   130

agt gtc acc gtc ttc gct cgc cgt cgc caa cgt ggc atc tgc gtt ttg
608
Ser Val Thr Val Phe Ala Arg Arg Arg Gln Arg Gly Ile Cys Val Leu
             135   140   145

583

```
agc gga aac ggc gcc gtt acc aac gtt acc ata aga caa cca gct tca
656
Ser Gly Asn Gly Ala Val Thr Asn Val Thr Ile Arg Gln Pro Ala Ser
        150                     155                 160

gta cct ggt ggt ggc tca tct gtc gtt aac tta cac gga cgt ttc gag
704
Val Pro Gly Gly Gly Ser Ser Val Val Asn Leu His Gly Arg Phe Glu
        165                     170                 175

att ctt tct ctc tcg gga tca ttc ctt cct cct ccg gct cca cca gct
752
Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala
180                     185                     190                 195

gcg tca ggt cta acg att tac tta gcc ggt ggt cag gga cag gtt gtt
800
Ala Ser Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln Val Val
            200                     205                 210

gga gga agc gtg gtt ggt cca ctc atg gct tca gga cct gta gtg att
848
Gly Gly Ser Val Val Gly Pro Leu Met Ala Ser Gly Pro Val Val Ile
            215                     220                 225

atg gca gct tcg ttt gga aac gct gcg tat gag aga ctg ccg ttg gag
896
Met Ala Ala Ser Phe Gly Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu
            230                     235                 240

gaa gac gat caa gaa gag caa aca gct gga gcg gtt gct aat aat atc
944
Glu Asp Asp Gln Glu Glu Gln Thr Ala Gly Ala Val Ala Asn Asn Ile
        245                     250                 255

gat gga aac gca aca atg ggt ggt gga acg caa acg caa act cag acg
992
Asp Gly Asn Ala Thr Met Gly Gly Gly Thr Gln Thr Gln Thr Gln Thr
260                     265                     270                 275

cag cag caa cag caa caa cag ttg atg caa gat ccg acg tcg ttt ata
1040
Gln Gln Gln Gln Gln Gln Gln Leu Met Gln Asp Pro Thr Ser Phe Ile
                280                     285                 290

caa ggg ttg cct ccg aat ctt atg aat tct gtt caa ttg cca gct gaa
1088
Gln Gly Leu Pro Pro Asn Leu Met Asn Ser Val Gln Leu Pro Ala Glu
                295                     300                 305

gct tat tgg gga act ccg aga cca tct ttc taa atcgcgaaga aaaaacaagt
1141
Ala Tyr Trp Gly Thr Pro Arg Pro Ser Phe
            310                     315
```

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tagatacgtt cgttgttttt aatttataat ctctcttctg tcaagtttta attttctttt
1201

tcttcttctt tgttttctaa agataattgt agtctttgac gaagattcgt ggtacgtatg
1261
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aatcgaagag aatcgttttg gtcatgggat tgctcgatct attaggtttg agaggggggtt
1321

tgtgttttgc gttgactagc agattataaa attgttgatt ttcgagtttt tattttcatg
1381

tgttggtgat aaa
1394

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330

Met Asp Gln Val Ser Arg Ser Leu Pro Pro Pro Phe Leu Ser Arg Asp
1   5   10   15

Leu His Leu His Pro His His Gln Phe Gln His Gln Gln Gln Gln Gln
        20   25   30

Gln Gln Asn His Gly His Asp Ile Asp Gln His Arg Ile Gly Gly Leu
        35   40   45

Lys Arg Asp Arg Asp Ala Asp Ile Asp Pro Asn Glu His Ser Ser Ala
    50   55   60

Gly Lys Asp Gln Ser Thr Pro Gly Ser Gly Gly Glu Ser Gly Gly Gly
65   70   75   80

Gly Gly Gly Asp Asn His Ile Thr Arg Arg Pro Arg Gly Arg Pro Ala
            85   90   ᶜ   95

Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser
            100   105   110

Ala Asn Ala Leu Lys Ser His Val Met Glu Val Ala Asn Gly Cys Asp
        115   120   125

Val Met Glu Ser Val Thr Val Phe Ala Arg Arg Arg Gln Arg Gly Ile
    130   135   140

Cys Val Leu Ser Gly Asn Gly Ala Val Thr Asn Val Thr Ile Arg Gln
145   150   155   160

Pro Ala Ser Val Pro Gly Gly Gly Ser Ser Val Val Asn Leu His Gly
            165   170   175

Arg Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala
            180   185   190

585

```
Pro Pro Ala Ala Ser Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly
        195                 200                 205


Gln Val Val Gly Gly Ser Val Val Gly Pro Leu Met Ala Ser Gly Pro
        210                 215                 220


Val Val Ile Met Ala Ala Ser Phe Gly Asn Ala Ala Tyr Glu Arg Leu
225                 230                 235                 240


Pro Leu Glu Glu Asp Asp Gln Glu Glu Gln Thr Ala Gly Ala Val Ala
                245                 250                 255


Asn Asn Ile Asp Gly Asn Ala Thr Met Gly Gly Gly Thr Gln Thr Gln
                260                 265                 270


Thr Gln Thr Gln Gln Gln Gln Gln Gln Gln Leu Met Gln Asp Pro Thr
        275                 280                 285


Ser Phe Ile Gln Gly Leu Pro Pro Asn Leu Met Asn Ser Val Gln Leu
    290                 295                 300


Pro Ala Glu Ala Tyr Trp Gly Thr Pro Arg Pro Ser Phe
305                 310                 315
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<221> CDS <222> (137)..(2059) <223> G610

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60

aatttaactg gcgccagatt gtgatccagg aatcgttggc ttgttaggtt gttgttttgt
120

tatgcataat tgagag atg gtg gtc aaa agg aag tta aat tgt ggt ggc tct
172
                 Met Val Val Lys Arg Lys Leu Asn Cys Gly Gly Ser
                 1               5                   10


gat ggt ttt gat ttc ccc aat att ccc aag gct cct cgt tca agc agg
220
Asp Gly Phe Asp Phe Pro Asn Ile Pro Lys Ala Pro Arg Ser Ser Arg
        15                  20                  25


agg aag gtc tca ggt aag aga tct gat gat gaa agt gag atc tgt gca
268
Arg Lys Val Ser Gly Lys Arg Ser Asp Asp Glu Ser Glu Ile Cys Ala
    30                  35                  40


att gat ttg cta gct tct ctt gct gga aag ttg ttg gaa gaa agt gaa
316
Ile Asp Leu Leu Ala Ser Leu Ala Gly Lys Leu Leu Glu Glu Ser Glu
```

586

```
45                    50                    55                    60

agt tcc tca acg tct acc tat gca tct gaa gct gat aat ctt gat cat
364
Ser Ser Ser Thr Ser Thr Tyr Ala Ser Glu Ala Asp Asn Leu Asp His
                65                    70                    75


ttg ggt gga ctg att aag caa gaa ctt gaa gat ggc tat act act aag
412
Leu Gly Gly Leu Ile Lys Gln Glu Leu Glu Asp Gly Tyr Thr Thr Lys
            80                    85                    90


cct tgt aaa tcc gag ttt ttc gat cca gga aac cct gct tca aag tcc
460
Pro Cys Lys Ser Glu Phe Phe Asp Pro Gly Asn Pro Ala Ser Lys Ser
        95                    100                   105


act agt gaa aat act agc gtg act tgt ttg cca ttt tcg tct ttc gaa
508
Thr Ser Glu Asn Thr Ser Val Thr Cys Leu Pro Phe Ser Ser Phe Glu
        110                   115                   120


aat gat tgc att ttg gag caa aca ccg gtt tct gat tgt aag agg gca
556
Asn Asp Cys Ile Leu Glu Gln Thr Pro Val Ser Asp Cys Lys Arg Ala
125                   130                   135                   140


tct ggt ttg aag tcc ctg gta ggg agc atc act gag gag aca tgt gtt
604
Ser Gly Leu Lys Ser Leu Val Gly Ser Ile Thr Glu Glu Thr Cys Val
                145                   150                   155


gtt aat gag gat gcc gga tct gaa caa ggt gct aat act ttc agc tta
652
Val Asn Glu Asp Ala Gly Ser Glu Gln Gly Ala Asn Thr Phe Ser Leu
                160                   165                   170


aag gat cca agt caa tta cat tcg cag tct cca gaa tcg gtc ctt ctg
700
Lys Asp Pro Ser Gln Leu His Ser Gln Ser Pro Glu Ser Val Leu Leu
            175                   180                   185


gat ggc gat gtg aaa tta gca cca tgc acg gat caa gtc cct aat gat
748
Asp Gly Asp Val Lys Leu Ala Pro Cys Thr Asp Gln Val Pro Asn Asp
        190                   195                   200


tct ttt aaa gga tat agg aat cat tct aag tta gtt tgc aga gat gat
796
Ser Phe Lys Gly Tyr Arg Asn His Ser Lys Leu Val Cys Arg Asp Asp
205                   210                   215                   220


gac gaa aac tat tgt aag tat tat aaa ttt agt gac aaa tgt aag tca
844
Asp Glu Asn Tyr Cys Lys Tyr Tyr Lys Phe Ser Asp Lys Cys Lys Ser
                225                   230                   235


tat agg cct ctc tcc cgg gtt ggc aat aga aga ata atg cag tcg gtg
892
Tyr Arg Pro Leu Ser Arg Val Gly Asn Arg Arg Ile Met Gln Ser Val
                240                   245                   250
```

587

aga gca atc tcc aag ttg aag tgt ttt gaa gac act aga aca gat ggt
940
Arg Ala Ile Ser Lys Leu Lys Cys Phe Glu Asp Thr Arg Thr Asp Gly
        255   260   265

cgt ttg aag gct ctc tac cgc aag aga aaa tta tgt tat ggt tac aac
988
Arg Leu Lys Ala Leu Tyr Arg Lys Arg Lys Leu Cys Tyr Gly Tyr Asn
    270   275   280

cca tgg aag cgt gag acc att cat agg aag aga aga ttg tct gac aaa
1036
Pro Trp Lys Arg Glu Thr Ile His Arg Lys Arg Arg Leu Ser Asp Lys
285   290   295   300

ggt ttg gtc gta aat tat gat ggt ggg ctc agt agt gaa agt gtt tcc
1084
Gly Leu Val Val Asn Tyr Asp Gly Gly Leu Ser Ser Glu Ser Val Ser
                305   310   315

aat tca cct gaa aag gga gaa tca gaa aat ggt gat ttc tct gct gca
1132
Asn Ser Pro Glu Lys Gly Glu Ser Glu Asn Gly Asp Phe Ser Ala Ala
        320   325   330

aaa ata ggt ctt ctt tcg aaa gac tcc cgt gta aag ttc agc atc aag
1180
Lys Ile Gly Leu Leu Ser Lys Asp Ser Arg Val Lys Phe Ser Ile Lys
        335   340   345

tcc ctt agg att ccg gag ctt gta att gaa gtt cca gaa aca gca aca
1228
Ser Leu Arg Ile Pro Glu Leu Val Ile Glu Val Pro Glu Thr Ala Thr
    350   355   360

gta ggc tta ctg aag agg acg gtg aag gag gcg gtt act gct tta ctc
1276
Val Gly Leu Leu Lys Arg Thr Val Lys Glu Ala Val Thr Ala Leu Leu
365   370   375   380

ggt ggt gga ata cgt att ggg gtg tta gtc caa ggg aaa aaa gtt aga
1324
Gly Gly Gly Ile Arg Ile Gly Val Leu Val Gln Gly Lys Lys Val Arg
                385   390   395

gat gac aac aac act cta tca cag act ggt ctt tcg tgt aga gaa aat
1372
Asp Asp Asn Asn Thr Leu Ser Gln Thr Gly Leu Ser Cys Arg Glu Asn
        400   405   410

ctt ggc aac ctt ggc ttc acc tta gag cct ggt ttg gaa aca ctg cct
1420
Leu Gly Asn Leu Gly Phe Thr Leu Glu Pro Gly Leu Glu Thr Leu Pro
    415   420   425

gta cct ctt tgt tct gaa act cct gtc ctt tct ctg cca act gac tct
1468
Val Pro Leu Cys Ser Glu Thr Pro Val Leu Ser Leu Pro Thr Asp Ser
    430   435   440

aca aag ttg tca gaa agg tcc gca gct tct cca gcg tta gag act gga
1516
Thr Lys Leu Ser Glu Arg Ser Ala Ala Ser Pro Ala Leu Glu Thr Gly
445   450   455   460

att cct ctc cct ccc caa gat gaa gat tac ttg att aat ttg gga aat
1564
Ile Pro Leu Pro Pro Gln Asp Glu Asp Tyr Leu Ile Asn Leu Gly Asn
                465   470   475

agt gtg gag aac aat gat gaa tta gtc cca cat ctg agt gac ata cca
1612
Ser Val Glu Asn Asn Asp Glu Leu Val Pro His Leu Ser Asp Ile Pro
                480   485   490

gct gat gaa caa cct tca tca gat tca aga gcg ctg gtt cca gtt ttg
1660
Ala Asp Glu Gln Pro Ser Ser Asp Ser Arg Ala Leu Val Pro Val Leu
            495   500   505

gcc ttg gag tcc gac gct ctt gca ctt gtt cca gtt aac gag aaa cct
1708
Ala Leu Glu Ser Asp Ala Leu Ala Leu Val Pro Val Asn Glu Lys Pro
        510   515   520

aag cgt aca gag ctt tca caa cgc aga acc agg aga cca ttc tct gtt
1756
Lys Arg Thr Glu Leu Ser Gln Arg Arg Thr Arg Arg Pro Phe Ser Val
525   530   535   540

aca gag gta gaa gct cta gta agc gca gtt gaa gaa gtt ggg act gga
1804
Thr Glu Val Glu Ala Leu Val Ser Ala Val Glu Glu Val Gly Thr Gly
                545   550   555

aga tgg cgt gat gtg aag ttg cgt tct ttt gag aat gca agt cat cga
1852
Arg Trp Arg Asp Val Lys Leu Arg Ser Phe Glu Asn Ala Ser His Arg
                560   565   570

acc tat gtg gac ttg aag gac aaa tgg aaa acg ttg gtt cac aca gca
1900
Thr Tyr Val Asp Leu Lys Asp Lys Trp Lys Thr Leu Val His Thr Ala
            575   580   585

agt ata tca cca cag caa cga aga gga gaa cca gtg cct caa gaa ctg
1948
Ser Ile Ser Pro Gln Gln Arg Arg Gly Glu Pro Val Pro Gln Glu Leu
        590   595   600

cta gac aga gtc tta gga gca cat agg tac tgg aca cag cac caa atg
1996
Leu Asp Arg Val Leu Gly Ala His Arg Tyr Trp Thr Gln His Gln Met
605   610   615   620

aaa cag aac ggg aaa cat cag gtg gct aca aca atg gtg gtt gaa gca
2044
Lys Gln Asn Gly Lys His Gln Val Ala Thr Thr Met Val Val Glu Ala
                625   630   635

ggt tcg tcc atg taa agaaggagaa tggtaataac aataactttc acttgacgac
2099
Gly Ser Ser Met
            640

taaggaacca aagtgggcaa ctgtacaaag ggaaacaaca aaatacagaa acatacttaa
2159

tttctgaaaa gaagagtcta tattttatt tttttaaat catagccggt agaaacaaga
2219

cgttccttga cacttttggt tacttttatg gtaggtctgt tcattccaaa tttctaattg
2279

.atttgattat gtaatttggt ggtaggacca tg
2311

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332

Met Val Val Lys Arg Lys Leu Asn Cys Gly Gly Ser Asp Gly Phe Asp
1   5   10   15

Phe Pro Asn Ile Pro Lys Ala Pro Arg Ser Ser Arg Arg Lys Val Ser
            20   25   .   30

Gly Lys Arg Ser Asp Asp Glu Ser Glu Ile Cys Ala Ile Asp Leu Leu
            35   40   45

Ala Ser Leu Ala Gly Lys Leu Leu Glu Glu Ser Glu Ser Ser Ser Thr
        50   55   60

Ser Thr Tyr Ala Ser Glu Ala Asp Asn Leu Asp His Leu Gly Gly Leu
65   70   75   80

Ile Lys Gln Glu Leu Glu Asp Gly Tyr Thr Thr Lys Pro Cys Lys Ser
                85   90   95

Glu Phe Phe Asp Pro Gly Asn Pro Ala Ser Lys Ser Thr Ser Glu Asn
            100   105   110

Thr Ser Val Thr Cys Leu Pro Phe Ser Ser Phe Glu Asn Asp Cys Ile
            115   120   125

Leu Glu Gln Thr Pro Val Ser Asp Cys Lys Arg Ala Ser Gly Leu Lys
        130   135   140

Ser Leu Val Gly Ser Ile Thr Glu Glu Thr Cys Val Val Asn Glu Asp
145   150   155   160

Ala Gly Ser Glu Gln Gly Ala Asn Thr Phe Ser Leu Lys Asp Pro Ser
            165   170   175

Gln Leu His Ser Gln Ser Pro Glu Ser Val Leu Leu Asp Gly Asp Val
            180   185   190

Lys Leu Ala Pro Cys Thr Asp Gln Val Pro Asn Asp Ser Phe Lys Gly
            195   200   205

Tyr Arg Asn His Ser Lys Leu Val Cys Arg Asp Asp Asp Glu Asn Tyr
    210   215   220

Cys Lys Tyr Tyr Lys Phe Ser Asp Lys Cys Lys Ser Tyr Arg Pro Leu
225   230   235   240

Ser Arg Val Gly Asn Arg Arg Ile Met Gln Ser Val Arg Ala Ile Ser
            245   250   255

Lys Leu Lys Cys Phe Glu Asp Thr Arg Thr Asp Gly Arg Leu Lys Ala
            260   265   270

Leu Tyr Arg Lys Arg Lys Leu Cys Tyr Gly Tyr Asn Pro Trp Lys Arg
            275   280   285

Glu Thr Ile His Arg Lys Arg Arg Leu Ser Asp Lys Gly Leu Val Val
    290   295   300

Asn Tyr Asp Gly Gly Leu Ser Ser Glu Ser Val Ser Asn Ser Pro Glu
305   310   315   320

Lys Gly Glu Ser Glu Asn Gly Asp Phe Ser Ala Ala Lys Ile Gly Leu
            325   330   335

Leu Ser Lys Asp Ser Arg Val Lys Phe Ser Ile Lys Ser Leu Arg Ile
            340   345   350

Pro Glu Leu Val Ile Glu Val Pro Glu Thr Ala Thr Val Gly Leu Leu
            355   360   365

Lys Arg Thr Val Lys Glu Ala Val Thr Ala Leu Leu Gly Gly Gly Ile
    370   375   380

Arg Ile Gly Val Leu Val Gln Gly Lys Lys Val Arg Asp Asp Asn Asn
385   390   395   400

Thr Leu Ser Gln Thr Gly Leu Ser Cys Arg Glu Asn Leu Gly Asn Leu

591

                    405   410   415

    Gly Phe Thr Leu Glu Pro Gly Leu Glu Thr Leu Pro Val Pro Leu Cys
            420   425   430

    Ser Glu Thr Pro Val Leu Ser Leu Pro Thr Asp Ser Thr Lys Leu Ser
            435   440   445

    Glu Arg Ser Ala Ala Ser Pro Ala Leu Glu Thr Gly Ile Pro Leu Pro
        450   455   460

    Pro Gln Asp Glu Asp Tyr Leu Ile Asn Leu Gly Asn Ser Val Glu Asn
    465   470   475   480

    Asn Asp Glu Leu Val Pro His Leu Ser Asp Ile Pro Ala Asp Glu Gln
                485   490   495

    Pro Ser Ser Asp Ser Arg Ala Leu Val Pro Val Leu Ala Leu Glu Ser
            500   505   510

    Asp Ala Leu Ala Leu Val Pro Val Asn Glu Lys Pro Lys Arg Thr Glu
            515   520   525

    Leu Ser Gln Arg Arg Thr Arg Arg Pro Phe Ser Val Thr Glu Val Glu
        530   535   540

    Ala Leu Val Ser Ala Val Glu Glu Val Gly Thr Gly Arg Trp Arg Asp
    545   550   555   560

    Val Lys Leu Arg Ser Phe Glu Asn Ala Ser His Arg Thr Tyr Val Asp
                565   570   575

    Leu Lys Asp Lys Trp Lys Thr Leu Val His Thr Ala Ser Ile Ser Pro
                580   585   590

    Gln Gln Arg Arg Gly Glu Pro Val Pro Gln Glu Leu Leu Asp Arg Val
            595   600   605

    Leu Gly Ala His Arg Tyr Trp Thr Gln His Gln Met Lys Gln Asn Gly
            610   615   620

    Lys His Gln Val Ala Thr Thr Met Val Val Glu Ala Gly Ser Ser Met
    625   630   635   640

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58

atg aga tca gga gaa tgt gat gaa gag gag att caa gca aag caa gaa
106
Met Arg Ser Gly Glu Cys Asp Glu Glu Glu Ile Gln Ala Lys Gln Glu
1   5   10   15

aga gat caa aat caa aat cat caa gta aac tta aac cac atg ttg caa
154
Arg Asp Gln Asn Gln Asn His Gln Val Asn Leu Asn His Met Leu Gln
            20   25   30

caa caa cag ccg agt tcg gta tca tct tca agg caa tgg act tca gct
202
Gln Gln Gln Pro Ser Ser Val Ser Ser Ser Arg Gln Trp Thr Ser Ala
            35   40   45

ttt agg aat cca aga atc gtt cga gtc tca aga aca ttc ggt ggc aaa
250
Phe Arg Asn Pro Arg Ile Val Arg Val Ser Arg Thr Phe Gly Gly Lys
        50   55   60

gac aga cac agc aaa gta tgt aca gtc cgt ggt ctt cga gac cgg agg
298
Asp Arg His Ser Lys Val Cys Thr Val Arg Gly Leu Arg Asp Arg Arg
65   70   75   80

ata agg ttg tcc gta cct aca gct att caa ctc tac gac ctt caa gat
346
Ile Arg Leu Ser Val Pro Thr Ala Ile Gln Leu Tyr Asp Leu Gln Asp
                85   90   95

cga tta ggg ctg agt cag cca agc aaa gtc att gat tgg tta ctc gaa
394
Arg Leu Gly Leu Ser Gln Pro Ser Lys Val Ile Asp Trp Leu Leu Glu
            100   105   110

gca gca aaa gat gac gta gac aag cta cct cct cta caa ttc cca cat
442
Ala Ala Lys Asp Asp Val Asp Lys Leu Pro Pro Leu Gln Phe Pro His
            115   120   125

gga ttt aac cag atg tat cca aat ctc atc ttc gga aac tcc ggg ttt
490
Gly Phe Asn Gln Met Tyr Pro Asn Leu Ile Phe Gly Asn Ser Gly Phe
        130   135   140

gga gaa tct cca tct tca act aca tca aca acg ttt cca gga acc aat
538
Gly Glu Ser Pro Ser Ser Thr Thr Ser Thr Thr Phe Pro Gly Thr Asn
145   150   155   160

ctc ggg ttc ttg gaa aat tgg gat ctt ggt ggt tct tca aga aca aga
586
Leu Gly Phe Leu Glu Asn Trp Asp Leu Gly Gly Ser Ser Arg Thr Arg
                165   170   175

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gca aga tta acc gat aca act acg acc caa aga gaa agt ttt gat ctt
634
Ala Arg Leu Thr Asp Thr Thr Thr Thr Gln Arg Glu Ser Phe Asp Leu
        180             185             190

gat aaa gga aaa tgg atc aaa aac gac gag aat agt aat caa gat cat
682
Asp Lys Gly Lys Trp Ile Lys Asn Asp Glu Asn Ser Asn Gln Asp His
        195             200             205

caa ggg ttt aac acc aat cat caa caa caa ttt cct ctg acc aat ccg
730
Gln Gly Phe Asn Thr Asn His Gln Gln Gln Phe Pro Leu Thr Asn Pro
    210             215             220

tac aac aac act tca gct tat tac aac ctt gga cat ctt caa caa tcg
778
Tyr Asn Asn Thr Ser Ala Tyr Tyr Asn Leu Gly His Leu Gln Gln Ser
225             230             235             240

tta gac caa tct ggt aat aac gtt act gtc gca ata tct aat gtt gct
826
Leu Asp Gln Ser Gly Asn Asn Val Thr Val Ala Ile Ser Asn Val Ala
        245             250             255

gct aat aat aac aat aat ctc aat ttg cat cct cct tcc tcg tct gcc
874
Ala Asn Asn Asn Asn Asn Leu Asn Leu His Pro Pro Ser Ser Ser Ala
        260             265             270

gga gat gga tct cag ctt ttt ttc ggt cct act cct ccg gca atg agc
922
Gly Asp Gly Ser Gln Leu Phe Phe Gly Pro Thr Pro Pro Ala Met Ser
        275             280             285

tct cta ttc ccg aca tac cct tcg ttt ctt gga gct tct cat cat cat
970
Ser Leu Phe Pro Thr Tyr Pro Ser Phe Leu Gly Ala Ser His His His
    290             295             300

cat gtc gtc gat gga gcc ggt cat ctt cag ctc ttt agc tcg aat tca
1018
His Val Val Asp Gly Ala Gly His Leu Gln Leu Phe Ser Ser Asn Ser
305             310             315             320

aat acc gca tcg cag caa cac atg atg ccg ggt aat acg agt ttg att
1066
Asn Thr Ala Ser Gln Gln His Met Met Pro Gly Asn Thr Ser Leu Ile
        325             330             335

aga cca ttt cat cat ttg atg agc tcg aat cat gat acg gat cat cat
1114
Arg Pro Phe His His Leu Met Ser Ser Asn His Asp Thr Asp His His
        340             345             350

agt agc gat aat gaa tca gat tct tga atgattttat atatctacac
1161
Ser Ser Asp Asn Glu Ser Asp Ser
        355             360
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594

tatacattga aaatgttata tgtatacgta ttcttctata ttttgatata tatgcgtatt
1221

gttggattgg tttatgtatc t
1242

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Met Arg Ser Gly Glu Cys Asp Glu Glu Glu Ile Gln Ala Lys Gln Glu
1   5   10   15

Arg Asp Gln Asn Gln Asn His Gln Val Asn Leu Asn His Met Leu Gln
            20   25   30

Gln Gln Gln Pro Ser Ser Val Ser Ser Ser Arg Gln Trp Thr Ser Ala
            35   40   45

Phe Arg Asn Pro Arg Ile Val Arg Val Ser Arg Thr Phe Gly Gly Lys
    50   55   60

Asp Arg His Ser Lys Val Cys Thr Val Arg Gly Leu Arg Asp Arg Arg
65   70   75   80

Ile Arg Leu Ser Val Pro Thr Ala Ile Gln Leu Tyr Asp Leu Gln Asp
                85   90   95

Arg Leu Gly Leu Ser Gln Pro Ser Lys Val Ile Asp Trp Leu Leu Glu
            100   105   110

Ala Ala Lys Asp Asp Val Asp Lys Leu Pro Pro Leu Gln Phe Pro His
            115   120   125

Gly Phe Asn Gln Met Tyr Pro Asn Leu Ile Phe Gly Asn Ser Gly Phe
    130   135   140

Gly Glu Ser Pro Ser Ser Thr Thr Ser Thr Thr Phe Pro Gly Thr Asn
145   150   155   160

Leu Gly Phe Leu Glu Asn Trp Asp Leu Gly Gly Ser Ser Arg Thr Arg
                165   170   175

Ala Arg Leu Thr Asp Thr Thr Thr Thr Gln Arg Glu Ser Phe Asp Leu
            180   ·   185   190

Asp Lys Gly Lys Trp Ile Lys Asn Asp Glu Asn Ser Asn Gln Asp His
            195   200   205

595

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Gln Gly Phe Asn Thr Asn His Gln Gln Gln Phe Pro Leu Thr Asn Pro
    210                 215                 220

Tyr Asn Asn Thr Ser Ala Tyr Tyr Asn Leu Gly His Leu Gln Gln Ser
225                 230                 235                 240

Leu Asp Gln Ser Gly Asn Asn Val Thr Val Ala Ile Ser Asn Val Ala
                245                 250                 255

Ala Asn Asn Asn Asn Asn Leu Asn Leu His Pro Pro Ser Ser Ser Ala
                260                 265                 270

Gly Asp Gly Ser Gln Leu Phe Phe Gly Pro Thr Pro Pro Ala Met Ser
            275                 280                 285

Ser Leu Phe Pro Thr Tyr Pro Ser Phe Leu Gly Ala Ser His His His
        290                 295                 300

His Val Val Asp Gly Ala Gly His Leu Gln Leu Phe Ser Ser Asn Ser
305                 310                 315                 320

Asn Thr Ala Ser Gln Gln His Met Met Pro Gly Asn Thr Ser Leu Ile
                325                 330                 335

Arg Pro Phe His His Leu Met Ser Ser Asn His Asp Thr Asp His His
            340                 345                 350

Ser Ser Asp Asn Glu Ser Asp Ser
        355                 360
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48
Met Ile Thr Glu Pro Ser Leu Thr Gly Ile Ser Gly Met Val Asn Arg
1               5                   10                  15

aac cgt tta tcc ggt tta ccc gat caa cct tct tcg cat agc ttc act
96
Asn Arg Leu Ser Gly Leu Pro Asp Gln Pro Ser Ser His Ser Phe Thr
            20                  25                  30

ccg gta aca cta tac gac ggt ttc aat tac aat ctc tcc tcc gat cat
144
Pro Val Thr Leu Tyr Asp Gly Phe Asn Tyr Asn Leu Ser Ser Asp His
            35                  40                  45
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ata aac acc gtt gta gca gcg ccg gag aat tca gtt ttt atc cgg gaa
192
Ile Asn Thr Val Val Ala Ala Pro Glu Asn Ser Val Phe Ile Arg Glu
    50   55   60

gaa gaa gaa gaa gag gat cca gct gat gat ttc gat ttc tct gac gct
240
Glu Glu Glu Glu Glu Asp Pro Ala Asp Asp Phe Asp Phe Ser Asp Ala
65   70   75   80

gtt tta gga tac att agt cag atg ttg aat gag gaa gac atg gat gat
288
Val Leu Gly Tyr Ile Ser Gln Met Leu Asn Glu Glu Asp Met Asp Asp
                85   90   95

aaa gtc tgc atg ctt caa gag tct cta gat ctc gaa gct gct gag aga
336
Lys Val Cys Met Leu Gln Glu Ser Leu Asp Leu Glu Ala Ala Glu Arg
            100   105   110

tcg tta tac gaa gct att ggt aag aag tat cct cca tct cca gaa cga
384
Ser Leu Tyr Glu Ala Ile Gly Lys Lys Tyr Pro Pro Ser Pro Glu Arg
        115   120   125

aac tta gct ttc gct gaa cga aac agc gag aat ctt gac cgt gtg gtt
432
Asn Leu Ala Phe Ala Glu Arg Asn Ser Glu Asn Leu Asp Arg Val Val
    130   135   140

cca gga aac tac act gga gga gat tgt ata ggt ttt ggg aac ggt gga
480
Pro Gly Asn Tyr Thr Gly Gly Asp Cys Ile Gly Phe Gly Asn Gly Gly
145   150   155   160

atc aag cct ttg agt agt ggt ttt act ttg gat ttt cga aat cct cag
528
Ile Lys Pro Leu Ser Ser Gly Phe Thr Leu Asp Phe Arg Asn Pro Gln
            165   170   175

agt tgt tct tcg att cta agt gtt cca caa tct aat ggt tta att act
576
Ser Cys Ser Ser Ile Leu Ser Val Pro Gln Ser Asn Gly Leu Ile Thr
            180   185   190

atc tac gga gat gga att gat gaa tcg tcg aag aac aat cgg gag aat
624
Ile Tyr Gly Asp Gly Ile Asp Glu Ser Ser Lys Asn Asn Arg Glu Asn
        195   200   205

cat caa tct gtt tgg ttg ttt agg cgt gag att gaa gaa gct aat agg
672
His Gln Ser Val Trp Leu Phe Arg Arg Glu Ile Glu Glu Ala Asn Arg
    210   215   220

ttt aat cct gaa gaa aac gag ttg att gtg aat ttc aga gag gag aat
720
Phe Asn Pro Glu Glu Asn Glu Leu Ile Val Asn Phe Arg Glu Glu Asn
225   230   235   240

597

tgt gtg agc aaa gca agg aag aac tct agc cgt gat gag att tgt gtt
768
Cys Val Ser Lys Ala Arg Lys Asn Ser Ser Arg Asp Glu Ile Cys Val
            245   250   255

gaa gaa gag agg agt agt aaa tta cct gca gtg ttt ggt gag gat att
816
Glu Glu Glu Arg Ser Ser Lys Leu Pro Ala Val Phe Gly Glu Asp Ile
            260   265   270

ttg agg tca gat gtt gta gat aag atc ttg gtt cat gta cca gga gga
864
Leu Arg Ser Asp Val Val Asp Lys Ile Leu Val His Val Pro Gly Gly
            275   280   285

gag agc atg aag gag ttt aat gcg ttg cgt gac gtt ttg aag aaa gga
912
Glu Ser Met Lys Glu Phe Asn Ala Leu Arg Asp Val Leu Lys Lys Gly
        290   295   300

gtg gag aag aag aaa gct tca gat gct caa ggt ggg aag aga cga gcc
960
Val Glu Lys Lys Lys Ala Ser Asp Ala Gln Gly Gly Lys Arg Arg Ala
305   310   315   320

aga gga aga gga cgt gga aga gga aga gga gga gga gga ggg caa aat
1008
Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Gly Gly Gly Gly Gln Asn
            325   330   335

ggg aaa aaa gaa gtt gtg gat ttg aga agt tta ttg ata cat tgt gct
1056
Gly Lys Lys Glu Val Val Asp Leu Arg Ser Leu Leu Ile His Cys Ala
            340   345   350

caa gct gtt gca gct gat gat cgt agg tgt gca ggt cag ttg tta aaa
1104
Gln Ala Val Ala Ala Asp Asp Arg Arg Cys Ala Gly Gln Leu Leu Lys
            355   360   365

cag ata aga ttg cat tct acg ccg ttt ggt gat ggg aat cag agg ttg
1152
Gln Ile Arg Leu His Ser Thr Pro Phe Gly Asp Gly Asn Gln Arg Leu
        370   375   380

gct cat tgt ttt gct aat ggt ctc gag gcg agg tta gcc ggt act gga
1200
Ala His Cys Phe Ala Asn Gly Leu Glu Ala Arg Leu Ala Gly Thr Gly
385   390   395   400

agc cag att tac aaa ggg att gtg agt aaa ccg aga tcc gct gca gct
1248
Ser Gln Ile Tyr Lys Gly Ile Val Ser Lys Pro Arg Ser Ala Ala Ala
            405   410   415

gtg ttg aag gct cac cag ctt ttt ctt gcg tgt tgt cct ttt aga aag
1296
Val Leu Lys Ala His Gln Leu Phe Leu Ala Cys Cys Pro Phe Arg Lys
            420   425   430

598

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ctc tct tat ttc ata act aat aag acg ata cgt gat ctt gtt ggg aac
1344
Leu Ser Tyr Phe Ile Thr Asn Lys Thr Ile Arg Asp Leu Val Gly Asn
        435                 440                 445

tct cag cgc gtt cat gtt att gat ttt ggt att ctt tac ggt ttc caa
1392
Ser Gln Arg Val His Val Ile Asp Phe Gly Ile Leu Tyr Gly Phe Gln
    450                 455                 460

tgg cca act ctt att cac cgg ttt tcg atg tat gga tca ccg aag gtt
1440
Trp Pro Thr Leu Ile His Arg Phe Ser Met Tyr Gly Ser Pro Lys Val
465                 470                 475                 480

agg atc acc ggg att gag ttt ccg cag ccc ggg ttt cgt ccg gca cag
1488
Arg Ile Thr Gly Ile Glu Phe Pro Gln Pro Gly Phe Arg Pro Ala Gln
                485                 490                 495

cgg gtt gaa gaa act ggt caa agg tta gca gcg tat gcc aaa ctc ttt
1536
Arg Val Glu Glu Thr Gly Gln Arg Leu Ala Ala Tyr Ala Lys Leu Phe
            500                 505                 510

ggg gtg cca ttt gag tat aaa gca att gct aag aag tgg gat gca att
1584
Gly Val Pro Phe Glu Tyr Lys Ala Ile Ala Lys Lys Trp Asp Ala Ile
        515                 520                 525

caa ctt gaa gat ctt gat atc gac agg gat gag att act gtt gtt aat
1632
Gln Leu Glu Asp Leu Asp Ile Asp Arg Asp Glu Ile Thr Val Val Asn
    530                 535                 540

tgc ctg tac cgg gct gag aat ttg cat gat gag tca gtc aaa gta gaa
1680
Cys Leu Tyr Arg Ala Glu Asn Leu His Asp Glu Ser Val Lys Val Glu
545                 550                 555                 560

agt tgt aga gac act gtt ctc aat ttg atc ggg aag atc aat cct gat
1728
Ser Cys Arg Asp Thr Val Leu Asn Leu Ile Gly Lys Ile Asn Pro Asp
                565                 570                 575

ctc ttt gtc ttt ggc att gtg aat ggt gca tac aac gca ccg ttt ttc
1776
Leu Phe Val Phe Gly Ile Val Asn Gly Ala Tyr Asn Ala Pro Phe Phe
                580                 585                 590

gta aca cgg ttt cgc gaa gct cta ttt cat ttc tcc tcg att ttt gac
1824
Val Thr Arg Phe Arg Glu Ala Leu Phe His Phe Ser Ser Ile Phe Asp
        595                 600                 605

atg ctt gag aca att gtg cca cga gaa gac gaa gag agg atg ttc ctt
1872
Met Leu Glu Thr Ile Val Pro Arg Glu Asp Glu Glu Arg Met Phe Leu
    610                 615                 620
```

599

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gag atg gag gtc ttt ggg aga gag gca ctg aat gtg att gct tgc gaa
1920
Glu Met Glu Val Phe Gly Arg Glu Ala Leu Asn Val Ile Ala Cys Glu
625                 630             635                 640

ggt tgg gaa aga gtg gag agg cct gag aca tac aag cag tgg cac gta
1968
Gly Trp Glu Arg Val Glu Arg Pro Glu Thr Tyr Lys Gln Trp His Val
            645             650                 655

cgg gct atg agg tca ggg ttg gtg cag gtt cca ttt gac cca agc att
2016
Arg Ala Met Arg Ser Gly Leu Val Gln Val Pro Phe Asp Pro Ser Ile
            660             665                 670

atg aag aca tcg ctg cat aag gtc cac aca ttc tac cac aag gat ttt
2064
Met Lys Thr Ser Leu His Lys Val His Thr Phe Tyr His Lys Asp Phe
        675             680                 685

gtg atc gat caa gat aac cgg tgg ctc ttg caa ggc tgg aag gga aga
2112
Val Ile Asp Gln Asp Asn Arg Trp Leu Leu Gln Gly Trp Lys Gly Arg
    690             695         --    700

act gtc atg gct ctt tct gtt tgg aaa cca gag tcc aag gct tga
2157
Thr Val Met Ala Leu Ser Val Trp Lys Pro Glu Ser Lys Ala
705             710             715
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Asn Arg Leu Ser Gly Leu Pro Asp Gln Pro Ser Ser His Ser Phe Thr
            20              25              30

Pro Val Thr Leu Tyr Asp Gly Phe Asn Tyr Asn Leu Ser Ser Asp His
        35              40              45

Ile Asn Thr Val Val Ala Ala Pro Glu Asn Ser Val Phe Ile Arg Glu
    50              55              60

Glu Glu Glu Glu Glu Asp Pro Ala Asp Asp Phe Asp Phe Ser Asp Ala
65              70              75              80

Val Leu Gly Tyr Ile Ser Gln Met Leu Asn Glu Glu Asp Met Asp Asp
            85              90              95

Lys Val Cys Met Leu Gln Glu Ser Leu Asp Leu Glu Ala Ala Glu Arg
            100             105             110
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Ser Leu Tyr Glu Ala Ile Gly Lys Lys Tyr Pro Pro Ser Pro Glu Arg
        115   120   125

Asn Leu Ala Phe Ala Glu Arg Asn Ser Glu Asn Leu Asp Arg Val Val
    130   135   140

Pro Gly Asn Tyr Thr Gly Gly Asp Cys Ile Gly Phe Gly Asn Gly Gly
145   150   155   160

Ile Lys Pro Leu Ser Ser Gly Phe Thr Leu Asp Phe Arg Asn Pro Gln
                165   170   175

Ser Cys Ser Ser Ile Leu Ser Val Pro Gln Ser Asn Gly Leu Ile Thr
            180   185   190

Ile Tyr Gly Asp Gly Ile Asp Glu Ser Ser Lys Asn Asn Arg Glu Asn
        195   200   205

His Gln Ser Val Trp Leu Phe Arg Arg Glu Ile Glu Glu Ala Asn Arg
    210   215   220

Phe Asn Pro Glu Glu Asn Glu Leu Ile Val Asn Phe Arg Glu Glu Asn
225   230   235   240

Cys Val Ser Lys Ala Arg Lys Asn Ser Ser Arg Asp Glu Ile Cys Val
                245   250   255

Glu Glu Glu Arg Ser Ser Lys Leu Pro Ala Val Phe Gly Glu Asp Ile
            260   265   270

Leu Arg Ser Asp Val Val Asp Lys Ile Leu Val His Val Pro Gly Gly
        275   280   285

Glu Ser Met Lys Glu Phe Asn Ala Leu Arg Asp Val Leu Lys Lys Gly
    290   295   300

Val Glu Lys Lys Lys Ala Ser Asp Ala Gln Gly Gly Lys Arg Arg Ala
305   310   315   320

Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Gly Gly Gly Gln Asn
                325   330   335

Gly Lys Lys Glu Val Val Asp Leu Arg Ser Leu Leu Ile His Cys Ala
            340   345   350

601

Gln Ala Val Ala Ala Asp Asp Arg Arg Cys Ala Gly Gln Leu Leu Lys
        355   360   365

Gln Ile Arg Leu His Ser Thr Pro Phe Gly Asp Gly Asn Gln Arg Leu
    370   375   380

Ala His Cys Phe Ala Asn Gly Leu Glu Ala Arg Leu Ala Gly Thr Gly
385   390   395   400

Ser Gln Ile Tyr Lys Gly Ile Val Ser Lys Pro Arg Ser Ala Ala Ala
            405   410   415

Val Leu Lys Ala His Gln Leu Phe Leu Ala Cys Cys Pro Phe Arg Lys
        420   425   430

Leu Ser Tyr Phe Ile Thr Asn Lys Thr Ile Arg Asp Leu Val Gly Asn
        435   440   445

Ser Gln Arg Val His Val Ile Asp Phe Gly Ile Leu Tyr Gly Phe Gln
    450   455   460

Trp Pro Thr Leu Ile His Arg Phe Ser Met Tyr Gly Ser Pro Lys Val
465   470   475   480

Arg Ile Thr Gly Ile Glu Phe Pro Gln Pro Gly Phe Arg Pro Ala Gln
            485   490   495

Arg Val Glu Glu Thr Gly Gln Arg Leu Ala Ala Tyr Ala Lys Leu Phe
        500   505   510

Gly Val Pro Phe Glu Tyr Lys Ala Ile Ala Lys Lys Trp Asp Ala Ile
        515   520   525

Gln Leu Glu Asp Leu Asp Ile Asp Arg Asp Glu Ile Thr Val Val Asn
    530   535   540

Cys Leu Tyr Arg Ala Glu Asn Leu His Asp Glu Ser Val Lys Val Glu
545   550   555   560

Ser Cys Arg Asp Thr Val Leu Asn Leu Ile Gly Lys Ile Asn·Pro Asp
            565   570   575

Leu Phe Val Phe Gly Ile Val Asn Gly Ala Tyr Asn Ala Pro Phe Phe
        580   585   590

Val Thr Arg Phe Arg Glu Ala Leu Phe His Phe Ser Ser Ile Phe Asp

602

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        595                      600                      605


Met Leu Glu Thr Ile Val Pro Arg Glu Asp Glu Glu Arg Met Phe Leu
        610                      615              620


Glu Met Glu Val Phe Gly Arg Glu Ala Leu Asn Val Ile Ala Cys Glu
625                      630              635                      640


Gly Trp Glu Arg Val Glu Arg Pro Glu Thr Tyr Lys Gln Trp His Val
                645                      650              655


Arg Ala Met Arg Ser Gly Leu Val Gln Val Pro Phe Asp Pro Ser Ile
                660                      665              670


Met Lys Thr Ser Leu His Lys Val His Thr Phe Tyr His Lys Asp Phe
        675                      680              685


Val Ile Asp Gln Asp Asn Arg Trp Leu Leu Gln Gly Trp Lys Gly Arg
    690                      695              700


Thr Val Met Ala Leu Ser Val Trp Lys Pro Glu Ser Lys Ala
705                      710              715
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Met Arg Lys Lys Val Ser Ser Ser Gly Asp Glu Gly Asn Asn Glu Tyr
1              5                    10                    15


aag aaa ggt ttg tgg aca gta gaa gaa gac aaa atc ctc atg gat tat
96
Lys Lys Gly Leu Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr
            20                    25                    30


gtc aaa gct cat ggc aaa ggt cac tgg aat cgt att gcc aaa aag act
144
Val Lys Ala His Gly Lys Gly His Trp Asn Arg Ile Ala Lys Lys Thr
        35                    40                    45


ggt tta aag aga tgt gga aag agt tgt aga ttg agg tgg atg aat tat
192
Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr
    50                    55                    60


ctc agc cct aat gtg aaa aga ggc aat ttc acc gag caa gaa gag gat
240
Leu Ser Pro Asn Val Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Asp
65                    70                    75                    80
```

```
ctt atc att agg ctc cac aag ttg ctt ggt aat agg tgg tct tta att
288
Leu Ile Ile Arg Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile
            85                  90                  95

gct aaa aga gtg ccg ggt cga acg gat aat caa gtg aag aac tat tgg
336
Ala Lys Arg Val Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp
            100                 105                 110

aac acg cat ctt agt aag aaa ctc gga atc aaa gat cag aaa acc aaa
384
Asn Thr His Leu Ser Lys Lys Leu Gly Ile Lys Asp Gln Lys Thr Lys
            115                 120                 125

cag agc aat ggt gat att gtt tat caa atc aat ctc ccg aat cct acc
432
Gln Ser Asn Gly Asp Ile Val Tyr Gln Ile Asn Leu Pro Asn Pro Thr
        130                 135                 140

gaa aca tca gaa gaa acg aaa atc tcg aat att gtc gat aac aat aat
480
Glu Thr Ser Glu Glu Thr Lys Ile Ser Asn Ile Val Asp Asn Asn Asn
145                 150                 155                 160

atc ctc gga gat gaa att caa gaa gat cat caa gga agt aac tac ttg
528
Ile Leu Gly Asp Glu Ile Gln Glu Asp His Gln Gly Ser Asn Tyr Leu
            165                 170                 175

agt tca ctt tgg gtt cat gag gat gag ttt gag ctt agc aca ctc acc
576
Ser Ser Leu Trp Val His Glu Asp Glu Phe Glu Leu Ser Thr Leu Thr
            180                 185                 190

aac atg atg gac ttt ata gat gga cac tgt ttt tga
612
Asn Met Met Asp Phe Ile Asp Gly His Cys Phe
            195                 200


<210>  338 <211>  203 <212>  PRT <213>  Arabidopsis thaliana  <400>
338

Met Arg Lys Lys Val Ser Ser Ser Gly Asp Glu Gly Asn Asn Glu Tyr
1               5                   10                  15


Lys Lys Gly Leu Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr
            20                  25                  30


Val Lys Ala His Gly Lys Gly His Trp Asn Arg Ile Ala Lys Lys Thr
            35                  40                  45


Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr
    50                  55                  60


Leu Ser Pro Asn Val Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Asp
```

604

```
65                      70              75                  80
```

```
Leu Ile Ile Arg Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile
                85                  90                  95
```

```
Ala Lys Arg Val Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp
                100                 105                 110
```

```
Asn Thr His Leu Ser Lys Lys Leu Gly Ile Lys Asp Gln Lys Thr Lys
            115                 120                 125
```

```
Gln Ser Asn Gly Asp Ile Val Tyr Gln Ile Asn Leu Pro Asn Pro Thr
        130                 135                 140
```

```
Glu Thr Ser Glu Glu Thr Lys Ile Ser Asn Ile Val Asp Asn Asn Asn
145                 150                 155                 160
```

```
Ile Leu Gly Asp Glu Ile Gln Glu Asp His Gln Gly Ser Asn Tyr Leu
                165                 170                 175
```

```
Ser Ser Leu Trp Val His Glu Asp Glu Phe Glu Leu Ser Thr Leu Thr
                180                 185                 190
```

```
Asn Met Met Asp Phe Ile Asp Gly His Cys Phe
            195                 200
```

```
<210>  339 <211>  705 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (1)..(705) <223>  G715
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```
<400>  339
atg gat acc aac aac cag caa cca cct ccc tcc gcc gcc gga atc cct
48
Met Asp Thr Asn Asn Gln Gln Pro Pro Pro Ser Ala Ala Gly Ile Pro
1               5               10                  15
```

```
cct cca cca cct gga acc acc atc tcc gcc gca gga gga gga gct tct
96
Pro Pro Pro Pro Gly Thr Thr Ile Ser Ala Ala Gly Gly Gly Ala Ser
            20                  25                  30
```

```
tac cac cac ctt ctc caa caa caa caa caa cag ctc caa cta ttc tgg
144
Tyr His His Leu Leu Gln Gln Gln Gln Gln Gln Leu Gln Leu Phe Trp
            35                  40                  45
```

```
acc tac caa cgc caa gag atc gaa caa gtt aac gat ttc aaa aac cat
192
Thr Tyr Gln Arg Gln Glu Ile Glu Gln Val Asn Asp Phe Lys Asn His
        50                  55                  60
```

```
cag ctt cca cta gct agg ata aaa aag atc atg aaa gcc gat gaa gat
240
```

Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp
65   70   75   80

gtt cgt atg atc tcc gca gaa gca ccg att ctc ttc gcg aaa gct tgt
288
Val Arg Met Ile Ser Ala Glu Ala Pro Ile Leu Phe Ala Lys Ala Cys
                85   90   95

gag ctt ttc att ctc gag ctc acg atc aga tct tgg ctt cac gct gag
336
Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg Ser Trp Leu His Ala Glu
            100   105   110

gag aat aaa cgt cgt acg ctt cag aaa aac gat atc gct gct gcg att
384
Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala Ala Ile
        115   120   125

act agg act gat atc ttc gat ttc ctt gtt gat att gtt cct aga gat
432
Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro Arg Asp
    130   135   140

gag att aag gac gaa gcc gca gtc ctc ggt ggt gga atg gtg gtg gct
480
Glu Ile Lys Asp Glu Ala Ala Val Leu Gly Gly Gly Met Val Val Ala
145   150   155   160

cct acc gcg agc ggc gtg cct tac tat tat ccg ccg atg gga caa cca
528
Pro Thr Ala Ser Gly Val Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro
                165   170   175

gct ggt cct gga ggg atg atg att ggg aga cca gct atg gat ccg aat
576
Ala Gly Pro Gly Gly Met Met Ile Gly Arg Pro Ala Met Asp Pro Asn
            180   185   190

ggt gtt tat gtc cag cct ccg tct cag gcg tgg cag agt gtt tgg cag
624
Gly Val Tyr Val Gln Pro Pro Ser Gln Ala Trp Gln Ser Val Trp Gln
        195   200   205

act tcg acg ggg acg gga gat gat gtc tct tat ggt agt ggt gga agt
672
Thr Ser Thr Gly Thr Gly Asp Asp Val Ser Tyr Gly Ser Gly Gly Ser
    210   215   220

tcc ggt caa ggg aat ctc gac ggc caa ggg taa
705
Ser Gly Gln Gly Asn Leu Asp Gly Gln Gly
225   230

<210> 340 <211> 234 <212> PRT <213> Arabidopsis thaliana <400>
340

Met Asp Thr Asn Asn Gln Gln Pro Pro Pro Ser Ala Ala Gly Ile Pro
1   5   10   15

```
Pro Pro Pro Pro Gly Thr Thr Ile Ser Ala Ala Gly Gly Gly Ala Ser
        20                      25                30

Tyr His His Leu Leu Gln Gln Gln Gln Gln Gln Leu Gln Leu Phe Trp
        35                  40                  45

Thr Tyr Gln Arg Gln Glu Ile Glu Gln Val Asn Asp Phe Lys Asn His
    50                  55                  60

Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp
65                  70                  75                  80

Val Arg Met Ile Ser Ala Glu Ala Pro Ile Leu Phe Ala Lys Ala Cys
                85                  90                  95

Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg Ser Trp Leu His Ala Glu
            100                 105                 110

Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala Ala Ile
        115                 120                 125

Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro Arg Asp
    130                 135                 140

Glu Ile Lys Asp Glu Ala Ala Val Leu Gly Gly Gly Met Val Val Ala
145                 150                 155                 160

Pro Thr Ala Ser Gly Val Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro
                165                 170                 175

Ala Gly Pro Gly Gly Met Met Ile Gly Arg Pro Ala Met Asp Pro Asn
            180                 185                 190

Gly Val Tyr Val Gln Pro Pro Ser Gln Ala Trp Gln Ser Val Trp Gln
        195                 200                 205

Thr Ser Thr Gly Thr Gly Asp Asp Val Ser Tyr Gly Ser Gly Gly Ser
    210                 215                 220

Ser Gly Gln Gly Asn Leu Asp Gly Gln Gly
225                 230
```

<210> 341 <211> 1824 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (521)..(1549) <223> G761

<400> 341

ggggccgacc ggccgcccgg gcaggtctag gttcaaaagg actcacaaga gagagatagt
60

atgattgata gggaaagaga gagagatgaa agaaagtaaa atatataata gattattagg
120

acacgagtgt catcttttga tttgtgtctt gtgtgctctc tctttcttct cttcctcgaa
180

tgatcatctt tatataaccc tactctcttt ctcttttccc attctttcat atcattctcc
240

ctttctctct cgggatctga tctctctttc cagtaaccta ttcccgagga gcactgtcaa
300

atcttgtcca ctctttgatc ttatctcgat ctctttctct ttctagtctt gtgtagtctt
360

caaacttgtg atgttatcta tatagtaatc acgagagaga atcatacaat agctgaaaca
420

taaagctttc ttagaagctt taaaaaggtc tcatctggat tatcctgttt aatttctaga
480

gtttcttcag gcagattatt aaccgatcaa gaagacaaac atg aat tca ttt tcc
535
                                                Met Asn Ser Phe Ser
                                                1   5

cac gtc cct ccg ggt ttt aga ttt cac ccg aca gat gaa gaa ctt gta
583
His Val Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val
            10   15   20

gac tac tac ctg agg aaa aaa gtc gca tcg aag aga ata gaa att gat
631
Asp Tyr Tyr Leu Arg Lys Lys Val Ala Ser Lys Arg Ile Glu Ile Asp
        25   30   35

ttc ata aag gac att gat ctt tac aag att gag cca tgg gac ctt caa
679
Phe Ile Lys Asp Ile Asp Leu Tyr Lys Ile Glu Pro Trp Asp Leu Gln
        40   45   50

gag ttg tgc aaa att ggg cat gaa gag cag agt gat tgg tac ttc ttt
727
Glu Leu Cys Lys Ile Gly His Glu Glu Gln Ser Asp Trp Tyr Phe Phe
        55   60   65

agc cat aaa gac aag aag tat ccc aca ggg act cga acc aat aga gca
775
Ser His Lys Asp Lys Lys Tyr Pro Thr Gly Thr Arg Thr Asn Arg Ala
70   75   80   85

aca aaa gca ggg ttt tgg aaa gcc acc gga aga gat aag gct atc tat
823
Thr Lys Ala Gly Phe Trp Lys Ala Thr Gly Arg Asp Lys Ala Ile Tyr
            90   95   100

ttg agg cat agt cta att ggc atg agg aaa aca ctt gtg ttt tac aag
871

608

```
Leu Arg His Ser Leu Ile Gly Met Arg Lys Thr Leu Val Phe Tyr Lys
        105                     110                 115


gga aga gcc cca aat gga caa aag tct gat tgg atc atg cac gaa tac
919
Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp Ile Met His Glu Tyr
        120                     125                 130


cgc tta gaa acc gat gaa aac gga act cct cag gaa gaa gga tgg gtt
967
Arg Leu Glu Thr Asp Glu Asn Gly Thr Pro Gln Glu Glu Gly Trp Val
    135                     140                 145


gtg tgt agg gtt ttc aag aag aga ttg gct gca gtt aga cga atg gga
1015
Val Cys Arg Val Phe Lys Lys Arg Leu Ala Ala Val Arg Arg Met Gly
150                 155                     160                 165


gat tac gac tca tcc cct tca cat tgg tac gat gat caa ctt tct ttt
1063
Asp Tyr Asp Ser Ser Pro Ser His Trp Tyr Asp Asp Gln Leu Ser Phe
                170                     175                 180


atg gcc tcc gag ctc gag aca aac ggt caa cga cgg att ctc ccc aat
1111
Met Ala Ser Glu Leu Glu Thr Asn Gly Gln Arg Arg Ile Leu Pro Asn
                185                     190                 195


cat cat cag cag cag cag cac gag cac caa caa cat atg cca tat ggc
1159
His His Gln Gln Gln Gln His Glu His Gln Gln His Met Pro Tyr Gly
            200                     205                 210


ctc aat gca tct gct tac gct ctc aac aac cct aac ttg caa tgc aag
1207
Leu Asn Ala Ser Ala Tyr Ala Leu Asn Asn Pro Asn Leu Gln Cys Lys
        215                     220                 225


caa gag cta gaa cta cac tac aac cac ctg caa tca aat atc gcg cat
1255
Gln Glu Leu Glu Leu His Tyr Asn His Leu Gln Ser Asn Ile Ala His
230                 235                     240                 245


gag gaa caa ttg aat caa gga aat cag aac ttc agc tct cta tac atg
1303
Glu Glu Gln Leu Asn Gln Gly Asn Gln Asn Phe Ser Ser Leu Tyr Met
                250                     255                 260


aac agc ggc aac gag caa gtg atg gac caa gtc aca gac tgg aga gtt
1351
Asn Ser Gly Asn Glu Gln Val Met Asp Gln Val Thr Asp Trp Arg Val
                265                     270                 275


ctc gat aaa ttt gtt gct tct cag cta agc aac gag gag gct gcc aca
1399
Leu Asp Lys Phe Val Ala Ser Gln Leu Ser Asn Glu Glu Ala Ala Thr
            280                     285                 290


gct tct gca tct ata cag aat aat gcc aag gac aca agc aat gct gag
1447
Ala Ser Ala Ser Ile Gln Asn Asn Ala Lys Asp Thr Ser Asn Ala Glu
```

```
      295                   300                   305

tac caa gtt gat gaa gaa aaa gat ccg aaa agg gct tca gac atg gga
1495
Tyr Gln Val Asp Glu Glu Lys Asp Pro Lys Arg Ala Ser Asp Met Gly
310                   315                   320                   325

gaa gaa tat act gct tct act tct tcg agt tgt cag att gat cta tgg
1543
Glu Glu Tyr Thr Ala Ser Thr Ser Ser Ser Cys Gln Ile Asp Leu Trp
                330                   335                   340

aag tga gctgaaagag aagacatata aatgcatata tacatatata tatatacgta
1599
Lys


cacacgaaca ctaatcaagt gtagatgatg atgatggtac agatttatat ttgctttgat
1659


tgattcttac tacattattg aacttatgtc atatgcatat atacattgcg tatctatgca
1719


tatttatact tgtactcaat atgattaacc atatataaac tctaatctaa atgtaactcc
1779


aatatttttt aaatagacaa ttgtctcttc ttattagaaa aaaaa
1824


<210> 342 <211> 342 <212> PRT <213> Arabidopsis thaliana <400>
342

Met Asn Ser Phe Ser His Val Pro Pro Gly Phe Arg Phe His Pro Thr
1               5                   10                  15


Asp Glu Glu Leu Val Asp Tyr Tyr Leu Arg Lys Lys Val Ala Ser Lys
                20                  25                  30


Arg Ile Glu Ile Asp Phe Ile Lys Asp Ile Asp Leu Tyr Lys Ile Glu
        35                  40                  45


Pro Trp Asp Leu Gln Glu Leu Cys Lys Ile Gly His Glu Glu Gln Ser
    50                  55                  60


Asp Trp Tyr Phe Phe Ser His Lys Asp Lys Lys Tyr Pro Thr Gly Thr
65                  70                  75                  80


Arg Thr Asn Arg Ala Thr Lys Ala Gly Phe Trp Lys Ala Thr Gly Arg
                85                  90                  95


Asp Lys Ala Ile Tyr Leu Arg His Ser Leu Ile Gly Met Arg Lys Thr
            100                 105                 110
```

```
Leu Val Phe Tyr Lys Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp
        115                 120             125

Ile Met His Glu Tyr Arg Leu Glu Thr Asp Glu Asn Gly Thr Pro Gln
    130                 135             140

Glu Glu Gly Trp Val Val Cys Arg Val Phe Lys Lys Arg Leu Ala Ala
145                 150             155                 160

Val Arg Arg Met Gly Asp Tyr Asp Ser Ser Pro Ser His Trp Tyr Asp
            165             170             175

Asp Gln Leu Ser Phe Met Ala Ser Glu Leu Glu Thr Asn Gly Gln Arg
        180             185             190

Arg Ile Leu Pro Asn His His Gln Gln Gln Gln His Glu His Gln Gln
        195             200             205

His Met Pro Tyr Gly Leu Asn Ala Ser Ala Tyr Ala Leu Asn Asn Pro
    210             215             220

Asn Leu Gln Cys Lys Gln Glu Leu Glu Leu His Tyr Asn His Leu Gln
225             230             235                 240

Ser Asn Ile Ala His Glu Glu Gln Leu Asn Gln Gly Asn Gln Asn Phe
            245             250             255

Ser Ser Leu Tyr Met Asn Ser Gly Asn Glu Gln Val Met Asp Gln Val
            260             265             270

Thr Asp Trp Arg Val Leu Asp Lys Phe Val Ala Ser Gln Leu Ser Asn
        275             280             285

Glu Glu Ala Ala Thr Ala Ser Ala Ser Ile Gln Asn Asn Ala Lys Asp
    290             295             300

Thr Ser Asn Ala Glu Tyr Gln Val Asp Glu Glu Lys Asp Pro Lys Arg
305             310             315                 320

Ala Ser Asp Met Gly Glu Glu Tyr Thr Ala Ser Thr Ser Ser Ser Cys
            325             330             335

Gln Ile Asp Leu Trp Lys
            340
```

<210> 343 <211> 1008 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (110)..(790) <223> G792

<400> 343
tctttttttct tccgttttttc cacacattgt ctctaccttt cccttttttca gatttgaccc
60

tttgttttca aaagaaacga tttttagtag ccgccgggga atcaggaga atg gtg tct
118
                                                            Met Val Ser
                                                            1

ccg gag aat acg aac tgg.ctt agt gat tac cct ttg att gaa ggt gct
166
Pro Glu Asn Thr Asn Trp Leu Ser Asp Tyr Pro Leu Ile Glu Gly Ala
    5   10   15

ttc tct gat cag aac ccc act ttc cct tgg cag ata gat ggc tca gct
214
Phe Ser Asp Gln Asn Pro Thr Phe Pro Trp Gln Ile Asp Gly Ser Ala
20   25   30   35

act gtc agt gtt gaa gtg gat ggc ttc ctt tgt gat gca gat gtg atc
262
Thr Val Ser Val Glu Val Asp Gly Phe Leu Cys Asp Ala Asp Val Ile
            40   45   50

aaa gaa cca agt tca agg aag agg atc aaa act gaa tct tgc act ggt
310
Lys Glu Pro Ser Ser Arg Lys Arg Ile Lys Thr Glu Ser Cys Thr Gly
            55   60   65

tct aac tcg aaa gct tgt agg gag aaa caa aga cgt gat aga cta aat
358
Ser Asn Ser Lys Ala Cys Arg Glu Lys Gln Arg Arg Asp Arg Leu Asn
        70   75   80

gac aag ttt acg gag ttg agt tcc gta ttg gaa cct ggg aga act cca
406
Asp Lys Phe Thr Glu Leu Ser Ser Val Leu Glu Pro Gly Arg Thr Pro
    85   90   95

aaa aca gac aag gtt gct att atc aat gat gca att cgc atg gtg aat
454
Lys Thr Asp Lys Val Ala Ile Ile Asn Asp Ala Ile Arg Met Val Asn
100   105   110   115

caa gca aga gat gaa gcg cag aaa cta aag gac ttg aac tca agc ctc
502
Gln Ala Arg Asp Glu Ala Gln Lys Leu Lys Asp Leu Asn Ser Ser Leu
                120   125   130

cag gag aaa atc aag gag ttg aag gat gag aag aac gag ctg cgt gat
550
Gln Glu Lys Ile Lys Glu Leu Lys Asp Glu Lys Asn Glu Leu Arg Asp
            135   140   145

gag aaa cag aag ctt aag gtc gag aag gag aga atc gat cag caa ctg
598
Glu Lys Gln Lys Leu Lys Val Glu Lys Glu Arg Ile Asp Gln Gln Leu
            150   155   160

612

aaa gct att aag aca cag cct cag cct caa cct tgt ttc tta cca aat
646
Lys Ala Ile Lys Thr Gln Pro Gln Pro Gln Pro Cys Phe Leu Pro Asn
       165   170   175

ccg caa aca ctc tct caa gct caa gct cct gga agc aag ctt gtc cct
694
Pro Gln Thr Leu Ser Gln Ala Gln Ala Pro Gly Ser Lys Leu Val Pro
180   185   190   195

ttc aca act tat ccc ggc ttt gca atg tgg caa ttc atg cct cct gct
742
Phe Thr Thr Tyr Pro Gly Phe Ala Met Trp Gln Phe Met Pro Pro Ala
             200   205   210

gct gtt gat acc tca cag gac cat gtc ctt cgt cct cca gtt gct taa
790
Ala Val Asp Thr Ser Gln Asp His Val Leu Arg Pro Pro Val Ala
             215   220   225

agctgctgct tctctctact actattaacg gttctgtaag attacttctt acgcgctttt
850

ttctgatgta atgattctca cattctgtga ttggtgacat agtccactgc aacttaaaat
910

gtaaaattga ataagcttg cactaaaaat caaatctcat tgtgcaaaaa gttggataat
970

ttggaaatca ttgttttaca aaaaaaaaac ccccgag
1008

<210> 344 <211> 226 <212> PRT <213> Arabidopsis thaliana <400>
344

Met Val Ser Pro Glu Asn Thr Asn Trp Leu Ser Asp Tyr Pro Leu Ile
1   5   10   15

Glu Gly Ala Phe Ser Asp Gln Asn Pro Thr Phe Pro Trp Gln Ile Asp
          20   25   30

Gly Ser Ala Thr Val Ser Val Glu Val Asp Gly Phe Leu Cys Asp Ala
          35   40   45

Asp Val Ile Lys Glu Pro Ser Ser Arg Lys Arg Ile Lys Thr Glu Ser
     50   55   60

Cys Thr Gly Ser Asn Ser Lys Ala Cys Arg Glu Lys Gln Arg Arg Asp
65   70   75   80

Arg Leu Asn Asp Lys Phe Thr Glu Leu Ser Ser Val Leu Glu Pro Gly
               85   90   95

Arg Thr Pro Lys Thr Asp Lys Val Ala Ile Ile Asn Asp Ala Ile Arg
            100   105   110

Met Val Asn Gln Ala Arg Asp Glu Ala Gln Lys Leu Lys Asp Leu Asn
            115   120   125   .

Ser Ser Leu Gln Glu Lys Ile Lys Glu Leu Lys Asp Glu Lys Asn Glu
    130   135   140

Leu Arg Asp Glu Lys Gln Lys Leu Lys Val Glu Lys Glu Arg Ile Asp
145   150   155   160

Gln Gln Leu Lys Ala Ile Lys Thr Gln Pro Gln Pro Gln Pro Cys Phe
                165   170   175

Leu Pro Asn Pro Gln Thr Leu Ser Gln Ala Gln Ala Pro Gly Ser Lys
            180   185   190

Leu Val Pro Phe Thr Thr Tyr Pro Gly Phe Ala Met Trp Gln Phe Met
            195   200   205
                                              '

Pro Pro Ala Ala Val Asp Thr Ser Gln Asp His Val Leu Arg Pro Pro
    210   215   220

Val Ala
225

<210> 345 <211> 2079 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (92)..(1987) <223> G831

 <400> 345
ttctttcatc gttgtgtcta ttataaatat atgtcaattt ggtttctaaa aaattctacc
60

attgattgat tgattttttt ttctttaaga g atg aat tta ttt aca aga atc
112
                                  Met Asn Leu Phe Thr Arg Ile
                                  1   5

tca tct cgg act aag aag gcc aat ctt tac tac gta acc cta gtt gct
160
Ser Ser Arg Thr Lys Lys Ala Asn Leu Tyr Tyr Val Thr Leu Val Ala
        10   15   20

ctt ctc tgc atc gct agc tac ctt ctc ggt att tgg caa aac acg gcg
208
Leu Leu Cys Ile Ala Ser Tyr Leu Leu Gly Ile Trp Gln Asn Thr Ala
        25   30   35

gtt aat cca cgc gcc gcc ttc gat gat tca gac ggt aca ccg tgc gag
256
Val Asn Pro Arg Ala Ala Phe Asp Asp Ser Asp Gly Thr Pro Cys Glu

614

```
40                    45                    50                    55

gga ttc acc aga cct aat tct acg aaa gat ctc gac ttc gac gcg cat
304
Gly Phe Thr Arg Pro Asn Ser Thr Lys Asp Leu Asp Phe Asp Ala His
            60                    65                    70

cac aac att caa gat cca cct ccg gtg acg gaa acc gcc gtt agt ttc
352
His Asn Ile Gln Asp Pro Pro Pro Val Thr Glu Thr Ala Val Ser Phe
            75                    80                    85

ccg tcg tgt gcc gcc gcg ttg agc gag cac acg cca tgc gaa gac gcg
400
Pro Ser Cys Ala Ala Ala Leu Ser Glu His Thr Pro Cys Glu Asp Ala
            90                    95                    100

aag cga tcg ttg aaa ttc tcg agg gag aga ttg gag tat agg caa agg
448
Lys Arg Ser Leu Lys Phe Ser Arg Glu Arg Leu Glu Tyr Arg Gln Arg
        105                   110                   115

cat tgt ccc gag aga gaa gaa atc ttg aag tgc aga att ccg gcg ccg
496
His Cys Pro Glu Arg Glu Glu Ile Leu Lys Cys Arg Ile Pro Ala Pro
120                   125                   130                   135

tac ggt tac aaa acg ccg ttc cga tgg ccg gcg agt cgt gac gtg gcg
544
Tyr Gly Tyr Lys Thr Pro Phe Arg Trp Pro Ala Ser Arg Asp Val Ala
            140                   145                   150

tgg ttc gct aat gtg cct cac acg gag ctt acg gtt gag aaa aag aat
592
Trp Phe Ala Asn Val Pro His Thr Glu Leu Thr Val Glu Lys Lys Asn
            155                   160                   165

cag aat tgg gtc cgg tac gag aat gat cgg ttt tgg ttc cct ggt gga
640
Gln Asn Trp Val Arg Tyr Glu Asn Asp Arg Phe Trp Phe Pro Gly Gly
            170                   175                   180

ggt acg atg ttt cca cgt ggc gct gat gct tac att gat gat atc gga
688
Gly Thr Met Phe Pro Arg Gly Ala Asp Ala Tyr Ile Asp Asp Ile Gly
        185                   190                   195

cgg ttg att gat ctc agc gac ggc tct atc cgt aca gcc atc gat acc
736
Arg Leu Ile Asp Leu Ser Asp Gly Ser Ile Arg Thr Ala Ile Asp Thr
200                   205                   210                   215

ggt tgc ggg gtg gct agc ttc ggt gca tat ctt tta tca aga aac att
784
Gly Cys Gly Val Ala Ser Phe Gly Ala Tyr Leu Leu Ser Arg Asn Ile
            220                   225                   230

aca acg atg tca ttt gca cca aga gac aca cac gaa gct caa gtc cag
832
Thr Thr Met Ser Phe Ala Pro Arg Asp Thr His Glu Ala Gln Val Gln
            235                   240                   245
```

ttc gca ctc gag cgt ggt gtg ccg gcg atg atc gga atc atg gct aca
880
Phe Ala Leu Glu Arg Gly Val Pro Ala Met Ile Gly Ile Met Ala Thr
        250   255   260

atc cgc cta ccg tac cct tct aga gcc ttt gat tta gca cat tgc tct
928
Ile Arg Leu Pro Tyr Pro Ser Arg Ala Phe Asp Leu Ala His Cys Ser
    265   270   275

cgt tgc ctt att ccg tgg ggc caa aac gat ggg gct tac ttg atg gag
976
Arg Cys Leu Ile Pro Trp Gly Gln Asn Asp Gly Ala Tyr Leu Met Glu
280   285   290   295

gtg gat agg gtt tta aga cca gga ggg tac tgg ata ctt tct gga ccg
1024
Val Asp Arg Val Leu Arg Pro Gly Gly Tyr Trp Ile Leu Ser Gly Pro
            300   305   310

ccg att aat tgg cag aaa cgg tgg aaa ggg tgg gaa cgg acc atg gat
1072
Pro Ile Asn Trp Gln Lys Arg Trp Lys Gly Trp Glu Arg Thr Met Asp
            315   320   325

gat ttg aat gca gag cag act cag atc gag cag gtc gcg aga agc ttg
1120
Asp Leu Asn Ala Glu Gln Thr Gln Ile Glu Gln Val Ala Arg Ser Leu
            330   335   340

tgt tgg aag aaa gtt gtt caa aga gat gat ctt gct att tgg caa aaa
1168
Cys Trp Lys Lys Val Val Gln Arg Asp Asp Leu Ala Ile Trp Gln Lys
        345   350   355

ccc ttt aac cac att gac tgt aag aaa acc aga gag gtt ttg aaa aat
1216
Pro Phe Asn His Ile Asp Cys Lys Lys Thr Arg Glu Val Leu Lys Asn
360   365   370   375

ccg gag ttt tgt cgt cat gat caa gat ccc gac atg gcc tgg tat acg
1264
Pro Glu Phe Cys Arg His Asp Gln Asp Pro Asp Met Ala Trp Tyr Thr
            380   385   390

aag atg gat tct tgt ttg aca cca tta cct gaa gtt gat gac gct gag
1312
Lys Met Asp Ser Cys Leu Thr Pro Leu Pro Glu Val Asp Asp Ala Glu
            395   400   405

gat cta aag acg gtg gcc gga ggg aag gta gaa aag tgg ccg gct aga
1360
Asp Leu Lys Thr Val Ala Gly Gly Lys Val Glu Lys Trp Pro Ala Arg
        410   415   420

tta aac gcg att cct ccg aga gta aac aaa ggc gct ctc gag gaa atc
1408
Leu Asn Ala Ile Pro Pro Arg Val Asn Lys Gly Ala Leu Glu Glu Ile
        425   430   435

616

```
aca cct gaa gct ttc ttg gag aac acg aaa ctg tgg aaa cag aga gtt
1456
Thr Pro Glu Ala Phe Leu Glu Asn Thr Lys Leu Trp Lys Gln Arg Val
440                 445             450                     455

tct tat tac aag aag tta gat tac cag ttg ggt gaa acc ggg aga tac
1504
Ser Tyr Tyr Lys Lys Leu Asp Tyr Gln Leu Gly Glu Thr Gly Arg Tyr
            460                 465                     470

aga aac tta gtc gac atg aac gct tac ctc ggt gga ttc gcg gcg gct
1552
Arg Asn Leu Val Asp Met Asn Ala Tyr Leu Gly Gly Phe Ala Ala Ala
            475                 480                 485

cta gcg gat gat ccg gtc tgg gtc atg aac gtt gtc ccg gtc gag gct
1600
Leu Ala Asp Asp Pro Val Trp Val Met Asn Val Val Pro Val Glu Ala
            490                 495                 500

aag ctc aat acg ctc ggt gtc atc tac gag cgt ggt cta atc gga acg
1648
Lys Leu Asn Thr Leu Gly Val Ile Tyr Glu Arg Gly Leu Ile Gly Thr
    505                 510                 515

tat caa aac tgg tgt gaa gcc atg tcg acg tat cca aga acg tat gat
1696
Tyr Gln Asn Trp Cys Glu Ala Met Ser Thr Tyr Pro Arg Thr Tyr Asp
520                 525                 530                     535

ttt atc cat gct gac tcg gtt ttc aca ttg tac caa ggt caa tgt gaa
1744
Phe Ile His Ala Asp Ser Val Phe Thr Leu Tyr Gln Gly Gln Cys Glu
            540                 545                 550

ccg gag gag ata ttg ttg gag atg gac cga att ctt aga ccg ggt ggt
1792
Pro Glu Glu Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Gly Gly
            555                 560                 565

ggt gtg att ata aga gat gac gtg gac gtt ttg atc aag gtt aag gaa
1840
Gly Val Ile Ile Arg Asp Asp Val Asp Val Leu Ile Lys Val Lys Glu
            570                 575                 580

tta acc aaa gga tta gaa tgg gaa ggt aga att gct gac cac gag aag
1888
Leu Thr Lys Gly Leu Glu Trp Glu Gly Arg Ile Ala Asp His Glu Lys
    585                 590                 595

ggt cct cat gaa aga gag aag att tac tat gcg gtg aaa cag tat tgg
1936
Gly Pro His Glu Arg Glu Lys Ile Tyr Tyr Ala Val Lys Gln Tyr Trp
600                 605                 610                     615

acc gtt cct gcg cct gat gaa gat aaa aac aac act agt gct ctc tcc
1984
Thr Val Pro Ala Pro Asp Glu Asp Lys Asn Asn Thr Ser Ala Leu Ser
            620                 625                 630
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tga tttttgagtt tttttttttct tacaatgttt tttttttttt tttttcaatt
2037

ttttatacaa caataaattc tcaataattg ttgtcgcggc cg
2079

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Met Asn Leu Phe Thr Arg Ile Ser Ser Arg Thr Lys Lys Ala Asn Leu
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Tyr Tyr Val Thr Leu Val Ala Leu Leu Cys Ile Ala Ser Tyr Leu Leu
              20   25   30

Gly Ile Trp Gln Asn Thr Ala Val Asn Pro Arg Ala Ala Phe Asp Asp
           35   40   45

Ser Asp Gly Thr Pro Cys Glu Gly Phe Thr Arg Pro Asn Ser Thr Lys
      50   55   –   60

Asp Leu Asp Phe Asp Ala His His Asn Ile Gln Asp Pro Pro Pro Val
65   70   75   80

Thr Glu Thr Ala Val Ser Phe Pro Ser Cys Ala Ala Ala Leu Ser Glu
                 85   90   95

His Thr Pro Cys Glu Asp Ala Lys Arg Ser Leu Lys Phe Ser Arg Glu
               100   105   110

Arg Leu Glu Tyr Arg Gln Arg His Cys Pro Glu Arg Glu Glu Ile Leu
           115   120   125

Lys Cys Arg Ile Pro Ala Pro Tyr Gly Tyr Lys Thr Pro Phe Arg Trp
      130   135   140

Pro Ala Ser Arg Asp Val Ala Trp Phe Ala Asn Val Pro His Thr Glu
145   150   155   160

Leu Thr Val Glu Lys Lys Asn Gln Asn Trp Val Arg Tyr Glu Asn Asp
                 165   170   175

Arg Phe Trp Phe Pro Gly Gly Gly Thr Met Phe Pro Arg Gly Ala Asp
               180   185   190

Ala Tyr Ile Asp Asp Ile Gly Arg Leu Ile Asp Leu Ser Asp Gly Ser
           195   200   205

618

Ile Arg Thr Ala Ile Asp Thr Gly Cys Gly Val Ala Ser Phe Gly Ala
210   215   220

Tyr Leu Leu Ser Arg Asn Ile Thr Thr Met Ser Phe Ala Pro Arg Asp
225   230   235   240

Thr His Glu Ala Gln Val Gln Phe Ala Leu Glu Arg Gly Val Pro Ala
                245   250   255

Met Ile Gly Ile Met Ala Thr Ile Arg Leu Pro Tyr Pro Ser Arg Ala
                260   265   270

Phe Asp Leu Ala His Cys Ser Arg Cys Leu Ile Pro Trp Gly Gln Asn
        275   280   285

Asp Gly Ala Tyr Leu Met Glu Val Asp Arg Val Leu Arg Pro Gly Gly
    290   295   300

Tyr Trp Ile Leu Ser Gly Pro Pro Ile Asn Trp Gln Lys Arg Trp Lys
305   310   315   320

Gly Trp Glu Arg Thr Met Asp Asp Leu Asn Ala Glu Gln Thr Gln Ile
                325   330   335

Glu Gln Val Ala Arg Ser Leu Cys Trp Lys Lys Val Val Gln Arg Asp
                340   345   350

Asp Leu Ala Ile Trp Gln Lys Pro Phe Asn His Ile Asp Cys Lys Lys
        355   360   365

Thr Arg Glu Val Leu Lys Asn Pro Glu Phe Cys Arg His Asp Gln Asp
    370   375   380

Pro Asp Met Ala Trp Tyr Thr Lys Met Asp Ser Cys Leu Thr Pro Leu
385   390   395   400

Pro Glu Val Asp Asp Ala Glu Asp Leu Lys Thr Val Ala Gly Gly Lys
                405   410   415

Val Glu Lys Trp Pro Ala Arg Leu Asn Ala Ile Pro Pro Arg Val Asn
                420   425   430

Lys Gly Ala Leu Glu Glu Ile Thr Pro Glu Ala Phe Leu Glu Asn Thr
                435   440   445

```
Lys Leu Trp Lys Gln Arg Val Ser Tyr Tyr Lys Lys Leu Asp Tyr Gln
    450             455             460
```

```
Leu Gly Glu Thr Gly Arg Tyr Arg Asn Leu Val Asp Met Asn Ala Tyr
465             470             475             480
```

```
Leu Gly Gly Phe Ala Ala Ala Leu Ala Asp Asp Pro Val Trp Val Met
            485             490             495
```

```
Asn Val Val Pro Val Glu Ala Lys Leu Asn Thr Leu Gly Val Ile Tyr
            500             505             510
```

```
Glu Arg Gly Leu Ile Gly Thr Tyr Gln Asn Trp Cys Glu Ala Met Ser
        515             520             525
```

```
Thr Tyr Pro Arg Thr Tyr Asp Phe Ile His Ala Asp Ser Val Phe Thr
    530             535             540
```

```
Leu Tyr Gln Gly Gln Cys Glu Pro Glu Glu Ile Leu Leu Glu Met Asp
545             550             555             560
```

```
Arg Ile Leu Arg Pro Gly Gly Gly Val Ile Ile Arg Asp Asp Val Asp
            565             570             575
```

```
Val Leu Ile Lys Val Lys Glu Leu Thr Lys Gly Leu Glu Trp Glu Gly
            580             585             590
```

```
Arg Ile Ala Asp His Glu Lys Gly Pro His Glu Arg Glu Lys Ile Tyr
        595             600             605
```

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Tyr Ala Val Lys Gln Tyr Trp Thr Val Pro Ala Pro Asp Glu Asp Lys
    610             615             620
```

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Asn Asn Thr Ser Ala Leu Ser
625             630
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taaactaggg ttcccccaca aatcatctta cacgtatcct ctattccttc cttcctttct
120

ccgtcatcat cattttttccc accgacaaca atctctcgga gtttgggtat tattacttct
180
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ctcatcaacc aattgtacca ctagatctcc cagattcctt cattatctct atcaata
237

atg gcg ttg aag tct agt tct gct gat ggt aaa acc aga agc tct gtt
285
Met Ala Leu Lys Ser Ser Ser Ala Asp Gly Lys Thr Arg Ser Ser Val
1   5   10   15

cag atc ttc att gtg ttt agt tta tgt tgc ttc ttt tac att ttg gga
333
Gln Ile Phe Ile Val Phe Ser Leu Cys Cys Phe Phe Tyr Ile Leu Gly
            20   25   30

gca tgg caa cga agt ggt ttt ggt aaa gga gac agt att gct ctt gag
381
Ala Trp Gln Arg Ser Gly Phe Gly Lys Gly Asp Ser Ile Ala Leu Glu
            35   40   45

atg acc aac agt gga gct gat tgc aac att gtt cct agc ttg aat ttc
429
Met Thr Asn Ser Gly Ala Asp Cys Asn Ile Val Pro Ser Leu Asn Phe
        50   55   60

gag act cat cac gct ggc gaa tca agt ctt gtt ggt gct tct gaa gct
477
Glu Thr His His Ala Gly Glu Ser Ser Leu Val Gly Ala Ser Glu Ala
65   70   75   80

gca aag gtc aag gct ttc gag ccc tgt gat ggt cgt tac acg gat tac
525
Ala Lys Val Lys Ala Phe Glu Pro Cys Asp Gly Arg Tyr Thr Asp Tyr
                85   90   95

act cct tgt caa gat cag aga cgt gcc atg act ttc ccg aga gat agt
573
Thr Pro Cys Gln Asp Gln Arg Arg Ala Met Thr Phe Pro Arg Asp Ser
            100   105   110

atg att tac cga gaa agg cat tgc gct cct gag aat gag aag ctc cat
621
Met Ile Tyr Arg Glu Arg His Cys Ala Pro Glu Asn Glu Lys Leu His
            115   120   125

tgt ctt ata ccg gct cct aaa gga tat gtg aca cct ttc tct tgg cct
669
Cys Leu Ile Pro Ala Pro Lys Gly Tyr Val Thr Pro Phe Ser Trp Pro
        130   135   140

aag agt cga gac tat gtg cct tat gct aat gcg ccg tat aaa gca ttg
717
Lys Ser Arg Asp Tyr Val Pro Tyr Ala Asn Ala Pro Tyr Lys Ala Leu
145   150   155   160

act gtt gag aag gct att cag aat tgg att cag tat gag gga gac gtt
765
Thr Val Glu Lys Ala Ile Gln Asn Trp Ile Gln Tyr Glu Gly Asp Val
            165   170   175

ttt aga ttc cct ggt ggt gga act cag ttc cct caa ggt gct gat aag
813
Phe Arg Phe Pro Gly Gly Gly Thr Gln Phe Pro Gln Gly Ala Asp Lys

                    180   185   190

tat atc gat cag ctt gct tcc gtg ata cct atg gag aac gga act gtt
861
Tyr Ile Asp Gln Leu Ala Ser Val Ile Pro Met Glu Asn Gly Thr Val
            195   200   205

agg act gct ttg gac act ggt tgt ggg gtt gca agt tgg gga gcg tac
909
Arg Thr Ala Leu Asp Thr Gly Cys Gly Val Ala Ser Trp Gly Ala Tyr
        210   215   220

tta tgg agc aga aat gtg cgt gca atg tct ttt gca cca aga gat tca
957
Leu Trp Ser Arg Asn Val Arg Ala Met Ser Phe Ala Pro Arg Asp Ser
225   230   235   240

cac gag gct cag gtc cag ttt gct ctc gag aga ggt gtt ccc gct gtt
1005
His Glu Ala Gln Val Gln Phe Ala Leu Glu Arg Gly Val Pro Ala Val
                245   250   255

att ggt gtt ctt ggt acc ata aag ttg cca tac cca aca cgt gct ttc
1053
Ile Gly Val Leu Gly Thr Ile Lys Leu Pro Tyr Pro Thr Arg Ala Phe
            260   265   270

gac atg gct cat tgc tct cgg tgt ttg att cca tgg gga gca aat gat
1101
Asp Met Ala His Cys Ser Arg Cys Leu Ile Pro Trp Gly Ala Asn Asp
        275   280   285

ggg atg tac ttg atg gaa gtt gac cgt gtg ctt aga cct ggt ggg tac
1149
Gly Met Tyr Leu Met Glu Val Asp Arg Val Leu Arg Pro Gly Gly Tyr
        290   295   300

tgg att ctg tct ggt cct cca atc aac tgg aaa gtc aac tac aag gca
1197
Trp Ile Leu Ser Gly Pro Pro Ile Asn Trp Lys Val Asn Tyr Lys Ala
305   310   315   320

tgg caa cgt ccc aag gag gac ctt caa gag gaa caa aga aag att gag
1245
Trp Gln Arg Pro Lys Glu Asp Leu Gln Glu Glu Gln Arg Lys Ile Glu
                325   330   335

gaa gct gct aaa ctt ctt tgt tgg gag aaa aag tat gaa cac ggt gag
1293
Glu Ala Ala Lys Leu Leu Cys Trp Glu Lys Lys Tyr Glu His Gly Glu
                340   345   350

att gca att tgg cag aag aga gtc aat gat gag gca tgc cga tca aga
1341
Ile Ala Ile Trp Gln Lys Arg Val Asn Asp Glu Ala Cys Arg Ser Arg
            355   360   365

caa gat gat cct aga gcc aat ttc tgc aaa acc gat gat acc gat gat
1389
Gln Asp Asp Pro Arg Ala Asn Phe Cys Lys Thr Asp Asp Thr Asp Asp
        370   375   380

                                    622

gtc tgg tac aag aaa atg gag gca tgt att aca ccg tat ccg gag aca
1437
Val Trp Tyr Lys Lys Met Glu Ala Cys Ile Thr Pro Tyr Pro Glu Thr
385   390   395   400

agt agc tca gat gaa gta gct ggt ggt gag ctt cag gct ttc cca gat
1485
Ser Ser Ser Asp Glu Val Ala Gly Gly Glu Leu Gln Ala Phe Pro Asp
              405   410   415

agg ctc aat gca gtg ccg ccc agg atc tct agc ggt tcg atc tct ggt
1533
Arg Leu Asn Ala Val Pro Pro Arg Ile Ser Ser Gly Ser Ile Ser Gly
              420   425   430

gtt act gtt gat gcc tat gaa gac gat aac aga cag tgg aaa aaa cat
1581
Val Thr Val Asp Ala Tyr Glu Asp Asp Asn Arg Gln Trp Lys Lys His
              435   440   445

gtg aaa gcc tac aag aga atc aac agt cta ctt gac act gga agg tac
1629
Val Lys Ala Tyr Lys Arg Ile Asn Ser Leu Leu Asp Thr Gly Arg Tyr
    450   455   460

cgt aac atc atg gac atg aac gca ggg ttt ggt gga ttt gct gct gct
1677
Arg Asn Ile Met Asp Met Asn Ala Gly Phe Gly Gly Phe Ala Ala Ala
465   470   475   480

ctt gaa tcc caa aag ctt tgg gtt atg aat gtt gtt ccc aca att gcc
1725
Leu Glu Ser Gln Lys Leu Trp Val Met Asn Val Val Pro Thr Ile Ala
              485   490   495

gaa aag aac aga ctc gga gtt gta tat gaa cga gga ctc atc ggt atc
1773
Glu Lys Asn Arg Leu Gly Val Val Tyr Glu Arg Gly Leu Ile Gly Ile
              500   505   510

tac cat gac tgg tgt gag gct ttc tct aca tat cca aga aca tat gac
1821
Tyr His Asp Trp Cys Glu Ala Phe Ser Thr Tyr Pro Arg Thr Tyr Asp
    515   520   525

ctg atc cac gcg aac cac ctc ttc agt cta tac aag aac aag tgc aat
1869
Leu Ile His Ala Asn His Leu Phe Ser Leu Tyr Lys Asn Lys Cys Asn
    530   535   540

gcg gat gat att ctt cta gag atg gat aga att ctc cga cca gaa gga
1917
Ala Asp Asp Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Glu Gly
545   550   555   560

gcg gtt ata atc cgg gat gat gtg gat aca ttg atc aag gtg aag aga
1965
Ala Val Ile Ile Arg Asp Asp Val Asp Thr Leu Ile Lys Val Lys Arg
              565   570   575

atc atc gct tgg aat gag atg gga tgc gaa gct tgt cga tca tga
2010
Ile Ile Ala Trp Asn Glu Met Gly Cys Glu Ala Cys Arg Ser
            580   585   590

ggatggtcct ttagttcctg agaaggtttt gattgccgtg aagcagtatt gggtcaccaa
2070

ctccacctcg actcactgaa gttactttat ttccggtgtg acctgacatt ttgatcaaat
2130

gatagagctt tcgtccttag ggaatgtgag agagctgcaa atcttgtctt taaacacttt
2190

ttgaagtatc tatttattga tgttatagtt tattttgtt tcccaatcca aaagcttgga
2250

actttgtggt gtaccattga attctc
2276

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Met Ala Leu Lys Ser Ser Ser Ala Asp Gly Lys Thr Arg Ser Ser Val
1   5   10   15

Gln Ile Phe Ile Val Phe Ser Leu Cys Cys Phe Phe Tyr Ile Leu Gly
                20   25   30

Ala Trp Gln Arg Ser Gly Phe Gly Lys Gly Asp Ser Ile Ala Leu Glu
            35   40   45

Met Thr Asn Ser Gly Ala Asp Cys Asn Ile Val Pro Ser Leu Asn Phe
        50   55   60

Glu Thr His His Ala Gly Glu Ser Ser Leu Val Gly Ala Ser Glu Ala
65   70   75   80

Ala Lys Val Lys Ala Phe Glu Pro Cys Asp Gly Arg Tyr Thr Asp Tyr
                85   90   95

Thr Pro Cys Gln Asp Gln Arg Arg Ala Met Thr Phe Pro Arg Asp Ser
                100   105   110

Met Ile Tyr Arg Glu Arg His Cys Ala Pro Glu Asn Glu Lys Leu His
            115   120   125

Cys Leu Ile Pro Ala Pro Lys Gly Tyr Val Thr Pro Phe Ser Trp Pro
        130   135   140

Lys Ser Arg Asp Tyr Val Pro Tyr Ala Asn Ala Pro Tyr Lys Ala Leu

624

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        145                150                155                160

Thr Val Glu Lys Ala Ile Gln Asn Trp Ile Gln Tyr Glu Gly Asp Val
            165                170                175

Phe Arg Phe Pro Gly Gly Gly Thr Gln Phe Pro Gln Gly Ala Asp Lys
            180                185                190

Tyr Ile Asp Gln Leu Ala Ser Val Ile Pro Met Glu Asn Gly Thr Val
            195                200                205

Arg Thr Ala Leu Asp Thr Gly Cys Gly Val Ala Ser Trp Gly Ala Tyr
    210                215                220

Leu Trp Ser Arg Asn Val Arg Ala Met Ser Phe Ala Pro Arg Asp Ser
225                230                235                240

His Glu Ala Gln Val Gln Phe Ala Leu Glu Arg Gly Val Pro Ala Val
            245                250                255

Ile Gly Val Leu Gly Thr Ile Lys Leu Pro Tyr Pro Thr Arg Ala Phe
            260                265                270

Asp Met Ala His Cys Ser Arg Cys Leu Ile Pro Trp Gly Ala Asn Asp
            275                280                285

Gly Met Tyr Leu Met Glu Val Asp Arg Val Leu Arg Pro Gly Gly Tyr
    290                295                300

Trp Ile Leu Ser Gly Pro Pro Ile Asn Trp Lys Val Asn Tyr Lys Ala
305                310                315                320

Trp Gln Arg Pro Lys Glu Asp Leu Gln Glu Glu Gln Arg Lys Ile Glu
            325                330                335

Glu Ala Ala Lys Leu Leu Cys Trp Glu Lys Lys Tyr Glu His Gly Glu
            340                345                350

Ile Ala Ile Trp Gln Lys Arg Val Asn Asp Glu Ala Cys Arg Ser Arg
            355                360                365

Gln Asp Asp Pro Arg Ala Asn Phe Cys Lys Thr Asp Asp Thr Asp Asp
    370                375                380

Val Trp Tyr Lys Lys Met Glu Ala Cys Ile Thr Pro Tyr Pro Glu Thr
385                390                395                400
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Ser Ser Ser Asp Glu Val Ala Gly Gly Glu Leu Gln Ala Phe Pro Asp
            405                 410             415


Arg Leu Asn Ala Val Pro Pro Arg Ile Ser Ser Gly Ser Ile Ser Gly
            420                 425             430


Val Thr Val Asp Ala Tyr Glu Asp Asp Asn Arg Gln Trp Lys Lys His
            435                 440             445


Val Lys Ala Tyr Lys Arg Ile Asn Ser Leu Leu Asp Thr Gly Arg Tyr
        450                 455             460


Arg Asn Ile Met Asp Met Asn Ala Gly Phe Gly Gly Phe Ala Ala Ala
465                 470             475                 480


Leu Glu Ser Gln Lys Leu Trp Val Met Asn Val Val Pro Thr Ile Ala
            485                 490             495


Glu Lys Asn Arg Leu Gly Val Val Tyr Glu Arg Gly Leu Ile Gly Ile
            500                 505             510


Tyr His Asp Trp Cys Glu Ala Phe Ser Thr Tyr Pro Arg Thr Tyr Asp
        515                 520             525


Leu Ile His Ala Asn His Leu Phe Ser Leu Tyr Lys Asn Lys Cys Asn
    530                 535             540


Ala Asp Asp Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Glu Gly
545                 550             555                 560


Ala Val Ile Ile Arg Asp Asp Val Asp Thr Leu Ile Lys Val Lys Arg
            565                 570             575


Ile Ile Ala Trp Asn Glu Met Gly Cys Glu Ala Cys Arg Ser
            580                 585             590
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atctctatat ccttggttgt gtcagattct cttagggttt attttctctc ccaattttgt
120

626

ttgattcctt gtccaaagtt tcttcctttc cttttgactt tttttgtgg tacattgaat
180

cagaggtgta agagtaatag tttcataact caaatcccca agtgtacaaa ttttcctctt
240

ttggttctgg gtttggttga ttccttgtta gaaatgtaaa tttagggctt ttgtatctga
300

aaccgatctt cagacttgtg taatcttctt gatcttcatg caagattgat aattctacaa
360

gaagaagaag aagagaaa atg gct act ttg act gag cca tca tca tct ttg
411
                     Met Ala Thr Leu Thr Glu Pro Ser Ser Ser Leu
                     1   5   10

agt ttc aca tct tct cat ttc tct tat ggt tct att ggg tcc aat cac
459
Ser Phe Thr Ser Ser His Phe Ser Tyr Gly Ser Ile Gly Ser Asn His
            15   20   25

ttc tca tca agc tca gct tct aat cct gaa gtt gtt agt cta acc aaa
507
Phe Ser Ser Ser Ser Ala Ser Asn Pro Glu Val Val Ser Leu Thr Lys
        30   35   40

ctc agc tcc aat ctt gag cag ctt ctt agt aat tca gat tgt gat tac
555
Leu Ser Ser Asn Leu Glu Gln Leu Leu Ser Asn Ser Asp Cys Asp Tyr
    45   50   55

agt gat gca gag atc att gtt gat ggt gtt cca gtt ggt gtt cat aga
603
Ser Asp Ala Glu Ile Ile Val Asp Gly Val Pro Val Gly Val His Arg
60   65   70   75

tgc att tta gct gca aga agt aag ttt ttc caa gat ttg ttt aag aaa
651
Cys Ile Leu Ala Ala Arg Ser Lys Phe Phe Gln Asp Leu Phe Lys Lys
                80   85   90

gaa aag aaa att tcg aaa act gag aaa cca aag tat cag ttg aga gag
699
Glu Lys Lys Ile Ser Lys Thr Glu Lys Pro Lys Tyr Gln Leu Arg Glu
                95   100   105

atg tta cct tat gga gct gtt gct cat gaa gct ttc ttg tat ttc ttg
747
Met Leu Pro Tyr Gly Ala Val Ala His Glu Ala Phe Leu Tyr Phe Leu
        110   115   120

agt tat ata tat act ggg aga tta aag cct ttt cca ttg gag gtt tcg
795
Ser Tyr Ile Tyr Thr Gly Arg Leu Lys Pro Phe Pro Leu Glu Val Ser
        125   130   135

act tgt gtt gat cca gtt tgt tct cat gat tgt tgt cga cct gcc att
843
Thr Cys Val Asp Pro Val Cys Ser His Asp Cys Cys Arg Pro Ala Ile
140   145   150   155

gat ttt gtt gtt caa ttg atg tat gct tcc tct gtt ctc caa gtg cct
891
Asp Phe Val Val Gln Leu Met Tyr Ala Ser Ser Val Leu Gln Val Pro
                160   165   170

gag cta gtt tca tct ttt cag cgg cgg ctt tgt aac ttt gtg gag aag
939
Glu Leu Val Ser Ser Phe Gln Arg Arg Leu Cys Asn Phe Val Glu Lys
            175   180   185

acc ctt gtt gag aat gtt ctt ccc att ctt atg gtt gct ttc aat tgt
987
Thr Leu Val Glu Asn Val Leu Pro Ile Leu Met Val Ala Phe Asn Cys
            190   195   200

aag ttg act cag ctt ctt gat cag tgt att gag aga gtg gcg agg tca
1035
Lys Leu Thr Gln Leu Leu Asp Gln Cys Ile Glu Arg Val Ala Arg Ser
        205   210   215

gat ctt tac agg ttc tgt att gaa aag gaa gtt cct ccc gaa gta gca
1083
Asp Leu Tyr Arg Phe Cys Ile Glu Lys Glu Val Pro Pro Glu Val Ala
220   225   230   235

gag aag att aaa cag ctt cga ctt ata tcc ccg caa gac gaa gaa acc
1131
Glu Lys Ile Lys Gln Leu Arg Leu Ile Ser Pro Gln Asp Glu Glu Thr
                240   245   250

agt ccc aag att tcg gag aaa ttg ctt gaa aga atc ggt aaa att ctc
1179
Ser Pro Lys Ile Ser Glu Lys Leu Leu Glu Arg Ile Gly Lys Ile Leu
            255   260   265

aag gcc ttg gat tca tat gat gtt ctt cat ttt gct gcg atg cgt aga
1227
Lys Ala Leu Asp Ser Tyr Asp Val Leu His Phe Ala Ala Met Arg Arg
        270   275   280

gag cca tcg atc att ata tcg ctt atc gat aaa ggc gcc aat gca tct
1275
Glu Pro Ser Ile Ile Ile Ser Leu Ile Asp Lys Gly Ala Asn Ala Ser
        285   290   295

gag ttt aca tct gac gga cgt agc gca gtt aat ata tta aga aga ctg
1323
Glu Phe Thr Ser Asp Gly Arg Ser Ala Val Asn Ile Leu Arg Arg Leu
300   305   310   315

aca aat cca aag gat tat cat acc aaa aca gct aaa ggg cgt gaa tct
1371
Thr Asn Pro Lys Asp Tyr His Thr Lys Thr Ala Lys Gly Arg Glu Ser
                320   325   330

agt aaa gcc agg tta tgc atc gat atc ttg gaa aga gaa atc agg aag
1419
Ser Lys Ala Arg Leu Cys Ile Asp Ile Leu Glu Arg Glu Ile Arg Lys
            335   340   345

628

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aac ccc atg gtt cta gat aca cca atg tgt tcc att tct atg cct gaa
1467
Asn Pro Met Val Leu Asp Thr Pro Met Cys Ser Ile Ser Met Pro Glu
        350                 355                 360

gat ctc cag atg aga ctg ttg tac cta gaa aag aga gtg ggg ctt gct
1515
Asp Leu Gln Met Arg Leu Leu Tyr Leu Glu Lys Arg Val Gly Leu Ala
    365                 370                 375

cag ttg ttc ttt cca acg gaa gct aaa gtt gct atg gac att ggt aac
1563
Gln Leu Phe Phe Pro Thr Glu Ala Lys Val Ala Met Asp Ile Gly Asn
380                 385                 390                 395

gta gaa ggt aca agt gag ttc acg ggt ttg tca cct cct tcg agt ggg
1611
Val Glu Gly Thr Ser Glu Phe Thr Gly Leu Ser Pro Pro Ser Ser Gly
                400                 405                 410

tta acc gga aac ttg agt cag gtt gat tta aac gaa act cct cat atg
1659
Leu Thr Gly Asn Leu Ser Gln Val Asp Leu Asn Glu Thr Pro His Met
                415                 420                 425

caa acc caa aga ctt ctt act cgt atg gtg gct cta atg aaa aca gtt
1707
Gln Thr Gln Arg Leu Leu Thr Arg Met Val Ala Leu Met Lys Thr Val
        430                 435                 440

gag act ggt cga agg ttt ttt cca tat ggt tca gag gtt cta gat aag
1755
Glu Thr Gly Arg Arg Phe Phe Pro Tyr Gly Ser Glu Val Leu Asp Lys
    445                 450                 455

tac atg gct gag tat ata gac gac gac atc ctc gac gat ttc cat ttt
1803
Tyr Met Ala Glu Tyr Ile Asp Asp Asp Ile Leu Asp Asp Phe His Phe
460                 465                 470                 475

gag aag gga tct aca cat gaa aga aga ttg aaa aga atg aga tat aga
1851
Glu Lys Gly Ser Thr His Glu Arg Arg Leu Lys Arg Met Arg Tyr Arg
                480                 485                 490

gag ctt aag gat gat gtc caa aag gca tat agc aaa gac aaa gag tct
1899
Glu Leu Lys Asp Asp Val Gln Lys Ala Tyr Ser Lys Asp Lys Glu Ser
            495                 500                 505

aag att gcg cgg tct tgt ctt tct gct tca tct tct cct tct tct tct
1947
Lys Ile Ala Arg Ser Cys Leu Ser Ala Ser Ser Ser Pro Ser Ser Ser
        510                 515                 520

tcc ata aga gat gac ctg cac aac aca aca tga aactgcacca taagtcaaat
2000
Ser Ile Arg Asp Asp Leu His Asn Thr Thr
    525                 530
```

gtaattagat atctttgtta aaagggtttt ttctttatgg atgttactca gattttatac
2060

agatgcttta ggttcagttt caataaagag agatggatag atagatgtac aagattagga
2120

gtgctgatta acccaaaacg ttctaactat acgcaatctt ttgttttcaa tacaaaaatc
2180

taatatttag gttaaa
2196

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Met Ala Thr Leu Thr Glu Pro Ser Ser Ser Leu Ser Phe Thr Ser Ser
1   5   10   15

His Phe Ser Tyr Gly Ser Ile Gly Ser Asn His Phe Ser Ser Ser Ser
            20   25   30

Ala Ser Asn Pro Glu Val Val Ser Leu Thr Lys Leu Ser Ser Asn Leu
        35   40   45

Glu Gln Leu Leu Ser Asn Ser Asp Cys Asp Tyr Ser Asp Ala Glu Ile
    50   55   60

Ile Val Asp Gly Val Pro Val Gly Val His Arg Cys Ile Leu Ala Ala
65   70   75   80

Arg Ser Lys Phe Phe Gln Asp Leu Phe Lys Lys Glu Lys Lys Ile Ser
            85   90   95

Lys Thr Glu Lys Pro Lys Tyr Gln Leu Arg Glu Met Leu Pro Tyr Gly
            100   105   110

Ala Val Ala His Glu Ala Phe Leu Tyr Phe Leu Ser Tyr Ile Tyr Thr
            115   120   125

Gly Arg Leu Lys Pro Phe Pro Leu Glu Val Ser Thr Cys Val Asp Pro
        130   135   140

Val Cys Ser His Asp Cys Cys Arg Pro Ala Ile Asp Phe Val Val Gln
145   150   155   160

Leu Met Tyr Ala Ser Ser Val Leu Gln Val Pro Glu Leu Val Ser Ser
                165   170   175

Phe Gln Arg Arg Leu Cys Asn Phe Val Glu Lys Thr Leu Val Glu Asn

```
           180                    185                    190

Val Leu Pro Ile Leu Met Val Ala Phe Asn Cys Lys Leu Thr Gln Leu
        195                 200                 205

Leu Asp Gln Cys Ile Glu Arg Val Ala Arg Ser Asp Leu Tyr Arg Phe
        210                 215                 220

Cys Ile Glu Lys Glu Val Pro Pro Glu Val Ala Glu Lys Ile Lys Gln
225                 230                 235                 240

Leu Arg Leu Ile Ser Pro Gln Asp Glu Glu Thr Ser Pro Lys Ile Ser
            245                 250                 255

Glu Lys Leu Leu Glu Arg Ile Gly Lys Ile Leu Lys Ala Leu Asp Ser
        260                 265                 270

Tyr Asp Val Leu His Phe Ala Ala Met Arg Arg Glu Pro Ser Ile Ile
        275                 280                 285

Ile Ser Leu Ile Asp Lys Gly Ala Asn Ala Ser Glu Phe Thr Ser Asp
    290                 295                 300

Gly Arg Ser Ala Val Asn Ile Leu Arg Arg Leu Thr Asn Pro Lys Asp
305                 310                 315                 320

Tyr His Thr Lys Thr Ala Lys Gly Arg Glu Ser Ser Lys Ala Arg Leu
            325                 330                 335

Cys Ile Asp Ile Leu Glu Arg Glu Ile Arg Lys Asn Pro Met Val Leu
            340                 345                 350

Asp Thr Pro Met Cys Ser Ile Ser Met Pro Glu Asp Leu Gln Met Arg
        355                 360                 365

Leu Leu Tyr Leu Glu Lys Arg Val Gly Leu Ala Gln Leu Phe Phe Pro
        370                 375                 380

Thr Glu Ala Lys Val Ala Met Asp Ile Gly Asn Val Glu Gly Thr Ser
385                 390                 395                 400

Glu Phe Thr Gly Leu Ser Pro Pro Ser Ser Gly Leu Thr Gly Asn Leu
            405                 410                 415

Ser Gln Val Asp Leu Asn Glu Thr Pro His Met Gln Thr Gln Arg Leu
            420                 425                 430
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631

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Leu Thr Arg Met Val Ala Leu Met Lys Thr Val Glu Thr Gly Arg Arg
      435                 440                 445


Phe Phe Pro Tyr Gly Ser Glu Val Leu Asp Lys Tyr Met Ala Glu Tyr
      450                 455                 460


Ile Asp Asp Asp Ile Leu Asp Asp Phe His Phe Glu Lys Gly Ser Thr
465                 470                 475                 480


His Glu Arg Arg Leu Lys Arg Met Arg Tyr Arg Glu Leu Lys Asp Asp
                485                 490                 495


Val Gln Lys Ala Tyr Ser Lys Asp Lys Glu Ser Lys Ile Ala Arg Ser
              500                 505                 510


Cys Leu Ser Ala Ser Ser Ser Pro Ser Ser Ser Ser Ile Arg Asp Asp
          515                 520                 525


Leu His Asn Thr Thr
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ccagatctcg tttcccgcga tctagtttat tctttgaaaa agtgatagaa gcagaa atg
119
                                                                 Met
                                                                 1

gga agg ggc aag atc gcg att aag agg atc aat aac tct acg agc cgt
167
Gly Arg Gly Lys Ile Ala Ile Lys Arg Ile Asn Asn Ser Thr Ser Arg
            5                  10                  15

cag gtt acg ttc tcg aag cga agg aat gga ttg ttg aag aaa gct aag
215
Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Lys
        20                  25                  30

gag ctt gcg att ctc tgc gat gct gag gtt ggt gtc atc atc ttc tcc
263
Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe Ser
      35                  40                  45

agc acc ggt agg ctc tac gat ttc tcc agc tcc agc atg aaa tcg gtc
311
Ser Thr Gly Arg Leu Tyr Asp Phe Ser Ser Ser Ser Met Lys Ser Val
50                  55                  60                  65
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ata gag aga tac agc gat gcc aaa gga gaa acc agt tca gaa aat gat
359
Ile Glu Arg Tyr Ser Asp Ala Lys Gly Glu Thr Ser Ser Glu Asn Asp
            70                  75                  80


ccc gct tca gaa att cag ttc tgg caa aag gag gct gcg att cta aag
407
Pro Ala Ser Glu Ile Gln Phe Trp Gln Lys Glu Ala Ala Ile Leu Lys
            85                  90                  95


cgt cag cta cat aac ttg caa gaa aac cac cgg caa atg atg ggg gag
455
Arg Gln Leu His Asn Leu Gln Glu Asn His Arg Gln Met Met Gly Glu
        100                 105                 110


gag ctc tct gga cta agt gta gaa gct tta cag aat ttg gaa aat cag
503
Glu Leu Ser Gly Leu Ser Val Glu Ala Leu Gln Asn Leu Glu Asn Gln
    115                 120                 125


ctt gaa ttg agc ctt cgt ggc gtt cga atg aaa aag gat caa atg tta
551
Leu Glu Leu Ser Leu Arg Gly Val Arg Met Lys Lys Asp Gln Met Leu
130                 135                 140                 145


atc gaa gaa ata caa gta ctt aac cga gag ggg aat ctc gtt cac caa
599
Ile Glu Glu Ile Gln Val Leu Asn Arg Glu Gly Asn Leu Val His Gln
            150                 155                 160


gag aat tta gac ctc cac aag aaa gta aac cta atg cac caa cag aac
647
Glu Asn Leu Asp Leu His Lys Lys Val Asn Leu Met His Gln Gln Asn
            165                 170                 175


atg gaa cta cat gaa aag gtt tca gag gtc gag ggt gtg aaa atc gca
695
Met Glu Leu His Glu Lys Val Ser Glu Val Glu Gly Val Lys Ile Ala
            180                 185                 190


aac aag aat tct ctt ctc aca aat ggt cta gac atg aga gat acc tcg
743
Asn Lys Asn Ser Leu Leu Thr Asn Gly Leu Asp Met Arg Asp Thr Ser
        195                 200                 205


aac gaa cat gtc cat ctt cag ctc agc caa ccg cag cat gat cat gag
791
Asn Glu His Val His Leu Gln Leu Ser Gln Pro Gln His Asp His Glu
210                 215                 220                 225


acg cat tca aaa gct atc caa ctc aac tat ttt tcc ttc att gca taa
839
Thr His Ser Lys Ala Ile Gln Leu Asn Tyr Phe Ser Phe Ile Ala
            230                 235                 240


tataattcgg tgtgccaaca cacttatgtt gacctcgtcg gaatcatatc acaattcact
899

gtgtcagctt gcctctgcat aagcgaaaat aaaaacataa acatgatcag tttgcattcc
959
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atatctatca aacaccagct ttgtaacttt taaaacttttt tctccgtgca aagacctttg
1019

gtttggcgct taagcatgta gtttgatgat caaaggaaat gggtgtttta gcataaagtt
1079

gtcacccttc cgttgcattt tagcttccca tccaaatcaa tttgtaaaat gtgagttagt
1139

ttgcagcatg aaagctgatt aaatatcagt cccgttatca caagaggtaa aaaaaaaaa
1199

aaaaaaaaaa a
1210
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352

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Met Gly Arg Gly Lys Ile Ala Ile Lys Arg Ile Asn Asn Ser Thr Ser
1               5                   10                  15


Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
            20                  25                  30


Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe
        35                  40                  45


Ser Ser Thr Gly Arg Leu Tyr Asp Phe Ser Ser Ser Ser Met Lys Ser
    50                  55                  60


Val Ile Glu Arg Tyr Ser Asp Ala Lys Gly Glu Thr Ser Ser Glu Asn
65                  70                  75                  80


Asp Pro Ala Ser Glu Ile Gln Phe Trp Gln Lys Glu Ala Ala Ile Leu
                85                  90                  95


Lys Arg Gln Leu His Asn Leu Gln Glu Asn His Arg Gln Met Met Gly
            100                 105                 110


Glu Glu Leu Ser Gly Leu Ser Val Glu Ala Leu Gln Asn Leu Glu Asn
        115                 120                 125


Gln Leu Glu Leu Ser Leu Arg Gly Val Arg Met Lys Lys Asp Gln Met
    130                 135                 140


Leu Ile Glu Glu Ile Gln Val Leu Asn Arg Glu Gly Asn Leu Val His
145                 150                 155                 160


Gln Glu Asn Leu Asp Leu His Lys Lys Val Asn Leu Met His Gln Gln
```

                    165   170   175

Asn Met Glu Leu His Glu Lys Val Ser Glu Val Glu Gly Val Lys Ile
            180   185   190

Ala Asn Lys Asn Ser Leu Leu Thr Asn Gly Leu Asp Met Arg Asp Thr
            195   200   205

Ser Asn Glu His Val His Leu Gln Leu Ser Gln Pro Gln His Asp His
            210   215   220

Glu Thr His Ser Lys Ala Ile Gln Leu Asn Tyr Phe Ser Phe Ile Ala
225   230   235   240

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58

atg ttt cgt ttt ccg gta agt ctt gga gga ggt cca cgt gag aat ctg
106
Met Phe Arg Phe Pro Val Ser Leu Gly Gly Gly Pro Arg Glu Asn Leu
1   5   10   15

aag cca tca gat gag cag cat caa cgt gcg gtg gtg aat gag gtt gac
154
Lys Pro Ser Asp Glu Gln His Gln Arg Ala Val Val Asn Glu Val Asp
            20   25   30

ttt ttc cga tca gcg gag aag aga gat agg gtt tca cgt gaa gaa caa
202
Phe Phe Arg Ser Ala Glu Lys Arg Asp Arg Val Ser Arg Glu Glu Gln
        35   40   45

aac att atc gcc gat gag act cat agg gtt cat gtc aaa agg gag aat
250
Asn Ile Ile Ala Asp Glu Thr His Arg Val His Val Lys Arg Glu Asn
    50   55   60

tca cgt gtt gat gat cat gac gat cgt tct act gat cac atc aat att
298
Ser Arg Val Asp Asp His Asp Asp Arg Ser Thr Asp His Ile Asn Ile
65   70   75   80

gga ctt aat ctt ctc act gcg aat acg gga agc gac gag tca atg gtg
346
Gly Leu Asn Leu Leu Thr Ala Asn Thr Gly Ser Asp Glu Ser Met Val
                85   90   95

gat gat gga ttg tct gtg gat atg gaa gag aaa cgt aca aag tgt gag
394
Asp Asp Gly Leu Ser Val Asp Met Glu Glu Lys Arg Thr Lys Cys Glu
            100   105   110

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aat gca caa ctt cgc gaa gag cta aag aag gcg agt gaa gat aat caa
442
Asn Ala Gln Leu Arg Glu Glu Leu Lys Lys Ala Ser Glu Asp Asn Gln
        115                 120                 125

aga cta aag caa atg cta agt caa aca acc aac aac ttc aat tcc ttg
490
Arg Leu Lys Gln Met Leu Ser Gln Thr Thr Asn Asn Phe Asn Ser Leu
    130                 135                 140

cag atg caa ctt gtt gct gtc atg agg caa caa gaa gat cat cat cac
538
Gln Met Gln Leu Val Ala Val Met Arg Gln Gln Glu Asp His His His
145                 150                 155                 160

cta gct acg acc gag aac aat gac aat gta aag aac cga cat gaa gtg
586
Leu Ala Thr Thr Glu Asn Asn Asp Asn Val Lys Asn Arg His Glu Val
                165                 170                 175

cct gaa atg gtt cca aga cag ttc atc gat ttg gga ccg cat tct gac
634
Pro Glu Met Val Pro Arg Gln Phe Ile Asp Leu Gly Pro His Ser Asp
            180                 185                 190

gaa gtg tcg tcc gag gag agg acg acg gtt cgg tcg gga tct cct ccc
682
Glu Val Ser Ser Glu Glu Arg Thr Thr Val Arg Ser Gly Ser Pro Pro
            195                 200                 205

tcg ctt cta gag aaa tct agc tca cgt caa aac gga aag aga gtg ctt
730
Ser Leu Leu Glu Lys Ser Ser Ser Arg Gln Asn Gly Lys Arg Val Leu
    210                 215                 220

gta aga gaa gaa agc ccg gaa acc gaa tcc aac ggc tgg aga aac cct
778
Val Arg Glu Glu Ser Pro Glu Thr Glu Ser Asn Gly Trp Arg Asn Pro
225                 230                 235                 240

aac aaa gtt cct aaa cac cat gca tca tcc agc att tgc ggt ggc aat
826
Asn Lys Val Pro Lys His His Ala Ser Ser Ser Ile Cys Gly Gly Asn
            245                 250                 255

ggc agt gaa aat gca agt agc aag gtc att gag caa gcg gcc gcc gaa
874
Gly Ser Glu Asn Ala Ser Ser Lys Val Ile Glu Gln Ala Ala Ala Glu
            260                 265                 270

gcc acc atg cgt aaa gcc cgt gtc tcg gtt cgt gct cga tcc gaa gct
922
Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala Arg Ser Glu Ala
        275                 280                 285

ccc atg tta agc gat gga tgt caa tgg aga aaa tac gga caa aaa atg
970
Pro Met Leu Ser Asp Gly Cys Gln Trp Arg Lys Tyr Gly Gln Lys Met
    290                 295                 300
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636

gcg aaa gga aac ccg tgc cct cga gct tat tac cgt tgc aca atg gct
1018
Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg Cys Thr Met Ala
305   310   315   320

gtt gga tgt cct gtt cgc aag caa gtg caa cgt tgc gcg gaa gat aga
1066
Val Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala Glu Asp Arg
                325   330   335

acc att ctc ata aca acc tac gaa gga aac cat aac cat cca tta cct
1114
Thr Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His Pro Leu Pro
                340   345   350

cct gcg gct atg aac atg gct tca act aca aca gca gcc gca agc atg
1162
Pro Ala Ala Met Asn Met Ala Ser Thr Thr Thr Ala Ala Ala Ser Met
            355   360   365

ctt ctc tca ggc tcc acc atg tcg aac caa gac ggt tta atg aac cca
1210
Leu Leu Ser Gly Ser Thr Met Ser Asn Gln Asp Gly Leu Met Asn Pro
        370   375   380

aca aat ctc ttg gct cga acc ata tta ccg tgt tcc tca agc atg gct
1258
Thr Asn Leu Leu Ala Arg Thr Ile Leu Pro Cys Ser Ser Ser Met Ala
385   390   395   400

act atc tca gcc tct gca cca ttc cca acc att aca tta gac ctc aca
1306
Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Ile Thr Leu Asp Leu Thr
                405   410   415

gag tca ccc aac ggg aac aat cca acc aat aac ccg ctg atg caa ttc
1354
Glu Ser Pro Asn Gly Asn Asn Pro Thr Asn Asn Pro Leu Met Gln Phe
                420   425   430

tct caa cgg tct ggt ttg gtg gag ttg aac caa tcg gtt ttg cct cat
1402
Ser Gln Arg Ser Gly Leu Val Glu Leu Asn Gln Ser Val Leu Pro His
        435   440   445

atg atg ggt cag gct ttg tac tac aac caa cag tct aag ttt tcg ggt
1450
Met Met Gly Gln Ala Leu Tyr Tyr Asn Gln Gln Ser Lys Phe Ser Gly
    450   455   460

tta cat atg ccg tct cag ccg cta aac gct ggt gag agt gtt agc gcc
1498
Leu His Met Pro Ser Gln Pro Leu Asn Ala Gly Glu Ser Val Ser Ala
465   470   475   480

gct act gcc gca atc gcc tcc aat ccc aac ttt gcc gcg gct cta gct
1546
Ala Thr Ala Ala Ile Ala Ser Asn Pro Asn Phe Ala Ala Ala Leu Ala
                485   490   495

637

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gca gcc ata act tcg att atc aac ggt tcg aac aat cag cag aat ggg
1594
Ala Ala Ile Thr Ser Ile Ile Asn Gly Ser Asn Asn Gln Gln Asn Gly
        500             505             510

aac aac aat aac agt aat gtt aca acg agc aac gtt gac aat agg caa
1642
Asn Asn Asn Asn Ser Asn Val Thr Thr Ser Asn Val Asp Asn Arg Gln
        515             520             525

taa catttttta taagttttag ttagggactt tttatcggtc gattttgttt
1695

tgtttttctt ttattacatt attttttagt tacggctttt ttttgttttt tcttttcttt
1755

cccaaacaac aagtattgag agcaattccc ccccccccc ct
1797
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1               5               10              15

Lys Pro Ser Asp Glu Gln His Gln Arg Ala Val Val Asn Glu Val Asp
        20              25              30

Phe Phe Arg Ser Ala Glu Lys Arg Asp Arg Val Ser Arg Glu Glu Gln
        35              40              45

Asn Ile Ile Ala Asp Glu Thr His Arg Val His Val Lys Arg Glu Asn
    50              55              60

Ser Arg Val Asp Asp His Asp Asp Arg Ser Thr Asp His Ile Asn Ile
65              70              75              80

Gly Leu Asn Leu Leu Thr Ala Asn Thr Gly Ser Asp Glu Ser Met Val
                85              90              95

Asp Asp Gly Leu Ser Val Asp Met Glu Glu Lys Arg Thr Lys Cys Glu
            100             105             110

Asn Ala Gln Leu Arg Glu Glu Leu Lys Lys Ala Ser Glu Asp Asn Gln
        115             120             125

Arg Leu Lys Gln Met Leu Ser Gln Thr Thr Asn Asn Phe Asn Ser Leu
    130             135             140

Gln Met Gln Leu Val Ala Val Met Arg Gln Gln Glu Asp His His His
145             150             155             160
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Leu Ala Thr Thr Glu Asn Asn Asp Asn Val Lys Asn Arg His Glu Val
              165   170   175

Pro Glu Met Val Pro Arg Gln Phe Ile Asp Leu Gly Pro His Ser Asp
              180   185   190

Glu Val Ser Ser Glu Glu Arg Thr Thr Val Arg Ser Gly Ser Pro Pro
          195   200   205

Ser Leu Leu Glu Lys Ser Ser Ser Arg Gln Asn Gly Lys Arg Val Leu
    210   215   220

Val Arg Glu Glu Ser Pro Glu Thr Glu Ser Asn Gly Trp Arg Asn Pro
225   230   235   240

Asn Lys Val Pro Lys His His Ala Ser Ser Ser Ile Cys Gly Gly Asn
              245   250   255

Gly Ser Glu Asn Ala Ser Ser Lys Val Ile Glu Gln Ala Ala Ala Glu
              260   265   270

Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala Arg Ser Glu Ala
          275   280   285

Pro Met Leu Ser Asp Gly Cys Gln Trp Arg Lys Tyr Gly Gln Lys Met
    290   295   300

Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg Cys Thr Met Ala
305   310   315   320

Val Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala Glu Asp Arg
              325   330   335

Thr Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His Pro Leu Pro
              340   345   350

Pro Ala Ala Met Asn Met Ala Ser Thr Thr Thr Ala Ala Ala Ser Met
          355   360   365

Leu Leu Ser Gly Ser Thr Met Ser Asn Gln Asp Gly Leu Met Asn Pro
    370   375   380

Thr Asn Leu Leu Ala Arg Thr Ile Leu Pro Cys Ser Ser Ser Met Ala
385   390   395   400

639

Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Ile Thr Leu Asp Leu Thr
                405   410   415

Glu Ser Pro Asn Gly Asn Asn Pro Thr Asn Asn Pro Leu Met Gln Phe
            420   425   430

Ser Gln Arg Ser Gly Leu Val Glu Leu Asn Gln Ser Val Leu Pro His
        435   440   445

Met Met Gly Gln Ala Leu Tyr Tyr Asn Gln Gln Ser Lys Phe Ser Gly
    450   455   460

Leu His Met Pro Ser Gln Pro Leu Asn Ala Gly Glu Ser Val Ser Ala
465   470   475   480

Ala Thr Ala Ala Ile Ala Ser Asn Pro Asn Phe Ala Ala Ala Leu Ala
            485   490   495

Ala Ala Ile Thr Ser Ile Ile Asn Gly Ser Asn Asn Gln Gln Asn Gly
            500   505   510

Asn Asn Asn Asn Ser Asn Val Thr Thr Ser Asn Val Asp Asn Arg Gln
        515   520   525

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48
Met Met Met Phe Asn Glu Met Gly Met Tyr Gly Asn Met Asp Phe Phe
1   5   10   15

tct tcc tcc aca tct ctc gat gtg tgt cca tta cca caa gct gaa caa
96
Ser Ser Ser Thr Ser Leu Asp Val Cys Pro Leu Pro Gln Ala Glu Gln
            20   25   30

gaa cct gta gtt gaa gat gtc gac tac acc gat gat gag atg gat gtg
144
Glu Pro Val Val Glu Asp Val Asp Tyr Thr Asp Asp Glu Met Asp Val
        35   40   45

gat gag ctt gag aag agg atg tgg aga gac aaa atg cgt ttg aaa cgt
192
Asp Glu Leu Glu Lys Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
    50   55   60

ctc aag gag caa cag agt aag tgt aaa gaa ggc gtc gat ggt tcg aaa
240
Leu Lys Glu Gln Gln Ser Lys Cys Lys Glu Gly Val Asp Gly Ser Lys
65   70   75   80

640

cag agg cag tcg caa gag caa gct agg agg aag aaa atg tct aga gcc
288
Gln Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala
              85   90   95

caa gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa
336
Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys
          100   105   110

gct caa ggc ttt gtt tat ggt att att cct gag aag ggt aag cct gtg
384
Ala Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro Val
          115   120   125

act ggt gct tcg gat aat ttg agg gaa tgg tgg aaa gat aag gtt agg
432
Thr Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg
      130   135   140

ttt gat cgt aat ggt cca gct gct att gct aag tat cag tca gag aat
480
Phe Asp Arg Asn Gly Pro Ala Ala Ile Ala Lys Tyr Gln Ser Glu Asn
145   150   155   160

aat att tct gga ggg agt aat gat tgt aac agc ttg gtt ggt cca aca
528
Asn Ile Ser Gly Gly Ser Asn Asp Cys Asn Ser Leu Val Gly Pro Thr
                  165   170   175

ccg cat acg ctt cag gag ctt cag gac acg act ctt ggt tcg ctt tta
576
Pro His Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu
              180   185   190

tcg gct ttg atg caa cat tgt gat cca ccg cag aga cgg ttt cct ttg
624
Ser Ala Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu
          195   200   205

gag aaa gga gtt tct cca cct tgg tgg cct aat ggg aat gaa gag tgg
672
Glu Lys Gly Val Ser Pro Pro Trp Trp Pro Asn Gly Asn Glu Glu Trp
      210   215   220

tgg cct cag ctt ggt tta cca aat gag caa ggt cct cct cct tat aag
720
Trp Pro Gln Leu Gly Leu Pro Asn Glu Gln Gly Pro Pro Pro Tyr Lys
225   230   235   240

aag cct cat gat ttg aag aaa gct tgg aaa gtc ggt gtt tta act gcg
768
Lys Pro His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala
              245   250   255

gtg atc aag cat atg tcg ccg gat att gcg aag atc cgt aag ctt gtg
816
Val Ile Lys His Met Ser Pro Asp Ile Ala Lys Ile Arg Lys Leu Val
              260   265   270

641

agg caa tca aaa tgc ttg cag gat aag atg acg gcg aaa gag agt gct
864
Arg Gln Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala
        275   280   285

act tgg ctt gcc att att aac caa gaa gag gtt gtg gct cgg gag ctt
912
Thr Trp Leu Ala Ile Ile Asn Gln Glu Glu Val Val Ala Arg Glu Leu
    290   295   300

tat ccc gag tca tgc cct cct ctt tct tct tct tca tca tta gga agc
960
Tyr Pro Glu Ser Cys Pro Pro Leu Ser Ser Ser Ser Ser Leu Gly Ser
305   310   315   320

ggg tcg ctt ctc att aat gat tgt agc gag tat gac gtt gaa ggt ttc
1008
Gly Ser Leu Leu Ile Asn Asp Cys Ser Glu Tyr Asp Val Glu Gly Phe
            325   330   335

gag aag gaa caa cat ggt ttc gat gtg gaa gag cgg aaa cca gag ata
1056
Glu Lys Glu Gln His Gly Phe Asp Val Glu Glu Arg Lys Pro Glu Ile
            340   345   -   350

gtg atg atg cat cct cta gca agc ttt ggg gtt gct aaa atg caa cat
1104
Val Met Met His Pro Leu Ala Ser Phe Gly Val Ala Lys Met Gln His
        355   360   365

ttt ccc ata aag gag gag gtc gcc acc acg gta aac tta gag ttc acg
1152
Phe Pro Ile Lys Glu Glu Val Ala Thr Thr Val Asn Leu Glu Phe Thr
    370   375   380

aga aag agg aag cag aac aat gat atg aat gtt atg gta atg gac aga
1200
Arg Lys Arg Lys Gln Asn Asn Asp Met Asn Val Met Val Met Asp Arg
385   390   395   400

tca gca ggt tac act tgt gag aat ggt cag tgt cct cac agc aaa atg
1248
Ser Ala Gly Tyr Thr Cys Glu Asn Gly Gln Cys Pro His Ser Lys Met
            405   410   415

aat ctt gga ttt caa gac agg agt tca agg gac aac cac cag atg gtt
1296
Asn Leu Gly Phe Gln Asp Arg Ser Ser Arg Asp Asn His Gln Met Val
            420   425   430

tgt cca tat aga gac aat cgt tta gcg tat gga gca tcc aag ttt cat
1344
Cys Pro Tyr Arg Asp Asn Arg Leu Ala Tyr Gly Ala Ser Lys Phe His
        435   440   445

atg ggt gga atg aaa cta gta gtt cct cag caa cca gtc caa ccg atc
1392
Met Gly Gly Met Lys Leu Val Val Pro Gln Gln Pro Val Gln Pro Ile
    450   455   460

```
gac cta tcg ggc gtt gga gtt ccg gaa aac ggg cag aag atg atc acc
1440
Asp Leu Ser Gly Val Gly Val Pro Glu Asn Gly Gln Lys Met Ile Thr
465                 470             475                 480

gag ctt atg gcc atg tac gac aga aat gtc caa agc aac caa acg cct
1488
Glu Leu Met Ala Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Pro
                485             490                 495

cct act ttg atg gaa aac caa agc atg gtc att gat gca aaa gca gct
1536
Pro Thr Leu Met Glu Asn Gln Ser Met Val Ile Asp Ala Lys Ala Ala
            500             505             510

cag aat cag cag ctg aat ttc aac agt ggc aat caa atg ttt atg caa
1584
Gln Asn Gln Gln Leu Asn Phe Asn Ser Gly Asn Gln Met Phe Met Gln
        515             520             525

caa ggg acg aac aac ggg gtt aac aat cgg ttc cag atg gtg ttt gat
1632
Gln Gly Thr Asn Asn Gly Val Asn Asn Arg Phe Gln Met Val Phe Asp
    530             535             540

tcg aca cca ttc gat atg gca gca ttc gat tac aga gat gat tgg caa
1680
Ser Thr Pro Phe Asp Met Ala Ala Phe Asp Tyr Arg Asp Asp Trp Gln
545             550             555                 560

acc gga gca atg gaa gga atg ggg aag cag cag cag cag cag cag cag
1728
Thr Gly Ala Met Glu Gly Met Gly Lys Gln Gln Gln Gln Gln Gln Gln
            565             570                 575

cag caa gat gta tca ata tgg ttc tga
1755
Gln Gln Asp Val Ser Ile Trp Phe
            580
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1               5               10                  15

Ser Ser Ser Thr Ser Leu Asp Val Cys Pro Leu Pro Gln Ala Glu Gln
            20              25              30

Glu Pro Val Val Glu Asp Val Asp Tyr Thr Asp Asp Glu Met Asp Val
        35              40              45

Asp Glu Leu Glu Lys Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
    50              55              60

Leu Lys Glu Gln Gln Ser Lys Cys Lys Glu Gly Val Asp Gly Ser Lys
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65   70   75   80

Gln Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala
            85   90   95

Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys
            100   105   110

Ala Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro Val
            115   120   125

Thr Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg
    130   135   140

Phe Asp Arg Asn Gly Pro Ala Ala Ile Ala Lys Tyr Gln Ser Glu Asn
145   150   155   160

Asn Ile Ser Gly Gly Ser Asn Asp Cys Asn Ser Leu Val Gly Pro Thr
                165   170   175

Pro His Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu
            180   185   190

Ser Ala Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu
            195   200   205

Glu Lys Gly Val Ser Pro Pro Trp Trp Pro Asn Gly Asn Glu Glu Trp
    210   215   220

Trp Pro Gln Leu Gly Leu Pro Asn Glu Gln Gly Pro Pro Pro Tyr Lys
225   230   235   240

Lys Pro His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala
            245   250   255

Val Ile Lys His Met Ser Pro Asp Ile Ala Lys Ile Arg Lys Leu Val
            260   265   270

Arg Gln Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala
            275   280   285

Thr Trp Leu Ala Ile Ile Asn Gln Glu Glu Val Val Ala Arg Glu Leu
    290   295   300

Tyr Pro Glu Ser Cys Pro Pro Leu Ser Ser Ser Ser Ser Leu Gly Ser
305   310   315   320

644

Gly Ser Leu Leu Ile Asn Asp Cys Ser Glu Tyr Asp Val Glu Gly Phe
            325   330   335

Glu Lys Glu Gln His Gly Phe Asp Val Glu Glu Arg Lys Pro Glu Ile
        340   345,   350

Val Met Met His Pro Leu Ala Ser Phe Gly Val Ala Lys Met Gln His
        355   360   365

Phe Pro Ile Lys Glu Glu Val Ala Thr Thr Val Asn Leu Glu Phe Thr
    370   375   380

Arg Lys Arg Lys Gln Asn Asn Asp Met Asn Val Met Val Met Asp Arg
385   390   395   400

Ser Ala Gly Tyr Thr Cys Glu Asn Gly Gln Cys Pro His Ser Lys Met
            405   410   415

Asn Leu Gly Phe Gln Asp Arg Ser Ser Arg Asp Asn His Gln Met Val
            420   425   430

Cys Pro Tyr Arg Asp Asn Arg Leu Ala Tyr Gly Ala Ser Lys Phe His
        435   440   445

Met Gly Gly Met Lys Leu Val Val Pro Gln Gln Pro Val Gln Pro Ile
    450   455   460

Asp Leu Ser Gly Val Gly Val Pro Glu Asn Gly Gln Lys Met Ile Thr
465   470   475   480

Glu Leu Met Ala Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Pro
            485   490   495

Pro Thr Leu Met Glu Asn Gln Ser Met Val Ile Asp Ala Lys Ala Ala
        500   505   510

Gln Asn Gln Gln Leu Asn Phe Asn Ser Gly Asn Gln Met Phe Met Gln
        515   520   525

Gln Gly Thr Asn Asn Gly Val Asn Asn Arg Phe Gln Met Val Phe Asp
    530   535   540

Ser Thr Pro Phe Asp Met Ala Ala Phe Asp Tyr Arg Asp Asp Trp Gln
545   550   555   560

645

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Thr Gly Ala Met Glu Gly Met Gly Lys Gln Gln Gln Gln Gln Gln
            565             570             575


Gln Gln Asp Val Ser Ile Trp Phe
        580


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gaaactaggg tttattatct tctccttctt tttcccatca ccatagaaaa ggcagagacc ·
120

tttttcttca tcattttat tctccttctt cttctgctgt tcatttctcc aggttaca
178

atg atg ttt aat gag atg gga atg tgt gga aac atg gat ttc ttc tct
226
Met Met Phe Asn Glu Met Gly Met Cys Gly Asn Met Asp Phe Phe Ser
1               5               10              15

tct gga tca ctt ggt gaa gtt gat ttc tgt cct gtt cca caa gct gag
274
Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu
            20              25              30

cct gat tcc att gtt gaa gat gac tat act gat gat gag att gat gtt
322
Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val
        35              40              45

gat gaa ttg gag agg agg atg tgg aga gac aaa atg cgg ctt aaa cgt
370
Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
    50              55              60

ctc aag gag cag gat aag ggt aaa gaa ggt gtt gat gct gct aaa cag
418
Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln
65              70              75              80

agg cag tct caa gag caa gct agg agg aag aaa atg tct aga gct caa
466
Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
            85              90              95

gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa gct
514
Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala
            100             105             110

caa ggc ttt gtt tat ggg att att ccg gag aat ggg aag cct gtg act
562
Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr
            115             120             125
```

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ggt gct tct gat aat tta agg gag tgg tgg aaa gat aag gtt agg ttt
610
Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe
    130             135             140

gat cgt aat ggt cct gcg gct att acc aag tat caa gcg gag aat aat
658
Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn
145             150             155             160

atc ccg ggg att cat gaa ggt aat aac ccg att gga ccg act cct cat
706
Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His
                165             170             175

acc ttg caa gag ctt caa gac acg act ctt gga tcg ctt ttg tct gcg
754
Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu Ser Ala
                180             185             190

ttg atg caa cac tgt gat cct cct cag aga cgt ttt cct ttg gag aaa
802
Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys
            195             200             205

gga gtt cct cct ccg tgg tgg cct aat ggg aaa gag gat tgg tgg cct
850
Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro
    210             215             220

caa ctt ggt ttg cct aaa gat caa ggt cct gca cct tac aag aag cct
898
Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro
225             230             235             240

cat gat ttg aag aag gcg tgg aaa gtc ggc gtt ttg act gcg gtt atc
946
His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile
            245             250             255

aag cat atg ttt cct gat att gct aag atc cgt aag ctc gtg agg caa
994
Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln
            260             265             270

tct aaa tgt ttg cag gat aag atg act gct aaa gag agt gct acc tgg
1042
Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp
            275             280             285

ctt gct att att aac caa gaa gag tcc ttg gct aga gag ctt tat ccc
1090
Leu Ala Ile Ile Asn Gln Glu Glu Ser Leu Ala Arg Glu Leu Tyr Pro
        290             295             300

gag tca tgt cca cct ctt tct ctg tct ggt gga agt tgc tcg ctt ctg
1138
Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu
305             310             315             320
```

647

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atg aat gat tgc agt caa tac gat gtt gaa ggt ttc gag aag gag tct
1186
Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser
            325                 330                 335

cac tat gaa gtg gaa gag ctc aag cca gaa aaa gtt atg aat tct tca
1234
His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser
            340                 345                 350

aac ttt ggg atg gtt gct aaa atg cat gac ttt cct gtc aaa gaa gaa
1282
Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu
        355                 360                 365

gtc cca gca gga aac tcg gaa ttc atg aga aag aga aag cca aac aga
1330
Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg
    370                 375                 380

gat ctg aac act att atg gac aga acc gtt ttc acc tgc gag aat ctt
1378
Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu
385                 390              -- 395                 400

ggg tgt gcg cac agc gaa atc agc cgg gga ttt ctg gat agg aat tcg
1426
Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser
            405                 410                 415

aga gac aac cat caa ctg gca tgt cca cat cga gac agt cgc tta ccg
1474
Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro
            420                 425                 430

tat gga gca gca cca tcc agg ttt cat gtc aat gaa gtt aag cct gta
1522
Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val
        435                 440                 445

gtt gga ttt cct cag cca agg cca gtg aac tca gta gcc caa cca att
1570
Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile
    450                 455                 460

gac tta acg ggt ata gtt cct gaa gat gga cag aag atg atc tca gag
1618
Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu
465                 470                 475                 480

ctc atg tcc atg tac gac aga aat gtc cag agc aac caa acc tct atg
1666
Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met
                485                 490                 495

gtc atg gaa aat caa agc gtg tca ctg ctt caa ccc aca gtc cat aac
1714
Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn
            500                 505                 510
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cat caa gaa cat ctc cag ttc cca gga aac atg gtg gaa gga agt ttc
1762
His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe
          515   520   525

ttt gaa gac ttg aac atc cca aac aga gca aac aac aac aac agc agc
1810
Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser
    530   535   540

aac aat caa acg ttt ttt caa ggg aac aac aac aac aac aat gtg ttt
1858
Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Asn Val Phe
545   550   555   560

aag ttc gac act gca gat cac aac aac ttt gaa gct gca cat aac aac
1906
Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn
          565   570 ·   575

aac aat aac agt agc ggc aac agg ttc cag ctt gtg ttt gat tcc aca
1954
Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr
          580   585   590

ccg ttc gac atg gcg tca ttc gat tac aga gat gat atg tcg atg cca
2002
Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro
          595   600   605

gga gta gta gga acg atg gat gga atg cag cag aag cag caa gat gta
2050
Gly Val Val Gly Thr Met Asp Gly Met Gln Gln Lys Gln Gln Asp Val
    610   615   620

tcc ata tgg ttc taa agtcttggta gtagatttca tcttctctta tttttatctt
2105
Ser Ile Trp Phe
625

ttgtgttctt acattcactc aaccatgtaa tatttttcc tgggtctctc tgtctctatc
2165

gcttgttatg atgtgtctgt aagagtctct aaaaactctc tgttactgtg tgtctttgtc
2225

tcggcttggt gaatctctct gtcatcatca gcttttagtt acacacccga cttggggatg
2285

aacgaacact aaatgtaagt tttca
2310

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Met Met Phe Asn Glu Met Gly Met Cys Gly Asn Met Asp Phe Phe Ser
1   5   10   15

Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu

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                20                      25                      30


Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val
        35                  40                  45


Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
        50                  55                  60


Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln
65                  70                  75                  80


Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
                85                  90                  95


Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala
            100                 105                 110


Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr
            115                 120                 125


Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe
    130                 135                 140


Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn
145                 150                 155                 160


Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His
            165                 170                 175


Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu Ser Ala
            180                 185                 190


Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys
        195                 200                 205


Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro
    210                 215                 220


Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro
225                 230                 235                 240


His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile
                245                 250                 255


Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln
            260                 265                 270
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650

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Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp
    275                 280             285

Leu Ala Ile Ile Asn Gln Glu Glu Ser Leu Ala Arg Glu Leu Tyr Pro
    290             295             300

Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu
305             310             315             320

Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser
            325             330             335

His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser
            340             345             350

Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu
        355             360             365

Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg
    370             375             380

Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu
385             390             395             400

Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser
            405             410             415

Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro
            420             425             430

Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val
        435             440             445

Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile
    450             455             460

Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu
465             470             475             480

Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met
            485             490             495

Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn
            500             505             510
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651

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His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe
        515                 520                 525


Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser
        530                 535                 540


Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Asn Val Phe
545                 550                 555                 560


Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn
                565                 570                 575


Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr
            580                 585                 590


Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro
        595                 600                 605


Gly Val Val Gly Thr Met Asp Gly Met Gln Gln Lys Gln Gln Asp Val
    610                 615                 620


Ser Ile Trp Phe
625
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atacatat atg gct gac cct aac aat cct atc act gaa cct aaa gct ata
110
        · Met Ala Asp Pro Asn Asn Pro Ile Thr Glu Pro Lys Ala Ile
          1                 5                 10

atc caa tct tct act tca tcg tca gtt act att gtg cca gtt ccc acg
158
Ile Gln Ser Ser Thr Ser Ser Ser Val Thr Ile Val Pro Val Pro Thr
15                  20                  25                  30

tgc ggt gac agc ctc tct gac tct gcc acg tgt gaa aac cct tgt cca
206
Cys Gly Asp Ser Leu Ser Asp Ser Ala Thr Cys Glu Asn Pro Cys Pro
                35                  40                  45

ctt gat act atc act act act act act gtt tgt ttt gcg gct cct
254
Leu Asp Thr Ile Thr Thr Thr Thr Thr Val Cys Phe Ala Ala Pro
            50                  55                  60
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tct tct act gca agt ggt aat gat att aat act tta atg gcc act gac
302
Ser Ser Thr Ala Ser Gly Asn Asp Ile Asn Thr Leu Met Ala Thr Asp
        65   70   75

acc gac atc tct cgc cgg aaa aag aat ccg gtt tat cgg gga att cgt
350
Thr Asp Ile Ser Arg Arg Lys Lys Asn Pro Val Tyr Arg Gly Ile Arg
    80   85   90

tgt cgg agt gga aaa tgg gtg tct gaa atc cga gag cct aaa aag act
398
Cys Arg Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Thr
95   100   105   110

aca cgt gtc tgg ctt ggg act tat ccg acg ccg gag atg gct gct gcc
446
Thr Arg Val Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala Ala
            115   120   125

gca tat gac gtg gcg gcg tta gct ctt aaa ggt gga gac act ctc ttg
494
Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu Leu
            130   135   140

aac ttc ccg gat tcc ctg gga tct tac ccc att ccc ctt tcc tct tcc
542
Asn Phe Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Leu Ser Ser Ser
        145   150   155

gca gct cat atc aga tgc gct gca gct gcg gct gct gcg act agg ggt
590
Ala Ala His Ile Arg Cys Ala Ala Ala Ala Ala Ala Thr Arg Gly
    160   165   170

gcg gct gga gcg gcc gtg aag gta ggt caa aag aag gaa gat aaa gtt
638
Ala Ala Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys Val
175   180   185   190

tat gat acg gcg gaa tct tca act atg ggg ttt gtg gat gaa gaa gag
686
Tyr Asp Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu Glu
                195   200   205

cta ttg aac atg cct ggt ttg cta gcg gat atg gcc aaa ggg atg atg
734
Leu Leu Asn Met Pro Gly Leu Leu Ala Asp Met Ala Lys Gly Met Met
            210   215   220

gtg gct cca ccg tgg atg gga tct cca ccg tca gat gat tcg cca gag
782
Val Ala Pro Pro Trp Met Gly Ser Pro Pro Ser Asp Asp Ser Pro Glu
        225   230   235

aat tct gat gga gag agc ttg tgg agc tat tga tcgattgaaa gcagtttaat
835
Asn Ser Asp Gly Glu Ser Leu Trp Ser Tyr
    240   245

atcttttttg gatcctttgt tcacgtttat gctagtcatc tttgtttctt tatcctatga
895

ttgttagaga tgatttgtta aatatataat cgtaatgatt ttcactttt tttattcaaa
955

aaaaaaaa
963

<210> 360 <211> 248 <212> PRT <213> Arabidopsis thaliana <400>
360

Met Ala Asp Pro Asn Asn Pro Ile Thr Glu Pro Lys Ala Ile Ile Gln
1   5   10   15

Ser Ser Thr Ser Ser Ser Val Thr Ile Val Pro Val Pro Thr Cys Gly
            20   25   30

Asp Ser Leu Ser Asp Ser Ala Thr Cys Glu Asn Pro Cys Pro Leu Asp
            35   40   45

Thr Ile Thr Thr Thr Thr Thr Thr Val Cys Phe Ala Ala Pro Ser Ser
        50   55   60

Thr Ala Ser Gly Asn Asp Ile Asn Thr Leu Met Ala Thr Asp Thr Asp
65   70   75   80

Ile Ser Arg Arg Lys Lys Asn Pro Val Tyr Arg Gly Ile Arg Cys Arg
                85   90   95

Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Thr Thr Arg
            100   105   110

Val Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala Ala Ala Tyr
        115   120   125

Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu Leu Asn Phe
    130   135   140

Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Leu Ser Ser Ser Ala Ala
145   150   155   160

His Ile Arg Cys Ala Ala Ala Ala Ala Ala Thr Arg Gly Ala Ala
                165   170   175

Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys Val Tyr Asp
            180   185   190

```
Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu Glu Leu Leu
        195                 200                 205


Asn Met Pro Gly Leu Leu Ala Asp Met Ala Lys Gly Met Met Val Ala
    210                 215                 220


Pro Pro Trp Met Gly Ser Pro Pro Ser Asp Asp Ser Pro Glu Asn Ser
225                 230                 235                 240


Asp Gly Glu Ser Leu Trp Ser Tyr
                245



<210> 361 <211> 1239 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (6)..(1091) <223> G993

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caaat atg gaa tac agc tgt gta gac gac agt agt aca acg tca gaa tct
50
      Met Glu Tyr Ser Cys Val Asp Asp Ser Ser Thr Thr Ser Glu Ser
      1               5                   10                  15

ctc tcc atc tct act act cca aag ccg aca acg acg acg gag aag aaa
98
Leu Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys
                20                  25                  30

ctc tct tct ccg ccg gcg acg tcg atg cgt ctc tac aga atg gga agc
146
Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser
            35                  40                  45

ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag
194
Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu
        50                  55                  60

tca cgt aag ctt cct tcg tcg aaa tat aaa ggc gtt gtg cct cag cct
242
Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro
    65                  70                  75

aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg
290
Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp
80                  85                  90                  95

ctc ggt act ttc aac gag gaa gaa gaa gct gcg tct tct tac gac atc
338
Leu Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile
                100                 105                 110

gcc gtg agg aga ttc cgc ggc cgc gac gcc gtc act aac ttc aaa tct
386
Ala Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser
            115                 120                 125
```

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caa gtt gat gga aac gac gcc gaa tcg gct ttt ctt gac gct cat tct
434
Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser
        130             135             140

aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag
482
Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu
    145             150             155

ttt gag cag agt aga cgg aag ttt gtt aac ggc gac gga aaa cgc tct
530
Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser
160             165             170             175

ggg ttg gag acg gcg acg tac gga aac gac gct gtt ttg aga gcg cgt
578
Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg
            180             185             190

gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg
626
Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu
        195             200             205

aac cgt tta gtg ata ccg aaa caa cac gcg gag aag cat ttt ccg tta
674
Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu
        210             215             220

ccg gcg atg acg acg gcg atg ggg atg aat ccg tct ccg acg aaa ggc
722
Pro Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly
    225             230             235

gtt ttg att aac ttg gaa gat aga aca ggg aaa gtg tgg cgg ttc cgt
770
Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg
240             245             250             255

tac agt tac tgg aac agc agt caa agt tac gtg ttg acc aag ggc tgg
818
Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp
            260             265             270

agc cgg ttc gtt aaa gag aag aat ctt cga gcc ggt gat gtg gtt tgt
866
Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys
            275             280             285

ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa
914
Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys
            290             295             300

gtc cgg tct agt ccg gtt cag act gtg gtt agg cta ttc gga gtc aac
962
Val Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn
    305             310             315
```

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att ttc aat gtg agt aac gag aaa cca aac gac gtc gca gta gag tgt
1010
Ile Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys
320              325              330                  335

gtt ggc aag aag aga tct cgg gaa gat gat ttg ttt tcg tta ggg tgt
1058
Val Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys
              340              345                  350

tcc aag aag cag gcg att atc aac atc ttg tga caaattcttt tttttggtt
1111
Ser Lys Lys Gln Ala Ile Ile Asn Ile Leu
              355              360

tttttcttca atttgtttct cctttttcaa tattttgtat tgaaatgaca agttgtaaat
1171

taggacaaga caagaaaaaa tgacaactag acaaatagt ttttgtttaa aaaaaaaaaa
1231

aaaaaaaa
1239
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<210> 362 <211> 361 <212> PRT <213> Arabidopsis thaliana <400>
362

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Met Glu Tyr Ser Cys Val Asp Asp Ser Ser Thr Thr Ser Glu Ser Leu
1               5               10                  15

Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys Leu
              20              25                  30

Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser Gly
          35              40              45

Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu Ser
      50              55              60

Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn
65              70              75                  80

Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu
              85              90                  95

Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile Ala
              100             105             110

Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser Gln
          115             120             125

Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser Lys
```

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        130                 135                 140


Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Phe
145                 150                 155                 160


Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser Gly
                165                 170                 175


Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg Glu
                180                 185                 190


Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn
                195                 200                 205


Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro
    210                 215                 220


Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly Val
225                 230                 235                 240


Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg Tyr
                245                 250                 255


Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
                260                 265                 270


Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe
    275                 280                 285


Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val
    290                 295                 300


Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile
305                 310                 315                 320


Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val
                325                 330                 335


Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys Ser
            340                 345                 350


Lys Lys Gln Ala Ile Ile Asn Ile Leu
            355                 360
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<210> 363 <211> 913 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (52)..(783) <223> G1006

<400> 363

gataaatcaa tcaacaaaac aaaaaaaact ctatagttag tttctctgaa a atg tac
57

　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　Met Tyr
　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　1

gga cag tgc aat ata gaa tcc gac tac gct ttg ttg gag tcg ata aca
105
Gly Gln Cys Asn Ile Glu Ser Asp Tyr Ala Leu Leu Glu Ser Ile Thr
　　　5　　　　　　　　　　　　10　　　　　　　　　　15

cgt cac ttg cta gga gga gga gga gag aac gag ctg cga ctc aat gag
153
Arg His Leu Leu Gly Gly Gly Gly Glu Asn Glu Leu Arg Leu Asn Glu
　　20　　　　　　　　　　25　　　　　　　　　　30

tca aca ccg agt tcg tgt ttc aca gag agt tgg gga ggt ttg cca ttg
201
Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu Pro Leu
35　　　　　　　　40　　　　　　　　　45　　　　　　　　　50

aaa gag aat gat tca gag gac atg ttg gtg tac gga ctc ctc aaa gat
249
Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu Lys Asp
　　　　　　　　55　　　　　　　　60　　　　　　　　65

gcc ttc cat ttt gac acg tca tca tcg gac ttg agc tgt ctt ttt gat
297
Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu Phe Asp
　　　　　70　　　　　　　　75　　　　　　　　80

ttt ccg gcg gtt aaa gtc gag cca act gag aac ttt acg gcg atg gag
345
Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala Met Glu
　　　　85　　　　　　　　90　　　　　　　　95

gag aaa cca aag aaa gcg ata ccg gtt acg gag acg gca gtg aag gcg
393
Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val Lys Ala
　　100　　　　　　　　105　　　　　　　　110

aag cat tac aga gga gtg agg cag aga ccg tgg ggg aaa ttc gcg gcg
441
Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala Ala
115　　　　　　　　120　　　　　　　　125　　　　　　　　130

gag ata cgt gat ccg gcg aag aat gga gct agg gtt tgg tta ggg acg
489
Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly Thr
　　　　　　　　135　　　　　　　　140　　　　　　　　145

ttt gag acg gcg gaa gat gcg gct tta gct tac gat ata gct gct ttt
537
Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala Ala Phe
　　　　　　　150　　　　　　　　155　　　　　　　　160

agg atg cgt ggt tcc cgc gct tta ttg aat ttt ccg ttg agg gtt aat
585
Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val Asn
　　　　　　165　　　　　　　　170　　　　　　　　175

659

tcc ggt gaa cct gac ccg gtt cgg atc acg tct aag aga tct tct tcg
633
Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser Ser Ser
    180   185   190

tcg tcg tcg tcg tcg tcc tct tct acg tcg tcg tct gaa aac ggg aag
681
Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn Gly Lys
195   200   205   210

ttg aaa cga agg aga aaa gca gag aat ctg acg tcg gag gtg gtg cag
729
Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val Val Gln
            215   220   225

gtg aag tgt gag gtt ggt gat gag aca cgt gtt gat gag tta ttg gtt
777
Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu Leu Val
        230   235   240

tca taa gtttgatctt gtgtgttttg tagttgaata gttttgctat aaatgttgag
833
Ser

gcaccaagta aaagtgttcc cgtgatgtaa attagttact aaacagagcc atatatcttc
893

aatcaaaaaa aaaaaaaaaa
913

<210> 364 <211> 243 <212> PRT <213> Arabidopsis thaliana <400>
364

Met Tyr Gly Gln Cys Asn Ile Glu Ser Asp Tyr Ala Leu Leu Glu Ser
1   5   10   15

Ile Thr Arg His Leu Leu Gly Gly Gly Glu Asn Glu Leu Arg Leu
        20   25   30

Asn Glu Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu
        35   40   45

Pro Leu Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu
    50   55   60

Lys Asp Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu
65   70   75   80

Phe Asp Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala
            85   90   95

Met Glu Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val

```
         100                    105                    110
```

Lys Ala Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe
    115   120   125

Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu
    130   .   135   140

Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala
145   150   155   160

Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg
                165   170   175

Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser
                180   185   190

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn
        195   200   205

Gly Lys Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val
    210   215   220

Val Gln Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu
225   230   235   240

Leu Val Ser

<210> 365 <211> 1291 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (66)..(1031) <223> G1051

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60

cttca atg gca caa ctc cct cct aaa atc ccc aac atg aca caa cat tgg
110
      Met Ala Gln Leu Pro Pro Lys Ile Pro Asn Met Thr Gln His Trp
      1   5   10   15

cct gat ttc tct tcc caa aag ctc tct cct ttc tct acc cca acc gca
158
Pro Asp Phe Ser Ser Gln Lys Leu Ser Pro Phe Ser Thr Pro Thr Ala
                20   25   30

acc gct gtc gcc acc gct aca acc acc gta caa aac ccc tca tgg gtc
206
Thr Ala Val Ala Thr Ala Thr Thr Thr Val Gln Asn Pro Ser Trp Val
            35   40   .   45
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```
gac gaa ttc ctc gac ttc tca gcg tct cgc cgt ggc aac cac cgt cgt
254
Asp Glu Phe Leu Asp Phe Ser Ala Ser Arg Arg Gly Asn His Arg Arg
        50              55              60

tcc atc agc gac tct atc gca ttc ctc gaa gct cca aca gtc agc atc
302
Ser Ile Ser Asp Ser Ile Ala Phe Leu Glu Ala Pro Thr Val Ser Ile
    65              70              75

gaa gac cac caa ttc gac agg ttc gat gac gaa cag ttc atg tcg atg
350
Glu Asp His Gln Phe Asp Arg Phe Asp Asp Glu Gln Phe Met Ser Met
80              85              90              95

ttc acc gac gac gac aac ctt cat agc aat cct tcc cat atc aac aac
398
Phe Thr Asp Asp Asp Asn Leu His Ser Asn Pro Ser His Ile Asn Asn
            100             105             110

aaa aat aac aat gtg ggg ccc acg gga tct tcc tcg aac aca tcc acg
446
Lys Asn Asn Asn Val Gly Pro Thr Gly Ser Ser Ser Asn Thr Ser Thr
            115             120             125

ccg tcc aat agc ttc aac gac gat aac aaa gaa tta cca ccg tcc gat
494
Pro Ser Asn Ser Phe Asn Asp Asp Asn Lys Glu Leu Pro Pro Ser Asp
        130             135             140

cat aac atg aac aat aat atc aac aac aac tat aac gat gaa gtc caa
542
His Asn Met Asn Asn Asn Ile Asn Asn Asn Tyr Asn Asp Glu Val Gln
    145             150             155

agc caa tgc aag atg gag cca gaa gat ggt acg gcg tcg aat aac aat
590
Ser Gln Cys Lys Met Glu Pro Glu Asp Gly Thr Ala Ser Asn Asn Asn
160             165             170             175

tcc ggt gat agc tcc ggc aac cgg att ctc gat ccc aaa agg gtt aag
638
Ser Gly Asp Ser Ser Gly Asn Arg Ile Leu Asp Pro Lys Arg Val Lys
            180             185             190

aga ata tta gca aat cgg caa tca gca cag aga tca agg gtg agg aaa
686
Arg Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser Arg Val Arg Lys
            195             200             205

ctg caa tac ata tca gag ctc gaa cgt agc gtc act tcg ttg cag gcg
734
Leu Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr Ser Leu Gln Ala
            210             215             220

gaa gtg tca gtg tta tcg cca aga gtt gca ttc ttg gat cat caa cgt
782
Glu Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu Asp His Gln Arg
    225             230             235
```

662

ttg ctt ctt aac gtt gac aac agc gct ctc aag caa cga atc gct gct
830
Leu Leu Leu Asn Val Asp Asn Ser Ala Leu Lys Gln Arg Ile Ala Ala
240   245   250   255

tta tct caa gac aag ctt ttc aaa gac gca cat caa gaa gca ttg aag
878
Leu Ser Gln Asp Lys Leu Phe Lys Asp Ala His Gln Glu Ala Leu Lys
            260   265   270

aga gaa ata gag aga ctt cga caa gtg tat aat caa caa agc ctc acg
926
Arg Glu Ile Glu Arg Leu Arg Gln Val Tyr Asn Gln Gln Ser Leu Thr
        275   280   285

aat gtg gaa aat gca aat cat tta tcg gcg acc gga gcc ggt gct act
974
Asn Val Glu Asn Ala Asn His Leu Ser Ala Thr Gly Ala Gly Ala Thr
        290   295   300

ccg gcc gtc gac atc aag tcg tcc gtt gaa aca gag cag ctc ctc aat
1022
Pro Ala Val Asp Ile Lys Ser Ser Val Glu Thr Glu Gln Leu Leu Asn
    305   310   315

gtc tca taa attaccatc atgcatcatc atcaacattt ctctcttta
1071
Val Ser
320

gcttcttggc aaaagttctt gactataaaa tctctttcgg gtaagaaatt caggagatat
1131

acatttttta ttctaatcac attgtttta agttgtgatg aattcagttt gatgtatctt
1191

atttatttg tttatgtcgt cttttttct tggggttgat ggaagggaat catcaattgt
1251

tgtttgtaca aagaactagt tgaatttttt ttttttttt
1291

<210> 366 <211> 321 <212> PRT <213> Arabidopsis thaliana. <400>
366

Met Ala Gln Leu Pro Pro Lys Ile Pro Asn Met Thr Gln His Trp Pro
1   5   10   15

Asp Phe Ser Ser Gln Lys Leu Ser Pro Phe Ser Thr Pro Thr Ala Thr
            20   25   30

Ala Val Ala Thr Ala Thr Thr Thr Val Gln Asn Pro Ser Trp Val Asp
        35   40   45

Glu Phe Leu Asp Phe Ser Ala Ser Arg Arg Gly Asn His Arg Arg Ser
    50   55   60

```
Ile Ser Asp Ser Ile Ala Phe Leu Glu Ala Pro Thr Val Ser Ile Glu
65                  70              75                  80


Asp His Gln Phe Asp Arg Phe Asp Asp Glu Gln Phe Met Ser Met Phe
                85                  90                  95


Thr Asp Asp Asp Asn Leu His Ser Asn Pro Ser His Ile Asn Asn Lys
            100             105             110


Asn Asn Asn Val Gly Pro Thr Gly Ser Ser Ser Asn Thr Ser Thr Pro
        115             120             125


Ser Asn Ser Phe Asn Asp Asp Asn Lys Glu Leu Pro Pro Ser Asp His
    130             135             140


Asn Met Asn Asn Asn Ile Asn Asn Asn Tyr Asn Asp Glu Val Gln Ser
145             150             155                 160


Gln Cys Lys Met Glu Pro Glu Asp Gly Thr Ala Ser Asn Asn Asn Ser
            165             170             175


Gly Asp Ser Ser Gly Asn Arg Ile Leu Asp Pro Lys Arg Val Lys Arg
        180             185             190


Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser Arg Val Arg Lys Leu
        195             200                 205


Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr Ser Leu Gln Ala Glu
    210             215             220


Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu Asp His Gln Arg Leu
225             230             235                 240


Leu Leu Asn Val Asp Asn Ser Ala Leu Lys Gln Arg Ile Ala Ala Leu
            245             250             255


Ser Gln Asp Lys Leu Phe Lys Asp Ala His Gln Glu Ala Leu Lys Arg
            260             265             270


Glu Ile Glu Arg Leu Arg Gln Val Tyr Asn Gln Gln Ser Leu Thr Asn
        275             280             285


Val Glu Asn Ala Asn His Leu Ser Ala Thr Gly Ala Gly Ala Thr Pro
    290             295             300
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664

Ala Val Asp Ile Lys Ser Ser Val Glu Thr Glu Gln Leu Leu Asn Val
305   310   315   320

Ser

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<221> CDS <222> (198)..(1076) <223> G1076

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60   .

tttcaataaa atagaaaaaa acatatacaa atctacagag aagagaagct ttattttaat
120

cttgtgtgtg tgtgtgtgtt ttatataatt tttattttt ttcaaattaa aatctcttct
180

ttgcttttga tgtgggc atg gct ggt ctt gat cta ggc aca gct ttt cgt
230
                    Met Ala Gly Leu Asp Leu Gly Thr Ala Phe Arg
                    1   5   10

tac gtt aat cac cag ctc cat cgt ccc gat ctc cac ctt cac cac aat
278
Tyr Val Asn His Gln Leu His Arg Pro Asp Leu His Leu His His Asn
            15   20   25

tcc tcc tcc gat gac gtc act ccc gga gcc ggg atg ggt cat ttc acc
326
Ser Ser Ser Asp Asp Val Thr Pro Gly Ala Gly Met Gly His Phe Thr
        30   35   40

gtc gac gac gaa gac aac aac aac aac cat caa ggt ctt gac tta gcc
374
Val Asp Asp Glu Asp Asn Asn Asn Asn His Gln Gly Leu Asp Leu Ala
    45   50   55

tct ggt gga gga tca gga agc tct gga gga gga gga ggt cac ggc ggg
422
Ser Gly Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Gly His Gly Gly
60   65   70   75

gga gga gac gtc gtt ggt cgt cgt cca cgt ggc aga cca ccg gga tcc
470
Gly Gly Asp Val Val Gly Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser
                80   85   90

aag aac aaa ccg aaa cct ccg gta att atc acg cgc gag agc gca aac
518
Lys Asn Lys Pro Lys Pro Pro Val Ile Ile Thr Arg Glu Ser Ala Asn
                95   100   105

act cta aga gct cac att ctt gaa gta aca aac ggc tgc gat gtt ttc
566
Thr Leu Arg Ala His Ile Leu Glu Val Thr Asn Gly Cys Asp Val Phe
            110   115   120

665

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gac tgc gtt gcg act tat gct cgt cgg aga cag cga ggg atc tgc gtt
614
Asp Cys Val Ala Thr Tyr Ala Arg Arg Arg Gln Arg Gly Ile Cys Val
    125             130             135

ctg agc ggt agc gga acg gtc acg aac gtc agc ata cgt cag cca tct
662
Leu Ser Gly Ser Gly Thr Val Thr Asn Val Ser Ile Arg Gln Pro Ser
140             145             150             155

gcg gct gga gcg gtt gtg acg cta caa gga acg ttc gag att ctt tct
710
Ala Ala Gly Ala Val Val Thr Leu Gln Gly Thr Phe Glu Ile Leu Ser
            160             165             170

ctc tcc gga tcg ttt ctt cct cct ccg gca cct ccc gga gca acg agt
758
Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser
            175             180             185

ttg aca att ttc tta gcc gga gga caa ggt cag gtg gtt gga gga agc
806
Leu Thr Ile Phe Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser
            190             195     -       200

gtt gtg ggt gag ctt acg gcg gct gga ccg gtg att gtg att gca gct
854
Val Val Gly Glu Leu Thr Ala Ala Gly Pro Val Ile Val Ile Ala Ala
    205             210             215

tcg ttt act aat gtt gct tat gag aga ctt cct tta gaa gaa gat gag
902
Ser Phe Thr Asn Val Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu
220             225             230             235

cag cag caa cag ctt gga gga gga tct aac ggc gga ggt aat ttg ttt
950
Gln Gln Gln Gln Leu Gly Gly Gly Ser Asn Gly Gly Gly Asn Leu Phe
            240             245             250

ccg gag gtg gca gct gga gga gga gga gga ctt ccg ttc ttt aat tta
998
Pro Glu Val Ala Ala Gly Gly Gly Gly Leu Pro Phe Phe Asn Leu
            255             260             265

ccg atg aat atg caa cca aat gtg caa ctt ccg gtg gaa ggt tgg ccg
1046
Pro Met Asn Met Gln Pro Asn Val Gln Leu Pro Val Glu Gly Trp Pro
            270             275             280

ggg aat tcc ggt gga aga ggt cct ttc tga tgtgtatata ttgataatca
1096
Gly Asn Ser Gly Gly Arg Gly Pro Phe
    285             290
```

```
ttatatatat accggcggag aagctttcc ggcgaagaat ttgcgagagt gaagaaaggt
1156


tagaaaagct tttaatggac taatgaattt caaattatca tcgtgatttc ggacattgtc
1216
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666

ttgttcatca tgttaagctt aggtttattt tttgtcgttt gtagaatttt atgtttgaat
1276

cctttttttt ttctgtgaaa ctctattgtg ttcgtctgcg aaggaaaaaa aaattctcaa
1336

aaaaaa
1342

<210> 368 <211> 292 <212> PRT <213> Arabidopsis thaliana <400>
368

Met Ala Gly Leu Asp Leu Gly Thr Ala Phe Arg Tyr Val Asn His Gln
1   5   10   15

Leu His Arg Pro Asp Leu His Leu His His Asn Ser Ser Ser Asp Asp
            20   25   30

Val Thr Pro Gly Ala Gly Met Gly His Phe Thr Val Asp Asp Glu Asp
        35   40   45

Asn Asn Asn Asn His Gln Gly Leu Asp Leu Ala Ser Gly Gly Gly Ser
    50   55   60

Gly Ser Ser Gly Gly Gly Gly Gly His Gly Gly Gly Gly Asp Val Val
65   70   75   80

Gly Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys
                85   90   95

Pro Pro Val Ile Ile Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala His
            100   105   110

Ile Leu Glu Val Thr Asn Gly Cys Asp Val Phe Asp Cys Val Ala Thr
        115   120   125

Tyr Ala Arg Arg Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Ser Gly
    130   135   140

Thr Val Thr Asn Val Ser Ile Arg Gln Pro Ser Ala Ala Gly Ala Val
145   150   155   160

Val Thr Leu Gln Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe
                165   170   175

Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe Leu
            180   185   190

```
Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Glu Leu
        195                 200                 205


Thr Ala Ala Gly Pro Val Ile Val Ile Ala Ala Ser Phe Thr Asn Val
    210                 215                 220


Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu Gln Gln Gln Gln Leu
225                 230                 235                 240


Gly Gly Gly Ser Asn Gly Gly Gly Asn Leu Phe Pro Glu Val Ala Ala
                245                 250                 255


Gly Gly Gly Gly Gly Leu Pro Phe Phe Asn Leu Pro Met Asn Met Gln
            260                 265                 270


Pro Asn Val Gln Leu Pro Val Glu Gly Trp Pro Gly Asn Ser Gly Gly
        275                 280                 285


Arg Gly Pro Phe
    290
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atg gag gag aga gaa gga act aac atc aac aac atc cca acc agt ttt
48
Met Glu Glu Arg Glu Gly Thr Asn Ile Asn Asn Ile Pro Thr Ser Phe
1               5                   10                  15


ggt ctg aaa caa cat gaa act cct ctt cct cct cct ggt tac cca cca
96
Gly Leu Lys Gln His Glu Thr Pro Leu Pro Pro Pro Gly Tyr Pro Pro
            20                  25                  30


cgg tct gaa aac cct aat ctt ttt ccg gtg ggt caa tcc agc act tcc
144
Arg Ser Glu Asn Pro Asn Leu Phe Pro Val Gly Gln Ser Ser Thr Ser
            35                  40                  45


tcc gcc gcc gcc gcg gtg aaa cct tct gag aat gtt gct cct cct ttt
192
Ser Ala Ala Ala Ala Val Lys Pro Ser Glu Asn Val Ala Pro Pro Phe
    50                  55                  60


agc tta aca atg ccg gtg gag aat tct tct tct gag ttg aag aag aag
240
Ser Leu Thr Met Pro Val Glu Asn Ser Ser Ser Glu Leu Lys Lys Lys
65                  70                  75                  80


aga ggg aga cca aga aag tat aac cct gac ggc tca ctc gct gtg act
288
Arg Gly Arg Pro Arg Lys Tyr Asn Pro Asp Gly Ser Leu Ala Val Thr
                85                  90                  95
```

```
ctc tct cct atg cct atc tca tcc tcc gtt ccg ttg acg tcg gag ttt
336
Leu Ser Pro Met Pro Ile Ser Ser Ser Val Pro Leu Thr Ser Glu Phe
            100             105             110

ggt tct cgg aaa cga gga aga ggt cga gga aga ggc aga gga aga gga
384
Gly Ser Arg Lys Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly
        115             120             125

cga gga cgt gga caa gga caa gga agc aga gag ccc aat aac aac aac
432
Arg Gly Arg Gly Gln Gly Gln Gly Ser Arg Glu Pro Asn Asn Asn Asn
    130             135             140

aac gac aac aat tgg ctc aag aat cct cag atg ttc gaa ttt aac aac
480
Asn Asp Asn Asn Trp Leu Lys Asn Pro Gln Met Phe Glu Phe Asn Asn
145             150             155             160

aac act cct act tct ggt gga gga gga cct gct gaa att gtc agt cca
528
Asn Thr Pro Thr Ser Gly Gly Gly Gly Pro Ala Glu Ile Val Ser Pro
                165             170             175

agt ttt aca cct cat gtg ctc aca gta aat gcc ggt gag gat gtg aca
576
Ser Phe Thr Pro His Val Leu Thr Val Asn Ala Gly Glu Asp Val Thr
            180             185             190

atg aag ata atg aca ttc tct caa caa ggc tcg cgt gct att tgt att
624
Met Lys Ile Met Thr Phe Ser Gln Gln Gly Ser Arg Ala Ile Cys Ile
        195             200             205

ctt tca gcg aac ggt ccc ata tcc aat gtt aca ctt cgt caa tct atg
672
Leu Ser Ala Asn Gly Pro Ile Ser Asn Val Thr Leu Arg Gln Ser Met
    210             215             220

aca tct ggt ggt act ctc act tat gag ggt cat ttt gag att ctt tct
720
Thr Ser Gly Gly Thr Leu Thr Tyr Glu Gly His Phe Glu Ile Leu Ser
225             230             235             240

ttg acg ggt tcg ttt ata cca agc gag agt gga gga acc cga agc aga
768
Leu Thr Gly Ser Phe Ile Pro Ser Glu Ser Gly Gly Thr Arg Ser Arg
                245             250             255

gct ggt ggg atg agt gtc tct ctt gca gga caa gat ggt cgt gtc ttt
816
Ala Gly Gly Met Ser Val Ser Leu Ala Gly Gln Asp Gly Arg Val Phe
            260             265             270

ggt ggt gga ctt gct ggt ctc ttt att gcc gct ggt cct gtt cag gta
864
Gly Gly Gly Leu Ala Gly Leu Phe Ile Ala Ala Gly Pro Val Gln Val
        275             280             285
```

atg gta ggg agt ttt ata gcg ggt cag gag gaa tcg cag cag cag cag
912
Met Val Gly Ser Phe Ile Ala Gly Gln Glu Glu Ser Gln Gln Gln Gln
    290   295   300

cag cag ata aag aag caa aga agg gaa aga ctc ggg atc ccg aca aca
960
Gln Gln Ile Lys Lys Gln Arg Arg Glu Arg Leu Gly Ile Pro Thr Thr
305   310   315   320

aca caa gct tct aat atc tca ttc ggt ggc tca gcg gaa gat cct aag
1008
Thr Gln Ala Ser Asn Ile Ser Phe Gly Gly Ser Ala Glu Asp Pro Lys
            325   330   335

gct aga tac ggg ctc aac aag cct gtt gtt att cag cca cca ccg gtg
1056
Ala Arg Tyr Gly Leu Asn Lys Pro Val Val Ile Gln Pro Pro Pro Val
            340   345   350

tct gca cca cct gtg tcc ttt tcg cat gaa cca agt act aac acc gtc
1104.
Ser Ala Pro Pro Val Ser Phe Ser His Glu Pro Ser Thr Asn Thr Val
            355   360   365

cat ggt tac tat gca aat aac aca gct aac cat atc aag gat ctc ttc
1152
His Gly Tyr Tyr Ala Asn Asn Thr Ala Asn His Ile Lys Asp Leu Phe
    370   375   380

tct tcc ctc cct gga gaa gat agg gaa gaa gat gag gat gat tta gaa
1200
Ser Ser Leu Pro Gly Glu Asp Arg Glu Glu Asp Glu Asp Asp Leu Glu
385   390   395   400

ggt gaa gat gat gaa gaa ttc gga ggc cat agc gaa tct gac acc gag
1248
Gly Glu Asp Asp Glu Glu Phe Gly Gly His Ser Glu Ser Asp Thr Glu
            405   410   415

gtt cca agc tga tgatcgatgg aaagaatccg acatatatgt gttatgaatc
1300
Val Pro Ser

ttgagttgtt ttatttcggt gtcttcagat ttttttagag cgtaatggta ttttttttct
1360

ttcagattgt tagttgttaa agtcttaaac agagatattt cactaaaagt tagggtttac
1420

tagaggatgt aatctttagg gttctttgac ttgtgtcttt cttttaatcc tcagatggtt
1480

gttgtaggct tgtagccaat cttagtgtgt gttcaaactc tctccttcaa tcaaactccc
1540

caatgacttc attttg
1556

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370

Met Glu Glu Arg Glu Gly Thr Asn Ile Asn Asn Ile Pro Thr Ser Phe
1   5   10   15

Gly Leu Lys Gln His Glu Thr Pro Leu Pro Pro Pro Gly Tyr Pro Pro
            20   25   30

Arg Ser Glu Asn Pro Asn Leu Phe Pro Val Gly Gln Ser Ser Thr Ser
        35   40   45

Ser Ala Ala Ala Ala Val Lys Pro Ser Glu Asn Val Ala Pro Pro Phe
    50   55   60

Ser Leu Thr Met Pro Val Glu Asn Ser Ser Ser Glu Leu Lys Lys Lys
65   70   75   80

Arg Gly Arg Pro Arg Lys Tyr Asn Pro Asp Gly Ser Leu Ala Val Thr
                85   90   95

Leu Ser Pro Met Pro Ile Ser Ser Ser Val Pro Leu Thr Ser Glu Phe
            100   105   110

Gly Ser Arg Lys Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly
        115   120   125

Arg Gly Arg Gly Gln Gly Gln Gly Ser Arg Glu Pro Asn Asn Asn Asn
    130   135   140

Asn Asp Asn Asn Trp Leu Lys Asn Pro Gln Met Phe Glu Phe Asn Asn
145   150   155   160

Asn Thr Pro Thr Ser Gly Gly Gly Gly Pro Ala Glu Ile Val Ser Pro
                165   170   175

Ser Phe Thr Pro His Val Leu Thr Val Asn Ala Gly Glu Asp Val Thr
            180   185   190

Met Lys Ile Met Thr Phe Ser Gln Gln Gly Ser Arg Ala Ile Cys Ile
            195   200   205

Leu Ser Ala Asn Gly Pro Ile Ser Asn Val Thr Leu Arg Gln Ser Met
    210   215   220

Thr Ser Gly Gly Thr Leu Thr Tyr Glu Gly His Phe Glu Ile Leu Ser
225   230   235   240

671

```
Leu Thr Gly Ser Phe Ile Pro Ser Glu Ser Gly Gly Thr Arg Ser Arg
            245                 250                 255

Ala Gly Gly Met Ser Val Ser Leu Ala Gly Gln Asp Gly Arg Val Phe
            260                 265                 270

Gly Gly Gly Leu Ala Gly Leu Phe Ile Ala Ala Gly Pro Val Gln Val
            275                 280                 285

Met Val Gly Ser Phe Ile Ala Gly Gln Glu Glu Ser Gln Gln Gln Gln
    290                 295                 300

Gln Gln Ile Lys Lys Gln Arg Arg Glu Arg Leu Gly Ile Pro Thr Thr
305                 310                 315                 320

Thr Gln Ala Ser Asn Ile Ser Phe Gly Gly Ser Ala Glu Asp Pro Lys
            325                 330                 335

Ala Arg Tyr Gly Leu Asn Lys Pro Val Val Ile Gln Pro Pro Pro Val
            340                 345                 350

Ser Ala Pro Pro Val Ser Phe Ser His Glu Pro Ser Thr Asn Thr Val
            355                 360                 365

His Gly Tyr Tyr Ala Asn Asn Thr Ala Asn His Ile Lys Asp Leu Phe
    370                 375                 380

Ser Ser Leu Pro Gly Glu Asp Arg Glu Glu Asp Glu Asp Asp Leu Glu
385                 390                 395                 400

Gly Glu Asp Asp Glu Glu Phe Gly Gly His Ser Glu Ser Asp Thr Glu
            405                 410                 415

Val Pro Ser


<210>  371  <211>  1322  <212>  DNA  <213>  Arabidopsis thaliana  <220>
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60

tattgtattc ctgtaaagtt cccttggctt aaactgcaag agc atg cct ctt gat
115
                                       Met Pro Leu Asp
                                         1
```

```
acc aaa cag cag aaa tgg ttg cca tta ggc tta aat cct caa gct tgt
163
Thr Lys Gln Gln Lys Trp Leu Pro Leu Gly Leu Asn Pro Gln Ala Cys
5                   10                  15                  20

gtc cag gac aag gcg act gag tat ttc cgt cct gga att cct ttt ccg
211
Val Gln Asp Lys Ala Thr Glu Tyr Phe Arg Pro Gly Ile Pro Phe Pro
                25                  30                  35

gaa ctc ggt aaa gtt tat gca gct gag cat cag ttt cgc tat ttg cag
259
Glu Leu Gly Lys Val Tyr Ala Ala Glu His Gln Phe Arg Tyr Leu Gln
            40                  45                  50

cca ccg ttc caa gcc tta ttg tct aga tat gat cag cag tct tgt gga
307
Pro Pro Phe Gln Ala Leu Leu Ser Arg Tyr Asp Gln Gln Ser Cys Gly
        55                  60                  65

aaa caa gtt tca tgt ttg aat ggg cga tct agc aac ggt gct gct cca
355
Lys Gln Val Ser Cys Leu Asn Gly Arg Ser Ser Asn Gly Ala Ala Pro
    70                  75                  80

gag ggg gca ctc aag tct tct cgg aaa aga ttt ata gta ttc gat cag
403
Glu Gly Ala Leu Lys Ser Ser Arg Lys Arg Phe Ile Val Phe Asp Gln
85                  90                  95                  100

tcg gga gag cag act cgt ttg tta caa tgt gga ttt cct ctg cgg ttt
451
Ser Gly Glu Gln Thr Arg Leu Leu Gln Cys Gly Phe Pro Leu Arg Phe
                105                 110                 115

cct tct tct atg gat gca gag cga ggg aac att ctc ggt gcc cta cac
499
Pro Ser Ser Met Asp Ala Glu Arg Gly Asn Ile Leu Gly Ala Leu His
            120                 125                 130

cca gag aaa ggg ttt agt aaa gat cat gcc att caa gaa aag ata ttg
547
Pro Glu Lys Gly Phe Ser Lys Asp His Ala Ile Gln Glu Lys Ile Leu
        135                 140                 145

caa cat gaa gat cat gaa aat ggc gaa gaa gac tcg gaa atg cac gaa
595
Gln His Glu Asp His Glu Asn Gly Glu Glu Asp Ser Glu Met His Glu
    150                 155                 160

gac act gag gaa atc aac gcg tta ctg tat tct gat gat gac gat aat
643
Asp Thr Glu Glu Ile Asn Ala Leu Leu Tyr Ser Asp Asp Asp Asp Asn
165                 170                 175                 180

gat gat tgg gaa agt gat gat gaa gta atg agc act ggt cac tct cca
691
Asp Asp Trp Glu Ser Asp Asp Glu Val Met Ser Thr Gly His Ser Pro
                185                 190                 195
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673

ttc aca gtt gaa caa caa gcg tgc aac ata aca aca gaa gag ctg gat
739
Phe Thr Val Glu Gln Gln Ala Cys Asn Ile Thr Thr Glu Glu Leu Asp
        200   205   210

gaa act gaa agc act gtt gat ggt cca ctt ctt aaa aga cag aaa cta
787
Glu Thr Glu Ser Thr Val Asp Gly Pro Leu Leu Lys Arg Gln Lys Leu
        215   220   225

ctg gac cat tcg tac aga gac tca tca cca tcc ctt gtg ggc acc act
835
Leu Asp His Ser Tyr Arg Asp Ser Ser Pro Ser Leu Val Gly Thr Thr
        230   235   240

aaa gtc aaa ggc tta tca gat gaa aac ctt cct gaa tca aac att tca
883
Lys Val Lys Gly Leu Ser Asp Glu Asn Leu Pro Glu Ser Asn Ile Ser
245   250   255   260

agc aaa caa gaa acg ggt tct ggt ttg agc gac gag cag tca aga aaa
931
Ser Lys Gln Glu Thr Gly Ser Gly Leu Ser Asp Glu Gln Ser Arg Lys
                265   270   275

gac aag att cac acc gct ctg aga atc ctg gag agt gta gtt cca ggg
979   '
Asp Lys Ile His Thr Ala Leu Arg Ile Leu Glu Ser Val Val Pro Gly
        280   285   290

gca aag gga aaa gaa gct ctt tta cta cta gac gaa gcc att gat tac
1027
Ala Lys Gly Lys Glu Ala Leu Leu Leu Leu Asp Glu Ala Ile Asp Tyr
        295   300   305

ctc aag ttg ctg aag caa agc tta aac tca tca aag ggt ttg aat aac
1075
Leu Lys Leu Leu Lys Gln Ser Leu Asn Ser Ser Lys Gly Leu Asn Asn
    310   315   320

cat tgg tga aaaacctaca acccctttg tcctattgat aaggcatgtt
1124
His Trp
325

tggttggtta aagagaagac atgggacaaa agataatcaa tgaggtaaag gactgatgaa
1184

gaagattctc tcaaattcat taacgtgggt ttgaaacaat tagaacacgc ctggtgaccc
1244

tagtgggacc gtatccactg ttcatctagc tggatcaata gtggtttact tttggatttg
1304

gcatgctctc tcaaaaaa
1322

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372

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Met Pro Leu Asp Thr Lys Gln Gln Lys Trp Leu Pro Leu Gly Leu Asn
1               5                   10                  15


Pro Gln Ala Cys Val Gln Asp Lys Ala Thr Glu Tyr Phe Arg Pro Gly
                20                  25                  30


Ile Pro Phe Pro Glu Leu Gly Lys Val Tyr Ala Ala Glu His Gln Phe
        35                  40                  45


Arg Tyr Leu Gln Pro Pro Phe Gln Ala Leu Leu Ser Arg Tyr Asp Gln
    50                  55                  60


Gln Ser Cys Gly Lys Gln Val Ser Cys Leu Asn Gly Arg Ser Ser Asn
65                  70                  75                  80


Gly Ala Ala Pro Glu Gly Ala Leu Lys Ser Ser Arg Lys Arg Phe Ile
                85                  90                  95


Val Phe Asp Gln Ser Gly Glu Gln Thr Arg Leu Leu Gln Cys Gly Phe
                100                 105                 110


Pro Leu Arg Phe Pro Ser Ser Met Asp Ala Glu Arg Gly Asn Ile Leu
        115                 120                 125


Gly Ala Leu His Pro Glu Lys Gly Phe Ser Lys Asp His Ala Ile Gln
    130                 135                 140


Glu Lys Ile Leu Gln His Glu Asp His Glu Asn Gly Glu Glu Asp Ser
145                 150                 155                 160


Glu Met His Glu Asp Thr Glu Glu Ile Asn Ala Leu Leu Tyr Ser Asp
                165                 170                 175


Asp Asp Asp Asn Asp Asp Trp Glu Ser Asp Asp Glu Val Met Ser Thr
                180                 185                 190


Gly His Ser Pro Phe Thr Val Glu Gln Gln Ala Cys Asn Ile Thr Thr
        195                 200                 205


Glu Glu Leu Asp Glu Thr Glu Ser Thr Val Asp Gly Pro Leu Leu Lys
    210                 215                 220


Arg Gln Lys Leu Leu Asp His Ser Tyr Arg Asp Ser Ser Pro Ser Leu
225                 230                 235                 240


Val Gly Thr Thr Lys Val Lys Gly Leu Ser Asp Glu Asn Leu Pro Glu
```

675

                    245   250   255

Ser Asn Ile Ser Ser Lys Gln Glu Thr Gly Ser Gly Leu Ser Asp Glu
            260   265   270

Gln Ser Arg Lys Asp Lys Ile His Thr Ala Leu Arg Ile Leu Glu Ser
        275   280   285

Val Val Pro Gly Ala Lys Gly Lys Glu Ala Leu Leu Leu Leu Asp Glu
    290   295   300

Ala Ile Asp Tyr Leu Lys Leu Leu Lys Gln Ser Leu Asn Ser Ser Lys
305   310   315   320

Gly Leu Asn Asn His Trp
                325

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<221> CDS <222> (89)..(2008) <223> G1186

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60

gttgcaagtc tttcatctct atgcacaa atg gcg aaa gag aac agt agt cat
112
                                 Met Ala Lys Glu Asn Ser Ser His
                                 1   5

agc ctt gca gaa gca aag aga aag aga ctc act tgg att ctt tgt gta
160
Ser Leu Ala Glu Ala Lys Arg Lys Arg Leu Thr Trp Ile Leu Cys Val
    10   15   20

agt gga ctt tgc ata ttg tct tat gtt ctt gga tct tgg caa acc aac
208
Ser Gly Leu Cys Ile Leu Ser Tyr Val Leu Gly Ser Trp Gln Thr Asn
25   30   35   40

act gtc cca act tct tcc tct gag gct tac tca aga atg gga tgt gat
256
Thr Val Pro Thr Ser Ser Ser Glu Ala Tyr Ser Arg Met Gly Cys Asp
            45   50   55

gaa aca tca aca acc act cgg gct cag act act cag act caa aca aat
304
Glu Thr Ser Thr Thr Thr Arg Ala Gln Thr Thr Gln Thr Gln Thr Asn
            60   65   70

cct tct tct gac gat act tct tcc tct ttg tct tcc tca gaa cca gtt
352
Pro Ser Ser Asp Asp Thr Ser Ser Ser Leu Ser Ser Ser Glu Pro Val
            75   80   85

```
gag tta gat ttc gaa agc cat cac aaa ctc gag ctg aag att acg aat
400
Glu Leu Asp Phe Glu Ser His His Lys Leu Glu Leu Lys Ile Thr Asn
    90               95              100

caa acc gta aag tac ttt gag cca tgt gac atg tct ttg agt gag tac
448
Gln Thr Val Lys Tyr Phe Glu Pro Cys Asp Met Ser Leu Ser Glu Tyr
105              110             115                 120

act cca tgt gaa gat cga gag aga gga aga aga ttt gat agg aac atg
496
Thr Pro Cys Glu Asp Arg Glu Arg Gly Arg Arg Phe Asp Arg Asn Met
             125             130                 135

atg aag tac aga gag aga cat tgt cct tct aaa gat gag ctt ctt tat
544
Met Lys Tyr Arg Glu Arg His Cys Pro Ser Lys Asp Glu Leu Leu Tyr
        140                 145                 150

tgt ctg att cct cct cca cca aac tac aag att cca ttc aag tgg cct
592
Cys Leu Ile Pro Pro Pro Pro Asn Tyr Lys Ile Pro Phe Lys Trp Pro
        155             160                 165

caa agt aga gat tat gct tgg tac gac aac att cca cac aag gag ctt
640
Gln Ser Arg Asp Tyr Ala Trp Tyr Asp Asn Ile Pro His Lys Glu Leu
    170             175                 180

agt att gag aaa gct atc cag aac tgg att caa gta gaa ggg gaa aga
688
Ser Ile Glu Lys Ala Ile Gln Asn Trp Ile Gln Val Glu Gly Glu Arg
185                 190             195                 200

ttc agg ttc cct ggt ggt ggc aca atg ttt cca cgt gga gct gat gct
736
Phe Arg Phe Pro Gly Gly Gly Thr Met Phe Pro Arg Gly Ala Asp Ala
        205             210                 215

tac att gat gat att gct aga ctc att cct ctt act gat gga gcc att
784
Tyr Ile Asp Asp Ile Ala Arg Leu Ile Pro Leu Thr Asp Gly Ala Ile
        220             225                 230

aga aca gct att gat aca gga tgt ggt gtg gcg agt ttt ggt gca tac
832
Arg Thr Ala Ile Asp Thr Gly Cys Gly Val Ala Ser Phe Gly Ala Tyr
        235             240                 245

ttg ttg aag agg gat att gtg gct atg tca ttt gct cca agg gac act
880
Leu Leu Lys Arg Asp Ile Val Ala Met Ser Phe Ala Pro Arg Asp Thr
        250             255                 260

cat gaa gct caa gtt caa ttt gcg ttg gaa cgt gga gtt cct gcg att
928
His Glu Ala Gln Val Gln Phe Ala Leu Glu Arg Gly Val Pro Ala Ile
265                 270             275                 280
```

677

atc ggg att atg gga tca aga agg ctt cct tat cca gct aga gct ttt
976
Ile Gly Ile Met Gly Ser Arg Arg Leu Pro Tyr Pro Ala Arg Ala Phe
            285   290   295

gat ctt gct cac tgt tct cgt tgt ttg att cct tgg ttt caa aat gat
1024
Asp Leu Ala His Cys Ser Arg Cys Leu Ile Pro Trp Phe Gln Asn Asp
            300   305   310

ggt ttg tac ttg acc gaa gtg gac cgg gtt tta aga ccg ggc ggt tat
1072
Gly Leu Tyr Leu Thr Glu Val Asp Arg Val Leu Arg Pro Gly Gly Tyr
            315   320   325

tgg atc ctt tcg ggt cca ccg atc aac tgg aag aaa tac tgg aaa ggc
1120
Trp Ile Leu Ser Gly Pro Pro Ile Asn Trp Lys Lys Tyr Trp Lys Gly
    330   335   340

tgg gaa aga tca caa gag gat ttg aag caa gag caa gat tct ata gaa
1168
Trp Glu Arg Ser Gln Glu Asp Leu Lys Gln Glu Gln Asp Ser Ile Glu
345   350   -   355   360

gat gca gca aga agt ctt tgt tgg aag aaa gtt aca gaa aag ggt gat
1216
Asp Ala Ala Arg Ser Leu Cys Trp Lys Lys Val Thr Glu Lys Gly Asp
            365   370   375

tta tca att tgg caa aag cct atc aat cac gtt gag tgt aac aaa ctc
1264
Leu Ser Ile Trp Gln Lys Pro Ile Asn His Val Glu Cys Asn Lys Leu
            380   385   390

aaa cga gtt cac aaa act cct cct cta tgc agt aaa tca gat tta ccc
1312
Lys Arg Val His Lys Thr Pro Pro Leu Cys Ser Lys Ser Asp Leu Pro
            395   400   405

gat ttt gct tgg tac aaa gat ttg gaa tct tgt gta aca cca tta cca
1360
Asp Phe Ala Trp Tyr Lys Asp Leu Glu Ser Cys Val Thr Pro Leu Pro
    410   415   420

gaa gca aac agt tca gac gaa ttc gca ggc ggt gca ttg gag gat tgg
1408
Glu Ala Asn Ser Ser Asp Glu Phe Ala Gly Gly Ala Leu Glu Asp Trp
425   430   435   440

cca aac cga gct ttt gcg gtg cca cct agg ata atc ggg gga acc att
1456
Pro Asn Arg Ala Phe Ala Val Pro Pro Arg Ile Ile Gly Gly Thr Ile
            445   450   455

ccg gac att aat gct gag aaa ttc aga gaa gac aat gaa gtg tgg aag
1504
Pro Asp Ile Asn Ala Glu Lys Phe Arg Glu Asp Asn Glu Val Trp Lys
            460   465   470

678

gag aga ata tca tat tac aaa cag ata atg cca gag ctt tca aga gga
1552
Glu Arg Ile Ser Tyr Tyr Lys Gln Ile Met Pro Glu Leu Ser Arg Gly
        475   480   485

aga ttt agg aac ata atg gac atg aat gca tac ttg gga gga ttt gct
1600
Arg Phe Arg Asn Ile Met Asp Met Asn Ala Tyr Leu Gly Gly Phe Ala
    490   495   500

gcg gca atg atg aaa tat cca tct tgg gtt atg aat gtg gtt cct gtg
1648
Ala Ala Met Met Lys Tyr Pro Ser Trp Val Met Asn Val Val Pro Val
505   510   515   520

gat gct gag aag caa acg tta ggg gtt atc ttt gaa cga gga ttt ata
1696
Asp Ala Glu Lys Gln Thr Leu Gly Val Ile Phe Glu Arg Gly Phe Ile
                525   530   535

ggg act tat caa gat tgg tgt gaa gga ttc tct acg tat ccg aga act
1744
Gly Thr Tyr Gln Asp Trp Cys Glu Gly Phe Ser Thr Tyr Pro Arg Thr
            540   545   550

tat gat ttg att cat gct ggt gga ttg ttc agc att tat gag aac agg
1792
Tyr Asp Leu Ile His Ala Gly Gly Leu Phe Ser Ile Tyr Glu Asn Arg
        555   560   565

tgt gat gtt aca tta ata cta ctt gag atg gat aga att ttg aga cca
1840
Cys Asp Val Thr Leu Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro
    570   575   580

gaa gga acc gtg gtg ttt aga gac act gtg gaa atg ttg acg aag ata
1888
Glu Gly Thr Val Val Phe Arg Asp Thr Val Glu Met Leu Thr Lys Ile
585   590   595   600

caa agc ata acc aat gga atg agg tgg aag agt cgg att ttg gat cat
1936
Gln Ser Ile Thr Asn Gly Met Arg Trp Lys Ser Arg Ile Leu Asp His
                605   610   615

gag aga ggt cct ttt aat cct gag aag atc ctt ctc gct gta aaa tcc
1984
Glu Arg Gly Pro Phe Asn Pro Glu Lys Ile Leu Leu Ala Val Lys Ser
            620   625   630

tat tgg acc ggt cct tct tct tag ctagttctag ctttcttgga actctctact
2038
Tyr Trp Thr Gly Pro Ser Ser
            635

ctaatctttt tcttatcttg tgtgtctcat ctttgtttta tttttaattg tttgttttaa
2098

aagatttcta tgattatata agaaaataca gggaggatca acatcttcag agaaa
2153

679

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Arg Leu Thr Trp Ile Leu Cys Val Ser Gly Leu Cys Ile Leu Ser Tyr
            20   25   30

Val Leu Gly Ser Trp Gln Thr Asn Thr Val Pro Thr Ser Ser Ser Glu
            35   40   45

Ala Tyr Ser Arg Met Gly Cys Asp Glu Thr Ser Thr Thr Thr Arg Ala
        50   55   60

Gln Thr Thr Gln Thr Gln Thr Asn Pro Ser Ser Asp Asp Thr Ser Ser
65   70   75   80

Ser Leu Ser Ser Ser Glu Pro Val Glu Leu Asp Phe Glu Ser His His
                85   90   95

Lys Leu Glu Leu Lys Ile Thr Asn Gln Thr Val Lys Tyr Phe Glu Pro
            100   105   110

Cys Asp Met Ser Leu Ser Glu Tyr Thr Pro Cys Glu Asp Arg Glu Arg
            115   120   125

Gly Arg Arg Phe Asp Arg Asn Met Met Lys Tyr Arg Glu Arg His Cys
    130   135   140

Pro Ser Lys Asp Glu Leu Leu Tyr Cys Leu Ile Pro Pro Pro Asn
145   150   155   160

Tyr Lys Ile Pro Phe Lys Trp Pro Gln Ser Arg Asp Tyr Ala Trp Tyr
                165   170   175

Asp Asn Ile Pro His Lys Glu Leu Ser Ile Glu Lys Ala Ile Gln Asn
            180   185   190

Trp Ile Gln Val Glu Gly Glu Arg Phe Arg Phe Pro Gly Gly Gly Thr
            195   200   205

Met Phe Pro Arg Gly Ala Asp Ala Tyr Ile Asp Asp Ile Ala Arg Leu
    210   215   220

Ile Pro Leu Thr Asp Gly Ala Ile Arg Thr Ala Ile Asp Thr Gly Cys

680

225   230   235   240

Gly Val Ala Ser Phe Gly Ala Tyr Leu Leu Lys Arg Asp Ile Val Ala
            245   250   255

Met Ser Phe Ala Pro Arg Asp Thr His Glu Ala Gln Val Gln Phe Ala
            260   265   270

Leu Glu Arg Gly Val Pro Ala Ile Ile Gly Ile Met Gly Ser Arg Arg
            275   280   285

Leu Pro Tyr Pro Ala Arg Ala Phe Asp Leu Ala His Cys Ser Arg Cys
        290   295   300

Leu Ile Pro Trp Phe Gln Asn Asp Gly Leu Tyr Leu Thr Glu Val Asp
305   310   315   320

Arg Val Leu Arg Pro Gly Gly Tyr Trp Ile Leu Ser Gly Pro Pro Ile
            325   330   335

Asn Trp Lys Lys Tyr Trp Lys Gly Trp Glu Arg Ser Gln Glu Asp Leu
            340   345   350

Lys Gln Glu Gln Asp Ser Ile Glu Asp Ala Ala Arg Ser Leu Cys Trp
            355   360   365

Lys Lys Val Thr Glu Lys Gly Asp Leu Ser Ile Trp Gln Lys Pro Ile
            370   375   380

Asn His Val Glu Cys Asn Lys Leu Lys Arg Val His Lys Thr Pro Pro
385   390   395   400

Leu Cys Ser Lys Ser Asp Leu Pro Asp Phe Ala Trp Tyr Lys Asp Leu
            405   410   415

Glu Ser Cys Val Thr Pro Leu Pro Glu Ala Asn Ser Ser Asp Glu Phe
            420   425   430

Ala Gly Gly Ala Leu Glu Asp Trp Pro Asn Arg Ala Phe Ala Val Pro
            435   440   445

Pro Arg Ile Ile Gly Gly Thr Ile Pro Asp Ile Asn Ala Glu Lys Phe
            450   455   460

Arg Glu Asp Asn Glu Val Trp Lys Glu Arg Ile Ser Tyr Tyr Lys Gln
465   470   475   480

                              681

Ile Met Pro Glu Leu Ser Arg Gly Arg Phe Arg Asn Ile Met Asp Met
            485   490   495

Asn Ala Tyr Leu Gly Gly Phe Ala Ala Ala Met Met Lys Tyr Pro Ser
            500   505   510

Trp Val Met Asn Val Val Pro Val Asp Ala Glu Lys Gln Thr Leu Gly
            515   520   525

Val Ile Phe Glu Arg Gly Phe Ile Gly Thr Tyr Gln Asp Trp Cys Glu
            530   535   540

Gly Phe Ser Thr Tyr Pro Arg Thr Tyr Asp Leu Ile His Ala Gly Gly
545   550   555   560

Leu Phe Ser Ile Tyr Glu Asn Arg Cys Asp Val Thr Leu Ile Leu Leu
            565   570   575

Glu Met Asp Arg Ile Leu Arg Pro Glu Gly Thr Val Val Phe Arg Asp
            580   585   590

Thr Val Glu Met Leu Thr Lys Ile Gln Ser Ile Thr Asn Gly Met Arg
            595   600   605

Trp Lys Ser Arg Ile Leu Asp His Glu Arg Gly Pro Phe Asn Pro Glu
            610   615   620

Lys Ile Leu Leu Ala Val Lys Ser Tyr Trp Thr Gly Pro Ser Ser
625   630   635

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1   5   10   15

gtt tcg agt tcc gat gat cgt aag atc gtt gca gat act ccc gat ttt
96
Val Ser Ser Ser Asp Asp Arg Lys Ile Val Ala Asp Thr Pro Asp Phe
            20   25   30

ata gac gaa tcc tct cta gtc atc aga aca acc act gga gtc cga atc
144
Ile Asp Glu Ser Ser Leu Val Ile Arg Thr Thr Thr Gly Val Arg Ile
            35   40   45

682

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tca gct cta ccg gcg gag caa agc ctt gtt gac tcc gat gga tct aac
192
Ser Ala Leu Pro Ala Glu Gln Ser Leu Val Asp Ser Asp Gly Ser Asn
    50              55              60

tcg gag gtt acg ctt ccg gcg aaa gac gag gta att agt gat ggt ttt
240
Ser Glu Val Thr Leu Pro Ala Lys Asp Glu Val Ile Ser Asp Gly Phe
65              70              75              80

act tgt gtg aac aaa gag att gta gaa tct gat tca ttt agg gag cag
288
Thr Cys Val Asn Lys Glu Ile Val Glu Ser Asp Ser Phe Arg Glu Gln
                85              90              95

aat cta gag att gga gaa cct gat tta gat gtt gag aat cgc aaa gaa
336
Asn Leu Glu Ile Gly Glu Pro Asp Leu Asp Val Glu Asn Arg Lys Glu
            100             105             110

gcg atg att att gat tcg ata gaa aat tct gtg gtt gaa att gtt tca
384
Ala Met Ile Ile Asp Ser Ile Glu Asn Ser Val Val Glu Ile Val Ser
            115             120             125

agt gct tct ggt gat gat tgt aat gtt aag gta gag gta gtg gaa cct
432
Ser Ala Ser Gly Asp Asp Cys Asn Val Lys Val Glu Val Val Glu Pro
    130             135             140

gaa ttg ctt gtt gag aat ctg gtg gtt gct aaa gaa gaa gaa gaa atg
480
Glu Leu Leu Val Glu Asn Leu Val Val Ala Lys Glu Glu Glu Glu Met
145             150             155             160

att gtt gat tct ata gaa gat tct gtt gtt gaa att gtt tca act gct
528
Ile Val Asp Ser Ile Glu Asp Ser Val Val Glu Ile Val Ser Thr Ala
            165             170             175

tcg ggt tgt gat tgt aat gtg aag gtt gag gta gtg gac cct gaa ttg
576
Ser Gly Cys Asp Cys Asn Val Lys Val Glu Val Val Asp Pro Glu Leu
            180             185             190

tgt gtt gat aat ctg gtg gtt gtt aaa gaa gaa gaa atg att gct gat
624
Cys Val Asp Asn Leu Val Val Val Lys Glu Glu Glu Met Ile Ala Asp
            195             200             205

tcg ata gcg gaa tct gtg gtt gaa act gtt tcg aga ggt tta gat tat
672
Ser Ile Ala Glu Ser Val Val Glu Thr Val Ser Arg Gly Leu Asp Tyr
    210             215             220

gag tgt gtt gat gtc aag gtg aaa gaa gaa cct gat tta ggt aca aaa
720
Glu Cys Val Asp Val Lys Val Lys Glu Glu Pro Asp Leu Gly Thr Lys
225             230             235             240
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ttg gaa gaa gat tct gtt ttt ccg aat gtg ctt gag aag aag gat gag
768
Leu Glu Glu Asp Ser Val Phe Pro Asn Val Leu Glu Lys Lys Asp Glu
            245         250                 255

gta atc aaa gtc ctg gaa gac cag cca agt gag att aat aag aag cta
816
Val Ile Lys Val Leu Glu Asp Gln Pro Ser Glu Ile Asn Lys Lys Leu
            260         265                 270

gag caa gag aat gat gat ctc ttt tcg tct gga gat tca gat ggt aca
864
Glu Gln Glu Asn Asp Asp Leu Phe Ser Ser Gly Asp Ser Asp Gly Thr
            275         280                 285

tca gcc aag aga agg aaa atg gag atg gaa tca tat gca cca gtc ggt
912
Ser Ala Lys Arg Arg Lys Met Glu Met Glu Ser Tyr Ala Pro Val Gly
            290         295                 300

gtg gaa agc tgt atc ctg gcg ccg acg cct ctt cga gtt gtg aaa cca
960
Val Glu Ser Cys Ile Leu Ala Pro Thr Pro Leu Arg Val Val Lys Pro
305             310         -   315                 320

gag aag ttg gat acc cct gaa gtt att gat ctg gaa tca gag aaa agt
1008
Glu Lys Leu Asp Thr Pro Glu Val Ile Asp Leu Glu Ser Glu Lys Ser
            325             330                 335

tat act cat gtg aag atg gaa cct gtt gag gaa ata aag gtg gaa gct
1056
Tyr Thr His Val Lys Met Glu Pro Val Glu Glu Ile Lys Val Glu Ala
            340             345                 350

gtt aag atg agt tct caa gtg gaa gat gtg aaa ttt agc cgt gag cag
1104
Val Lys Met Ser Ser Gln Val Glu Asp Val Lys Phe Ser Arg Glu Gln
            355             360                 365

aaa tct gtg tat gtg aag aag gaa cca gtt gga gca aga aag gtg aaa
1152
Lys Ser Val Tyr Val Lys Lys Glu Pro Val Gly Ala Arg Lys Val Lys
            370             375                 380

gtg gaa gat gga gat ttt ccg gtg gag aaa gat tgg tat ttg gtt ggg
1200
Val Glu Asp Gly Asp Phe Pro Val Glu Lys Asp Trp Tyr Leu Val Gly
385             390             395                 400

agg tca ctt gtt act gct act tct acg agt aaa gga agg aaa tta gaa
1248
Arg Ser Leu Val Thr Ala Thr Ser Thr Ser Lys Gly Arg Lys Leu Glu
                405             410                 415

gat aat gag att gtg aat ttc aca ttt tct tct gtt gca aaa tgg aaa
1296
Asp Asn Glu Ile Val Asn Phe Thr Phe Ser Ser Val Ala Lys Trp Lys
            420             425                 430
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gtc cca aac att gtt cgt ttc tct acc aaa aga tgt gga gag att ggt
1344
Val Pro Asn Ile Val Arg Phe Ser Thr Lys Arg Cys Gly Glu Ile Gly
        435   440   445

aga ctt ccg atg gag tgg tca aat tgg gct gtg agc ctt tta aga tct
1392
Arg Leu Pro Met Glu Trp Ser Asn Trp Ala Val Ser Leu Leu Arg Ser
    450   455   460

ggt aag gtc aag atg tta ggc aga tgt gta gcg gcg cca cca ttt ctt
1440
Gly Lys Val Lys Met Leu Gly Arg Cys Val Ala Ala Pro Pro Phe Leu
465   470   475   480

aca atg atg caa gaa att atg cta tat gtc agt ttt tac att cac agc
1488
Thr Met Met Gln Glu Ile Met Leu Tyr Val Ser Phe Tyr Ile His Ser
                485   490   495

tcg ata ttc act gat gtt agc aaa tcc act tgg cgg att ggt tct tcc
1536
Ser Ile Phe Thr Asp Val Ser Lys Ser Thr Trp Arg Ile Gly Ser Ser
            500   505   510

cca aac ctt gag tcc acc ctt cat cct ctt ctc cag ctt ttc aaa cac
1584
Pro Asn Leu Glu Ser Thr Leu His Pro Leu Leu Gln Leu Phe Lys His
        515   520   525

ttg aca atc aaa cct tat caa aag gcg gag ttt act cct gag gaa ctc
1632
Leu Thr Ile Lys Pro Tyr Gln Lys Ala Glu Phe Thr Pro Glu Glu Leu
    530   535   540

aac tct cgt aaa cgt tca ctg aat ttg gag gat gac tat gat gaa aga
1680
Asn Ser Arg Lys Arg Ser Leu Asn Leu Glu Asp Asp Tyr Asp Glu Arg
545   550   555   560

gca gca ttg ttg gcc ata gca aaa aga aga aaa ggt tgt caa cag tct
1728
Ala Ala Leu Leu Ala Ile Ala Lys Arg Arg Lys Gly Cys Gln Gln Ser
                565   570   575

ctg gag cag aac aaa gat gaa gaa gag gct cct gag tca tat atg aat
1776
Leu Glu Gln Asn Lys Asp Glu Glu Glu Ala Pro Glu Ser Tyr Met Asn
                580   585   590

cgg gtt gtc ggc gct gcc gat tca tac aac ctt gag gaa atg gaa gct
1824
Arg Val Val Gly Ala Ala Asp Ser Tyr Asn Leu Glu Glu Met Glu Ala
            595   600   605

cca agt aca ctc acg tgt aac ctg aga ccg tac cag aaa caa gct ctc
1872
Pro Ser Thr Leu Thr Cys Asn Leu Arg Pro Tyr Gln Lys Gln Ala Leu
    610   615   620

685

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tac tgg atg tcg gaa tct gag aaa gga att gat gtt gaa aag gca gct
1920
Tyr Trp Met Ser Glu Ser Glu Lys Gly Ile Asp Val Glu Lys Ala Ala
625                 630             635                 640

gaa act cta cat cct tgc tgg gag gct tat cga atc tgt gac gag agg
1968
Glu Thr Leu His Pro Cys Trp Glu Ala Tyr Arg Ile Cys Asp Glu Arg
                645             650             655

gca cct tct att tat ttg aac atc ttt agt ggt gaa gca aca atc cag
2016
Ala Pro Ser Ile Tyr Leu Asn Ile Phe Ser Gly Glu Ala Thr Ile Gln
                660             665             670

ttt cca aca gca acg cag atg gca aga ggc gga ata ttg gca gat gcc
2064
Phe Pro Thr Ala Thr Gln Met Ala Arg Gly Gly Ile Leu Ala Asp Ala
            675             680             685

atg gga ctt ggt aaa act gtg atg aca att gca cta ata ctt gca cgg
2112
Met Gly Leu Gly Lys Thr Val Met Thr Ile Ala Leu Ile Leu Ala Arg
        690             695             700

cca ggc cga ggt aac ccg gaa aat gaa gat gtc ttg gtg gca gat gtt
2160
Pro Gly Arg Gly Asn Pro Glu Asn Glu Asp Val Leu Val Ala Asp Val
705             710             715             720

aat gca gat aaa cgc aat agg aag gag att cat atg gca cta acg act
2208
Asn Ala Asp Lys Arg Asn Arg Lys Glu Ile His Met Ala Leu Thr Thr
                725             730             735

gtg aag gca aaa gga ggc act ctt att att tgt ccc atg gca ttg tta
2256
Val Lys Ala Lys Gly Gly Thr Leu Ile Ile Cys Pro Met Ala Leu Leu
            740             745             750

agc caa tgg aag gac gag ctt gag act cat tca aag cct gac act gtg
2304
Ser Gln Trp Lys Asp Glu Leu Glu Thr His Ser Lys Pro Asp Thr Val
            755             760             765

tct gtg tta gtt tac tat gga ggg gat agg aca cat gac gcg aaa gca
2352
Ser Val Leu Val Tyr Tyr Gly Gly Asp Arg Thr His Asp Ala Lys Ala
        770             775             780

ata gcg agt cat gat gtg gtt ttg aca act tat ggt gtt tta acc tca
2400
Ile Ala Ser His Asp Val Val Leu Thr Thr Tyr Gly Val Leu Thr Ser
785             790             795             800

gct tac aag cag gat atg gca aac agt att ttc cac agg att gat tgg
2448
Ala Tyr Lys Gln Asp Met Ala Asn Ser Ile Phe His Arg Ile Asp Trp
                805             810             815
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tat agg att gtt ctt gat gaa gct cac acg atc aaa tca tgg aaa act
2496
Tyr Arg Ile Val Leu Asp Glu Ala His Thr Ile Lys Ser Trp Lys Thr
        820                 825                 830

caa gct gct aaa gcc aca ttt gag tta tct tca cat tgc aga tgg tgt
2544
Gln Ala Ala Lys Ala Thr Phe Glu Leu Ser Ser His Cys Arg Trp Cys
        835                 840                 845

ctg act ggg act ccc tta caa aac aag ctc gaa gat cta tac agt ctt
2592
Leu Thr Gly Thr Pro Leu Gln Asn Lys Leu Glu Asp Leu Tyr Ser Leu
        850                 855                 860

cta tgt ttc ctg cat gtt gaa cca tgg tgc aat tgg gct tgg tgg agt
2640
Leu Cys Phe Leu His Val Glu Pro Trp Cys Asn Trp Ala Trp Trp Ser
865                 870                 875                 880

aag ttg ata cag aag cct tat gaa aat ggt gat cca cga gga ctg aag
2688
Lys Leu Ile Gln Lys Pro Tyr Glu Asn Gly Asp Pro Arg Gly Leu Lys
                885                 890                 895

ctg atc aag gcg att ttg agg cca ttg atg ctg aga aga aca aag gaa
2736
Leu Ile Lys Ala Ile Leu Arg Pro Leu Met Leu Arg Arg Thr Lys Glu
        900                 905                 910

aca agg gac aaa gaa gga agt cta att ctt gaa ctt cct cca acc gac
2784
Thr Arg Asp Lys Glu Gly Ser Leu Ile Leu Glu Leu Pro Pro Thr Asp
        915                 920                 925

gtc caa gtc att gaa tgt gaa caa tct gaa gca gaa cgt gac ttc tat
2832
Val Gln Val Ile Glu Cys Glu Gln Ser Glu Ala Glu Arg Asp Phe Tyr
        930                 935                 940

aca gcc ttg ttc aag aga tcc aaa gtc caa ttt gac cag ttt gtg gca
2880
Thr Ala Leu Phe Lys Arg Ser Lys Val Gln Phe Asp Gln Phe Val Ala
945                 950                 955                 960

caa gga aaa gtt ctt cac aac tat gca aac atc ctc gag ctc ctc ctc
2928
Gln Gly Lys Val Leu His Asn Tyr Ala Asn Ile Leu Glu Leu Leu Leu
                965                 970                 975

cgt cta cgc caa tgt tgt aac cac cct ttt cta gtt atg agc cga gca
2976
Arg Leu Arg Gln Cys Cys Asn His Pro Phe Leu Val Met Ser Arg Ala
                980                 985                 990

gat tca caa cag tac gct gac tta gat agc ctt gca agg agg ttt ctt
3024
Asp Ser Gln Gln Tyr Ala Asp Leu Asp Ser Leu Ala Arg Arg Phe Leu
        995                 1000                1005
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687

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gat aac  aac cct gac tct gtt  tcc caa aat gct cct  tct cgg gca
3069
Asp Asn  Asn Pro Asp Ser Val  Ser Gln Asn Ala Pro  Ser Arg Ala
    1010                 1015              1020


tat atc  gaa gaa gtt atc caa  gat tta cgc gat ggc  aat agc aaa
3114
Tyr Ile  Glu Glu Val Ile Gln  Asp Leu Arg Asp Gly  Asn Ser Lys
    1025                 1030              1035


gaa tgt  cca ata tgt ctg gag  tct gca gat gat ccc  gtt ctc aca
3159
Glu Cys  Pro Ile Cys Leu Glu  Ser Ala Asp Asp Pro  Val Leu Thr
    1040                 1045              1050


cct tgt  gct cac aga atg tgc  cgt gaa tgt ctc ctt  act agc tgg
3204
Pro Cys  Ala His Arg Met Cys  Arg Glu Cys Leu Leu  Thr Ser Trp
    1055                 1060              1065


cgc tct  cca tct tgt ggt cta  tgc cca atc tgc agg  aca atc ctg
3249
Arg Ser  Pro Ser Cys Gly Leu  Cys Pro Ile Cys Arg  Thr Ile Leu
    1070                 1075              1080


aag aga  acc gaa ctt atc tca  tgc ccg aca gat agt  ata ttc cgt
3294
Lys Arg  Thr Glu Leu Ile Ser  Cys Pro Thr Asp Ser  Ile Phe Arg
    1085                 1090              1095


gtt gat  gtg gta aag aac tgg  aag gag tct tca aag  gtt tcg gag
3339
Val Asp  Val Val Lys Asn Trp  Lys Glu Ser Ser Lys  Val Ser Glu
    1100                 1105              1110


ctg ctc  aag tgc tta gag aag  atc aag aaa tct ggt  tcg ggc gag
3384
Leu Leu  Lys Cys Leu Glu Lys  Ile Lys Lys Ser Gly  Ser Gly Glu
    1115                 1120              1125


aag agc  att gtc ttt agc cag  tgg act tca ttt ttg  gat ctt ttg
3429
Lys Ser  Ile Val Phe Ser Gln  Trp Thr Ser Phe Leu  Asp Leu Leu
    1130                 1135              1140


gag att  cca ttg cga aga aga  gga ttt gag ttt ctt  aga ttc gat
3474
Glu Ile  Pro Leu Arg Arg Arg  Gly Phe Glu Phe Leu  Arg Phe Asp
    1145                 1150              1155


ggg aag  ctg gct cag aag gga  aga gaa aag gtt ttg  aaa gag ttc
3519
Gly Lys  Leu Ala Gln Lys Gly  Arg Glu Lys Val Leu  Lys Glu Phe
    1160                 1165              1170


aat gaa  acc aaa cag aaa acg  att ctg ctt atg tct  ctg aaa gct
3564
Asn Glu  Thr Lys Gln Lys Thr  Ile Leu Leu Met Ser  Leu Lys Ala
    1175                 1180              1185
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688

gga gga gtc ggt ctg aat cta act gca gct tca agt gtc ttc tta
3609
Gly Gly Val Gly Leu Asn Leu Thr Ala Ala Ser Ser Val Phe Leu
    1190   1195   1200

atg gat cca tgg tgg aat cca gcg gtg gaa gag caa gcg atc atg
3654
Met Asp Pro Trp Trp Asn Pro Ala Val Glu Glu Gln Ala Ile Met
    1205   1210   1215

aga att cat cga ata ggg cag aaa cga acg gta ttc gtc aga aga
3699
Arg Ile His Arg Ile Gly Gln Lys Arg Thr Val Phe Val Arg Arg
    1220   1225   1230

ttc att gtc aag gat aca gtg gag gaa cgg atg cag caa gtt cag
3744
Phe Ile Val Lys Asp Thr Val Glu Glu Arg Met Gln Gln Val Gln
    1235   1240   1245

gca agg aag cag agg atg att gcc gga gct ttg aca gat gaa gaa
3789
Ala Arg Lys Gln Arg Met Ile Ala Gly Ala Leu Thr Asp Glu Glu
    1250   1255   1260

gtc cgg tct gca aga ctt gag gag ctt aaa atg ttg ttc cga tga
3834
Val Arg Ser Ala Arg Leu Glu Glu Leu Lys Met Leu Phe Arg
    1265   1270   1275

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1   5   10   15

Val Ser Ser Ser Asp Asp Arg Lys Ile Val Ala Asp Thr Pro Asp Phe
            20   25   30

Ile Asp Glu Ser Ser Leu Val Ile Arg Thr Thr Thr Gly Val Arg Ile
        35   40   45

Ser Ala Leu Pro Ala Glu Gln Ser Leu Val Asp Ser Asp Gly Ser Asn
    50   55   60

Ser Glu Val Thr Leu Pro Ala Lys Asp Glu Val Ile Ser Asp Gly Phe
65   70   75   80

Thr Cys Val Asn Lys Glu Ile Val Glu Ser Asp Ser Phe Arg Glu Gln
                85   90   95

Asn Leu Glu Ile Gly Glu Pro Asp Leu Asp Val Glu Asn Arg Lys Glu
                100   105   110

689

Ala Met Ile Ile Asp Ser Ile Glu Asn Ser Val Val Glu Ile Val Ser
        115   120   125

Ser Ala Ser Gly Asp Asp Cys Asn Val Lys Val Glu Val Val Glu Pro
    130   135   140

Glu Leu Leu Val Glu Asn Leu Val Val Ala Lys Glu Glu Glu Glu Met
145   150   155   160

Ile Val Asp Ser Ile Glu Asp Ser Val Val Glu Ile Val Ser Thr Ala
            165   170   175

Ser Gly Cys Asp Cys Asn Val Lys Val Glu Val Val Asp Pro Glu Leu
        180   185   190

Cys Val Asp Asn Leu Val Val Val Lys Glu Glu Glu Met Ile Ala Asp
        195   200   205

Ser Ile Ala Glu Ser Val Val Glu Thr Val Ser Arg Gly Leu Asp Tyr
    210   215   220

Glu Cys Val Asp Val Lys Val Lys Glu Glu Pro Asp Leu Gly Thr Lys
225   230   235   240

Leu Glu Glu Asp Ser Val Phe Pro Asn Val Leu Glu Lys Lys Asp Glu
            245   250   255

Val Ile Lys Val Leu Glu Asp Gln Pro Ser Glu Ile Asn Lys Lys Leu
        260   265   270

Glu Gln Glu Asn Asp Asp Leu Phe Ser Ser Gly Asp Ser Asp Gly Thr
    275   280   285

Ser Ala Lys Arg Arg Lys Met Glu Met Glu Ser Tyr Ala Pro Val Gly
    290   295   300

Val Glu Ser Cys Ile Leu Ala Pro Thr Pro Leu Arg Val Val Lys Pro
305   310   315   320

Glu Lys Leu Asp Thr Pro Glu Val Ile Asp Leu Glu Ser Glu Lys Ser
            325   330   335

Tyr Thr His Val Lys Met Glu Pro Val Glu Glu Ile Lys Val Glu Ala
            340   345   350

690

```
Val Lys Met Ser Ser Gln Val Glu Asp Val Lys Phe Ser Arg Glu Gln
        355             360             365

Lys Ser Val Tyr Val Lys Lys Glu Pro Val Gly Ala Arg Lys Val Lys
        370             375             380

Val Glu Asp Gly Asp Phe Pro Val Glu Lys Asp Trp Tyr Leu Val Gly
385             390             395             400

Arg Ser Leu Val Thr Ala Thr Ser Thr Ser Lys Gly Arg Lys Leu Glu
            405             410             415

Asp Asn Glu Ile Val Asn Phe Thr Phe Ser Ser Val Ala Lys Trp Lys
            420             425             430

Val Pro Asn Ile Val Arg Phe Ser Thr Lys Arg Cys Gly Glu Ile Gly
        435             440             445

Arg Leu Pro Met Glu Trp Ser Asn Trp Ala Val Ser Leu Leu Arg Ser
    450             455             460

Gly Lys Val Lys Met Leu Gly Arg Cys Val Ala Ala Pro Pro Phe Leu
465             470             475             480

Thr Met Met Gln Glu Ile Met Leu Tyr Val Ser Phe Tyr Ile His Ser
            485                 490             495

Ser Ile Phe Thr Asp Val Ser Lys Ser Thr Trp Arg Ile Gly Ser Ser
            500             505             510

Pro Asn Leu Glu Ser Thr Leu His Pro Leu Leu Gln Leu Phe Lys His
        515             520             525

Leu Thr Ile Lys Pro Tyr Gln Lys Ala Glu Phe Thr Pro Glu Glu Leu
        530             535             540

Asn Ser Arg Lys Arg Ser Leu Asn Leu Glu Asp Asp Tyr Asp Glu Arg
545             550             555             560

Ala Ala Leu Leu Ala Ile Ala Lys Arg Arg Lys Gly Cys Gln Gln Ser
            565             570             575

Leu Glu Gln Asn Lys Asp Glu Glu Glu Ala Pro Glu Ser Tyr Met Asn
        580             585             590

Arg Val Val Gly Ala Ala Asp Ser Tyr Asn Leu Glu Glu Met Glu Ala
```

595   600   605

Pro Ser Thr Leu Thr Cys Asn Leu Arg Pro Tyr Gln Lys Gln Ala Leu
    610   615   620

Tyr Trp Met Ser Glu Ser Glu Lys Gly Ile Asp Val Glu Lys Ala Ala
625   630   635   640

Glu Thr Leu His Pro Cys Trp Glu Ala Tyr Arg Ile Cys Asp Glu Arg
            645   650   655

Ala Pro Ser Ile Tyr Leu Asn Ile Phe Ser Gly Glu Ala Thr Ile Gln
            660   665   670

Phe Pro Thr Ala Thr Gln Met Ala Arg Gly Gly Ile Leu Ala Asp Ala
            675   680   685.

Met Gly Leu Gly Lys Thr Val Met Thr Ile Ala Leu Ile Leu Ala Arg
    690   695   700

Pro Gly Arg Gly Asn Pro Glu Asn Glu Asp Val Leu Val Ala Asp Val
705   710   715   720

Asn Ala Asp Lys Arg Asn Arg Lys Glu Ile His Met Ala Leu Thr Thr
            725   730   735

Val Lys Ala Lys Gly Gly Thr Leu Ile Ile Cys Pro Met Ala Leu Leu
            740   745   750

Ser Gln Trp Lys Asp Glu Leu Glu Thr His Ser Lys Pro Asp Thr Val
        755   760   765

Ser Val Leu Val Tyr Tyr Gly Gly Asp Arg Thr His Asp Ala Lys Ala
770   775   780

Ile Ala Ser His Asp Val Val Leu Thr Thr Tyr Gly Val Leu Thr Ser
785   790   795   800

Ala Tyr Lys Gln Asp Met Ala Asn Ser Ile Phe His Arg Ile Asp Trp
            805   810   815

Tyr Arg Ile Val Leu Asp Glu Ala His Thr Ile Lys Ser Trp Lys Thr
        820   825   830

Gln Ala Ala Lys Ala Thr Phe Glu Leu Ser Ser His Cys Arg Trp Cys
        835   840   845

692

```
Leu Thr Gly Thr Pro Leu Gln Asn Lys Leu Glu Asp Leu Tyr Ser Leu
    850                 855                 860


Leu Cys Phe Leu His Val Glu Pro Trp Cys Asn Trp Ala Trp Trp Ser
865                 870                 875                 880


Lys Leu Ile Gln Lys Pro Tyr Glu Asn Gly Asp Pro Arg Gly Leu Lys
                885                 890                 895


Leu Ile Lys Ala Ile Leu Arg Pro Leu Met Leu Arg Arg Thr Lys Glu
            900                 905                 910


Thr Arg Asp Lys Glu Gly Ser Leu Ile Leu Glu Leu Pro Pro Thr Asp
        915                 920                 925


Val Gln Val Ile Glu Cys Glu Gln Ser Glu Ala Glu Arg Asp Phe Tyr
    930                 935                 940


Thr Ala Leu Phe Lys Arg Ser Lys Val Gln Phe Asp Gln Phe Val Ala
945                 950                 955                 960


Gln Gly Lys Val Leu His Asn Tyr Ala Asn Ile Leu Glu Leu Leu Leu
                965                 970                 975


Arg Leu Arg Gln Cys Cys Asn His Pro Phe Leu Val Met Ser Arg Ala
            980                 985                 990


Asp Ser Gln Gln Tyr Ala Asp Leu  Asp Ser Leu Ala Arg  Arg Phe Leu
        995                 1000                1005


Asp Asn Asn Pro Asp Ser Val  Ser Gln Asn Ala Pro  Ser Arg Ala
    1010                1015                1020


Tyr Ile Glu Glu Val Ile Gln Asp Leu Arg Asp Gly Asn Ser Lys
    1025                1030                1035


Glu Cys Pro Ile Cys Leu Glu Ser Ala Asp Asp Pro Val Leu Thr
    1040                1045                1050


Pro Cys Ala His Arg Met Cys Arg Glu Cys Leu Leu Thr Ser Trp
    1055                1060                1065


Arg Ser Pro Ser Cys Gly Leu Cys Pro Ile Cys Arg Thr Ile Leu
    1070                1075                1080
```

693

```
Lys Arg Thr Glu Leu Ile Ser  Cys Pro Thr Asp Ser  Ile Phe Arg
    1085                1090               1095


Val Asp Val Val Lys Asn Trp  Lys Glu Ser Ser Lys  Val Ser Glu
    1100                1105               1110


Leu Leu Lys Cys Leu Glu Lys  Ile Lys Lys Ser Gly  Ser Gly Glu
    1115                1120               1125


Lys Ser Ile Val Phe Ser Gln  Trp Thr Ser Phe Leu  Asp Leu Leu
    1130                1135               1140


Glu Ile Pro Leu Arg Arg Arg  Gly Phe Glu Phe Leu  Arg Phe Asp
    1145                1150               1155


Gly Lys Leu Ala Gln Lys Gly  Arg Glu Lys Val Leu  Lys Glu Phe
    1160                1165               1170


Asn Glu Thr Lys Gln Lys Thr  Ile Leu Leu Met Ser  Leu Lys Ala
    1175                1180               1185


Gly Gly Val Gly Leu Asn Leu  Thr Ala Ala Ser Ser  Val Phe Leu
    1190                1195               1200


Met Asp Pro Trp Trp Asn Pro  Ala Val Glu Glu Gln  Ala Ile Met
    1205                1210               1215


Arg Ile His Arg Ile Gly Gln  Lys Arg Thr Val Phe  Val Arg Arg
    1220                1225               1230


Phe Ile Val Lys Asp Thr Val  Glu Glu Arg Met Gln  Gln Val Gln
    1235                1240               1245


Ala Arg Lys Gln Arg Met Ile  Ala Gly Ala Leu Thr  Asp Glu Glu
    1250                1255               1260


Val Arg Ser Ala Arg Leu Glu  Glu Leu Lys Met Leu  Phe Arg
    1265                1270               1275
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<221> CDS <222> (44)..(1120) <223> G1211

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tgaaacctag atttctgcaa ctgaattcct aattcgaaaa aga atg gag ggt tcg
55
                                            Met Glu Gly Ser
                                            1
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694

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tcg tcg acg ata gca agg aag aca tgg gaa cta gag aac agc att cta
103
Ser Ser Thr Ile Ala Arg Lys Thr Trp Glu Leu Glu Asn Ser Ile Leu
5               10              15              20

aca gta gac tca cct gat tca acc tcc gac aac atc ttc tac tac gac
151
Thr Val Asp Ser Pro Asp Ser Thr Ser Asp Asn Ile Phe Tyr Tyr Asp
            25              30              35

gat act tca cag act agg ttc cag caa gag aaa ccg tgg gag aat gat
199
Asp Thr Ser Gln Thr Arg Phe Gln Gln Glu Lys Pro Trp Glu Asn Asp
        40              45                  50

cct cac tac ttt aaa cga gtc aag atc tca gcg ctc gct ctt ctt aag
247
Pro His Tyr Phe Lys Arg Val Lys Ile Ser Ala Leu Ala Leu Leu Lys
        55              60              65

atg gtg gtt cac gct cgc tct ggt ggt aca att gaa ata atg ggt ctt
295
Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu Ile Met Gly Leu
    70              75              80

atg caa ggt aag acc gat ggt gat act atc att gtt atg gat gct ttt
343
Met Gln Gly Lys Thr Asp Gly Asp Thr Ile Ile Val Met Asp Ala Phe
85              90              95              100

gct tta cca gtg gaa ggt act gag aca agg gtt aat gct cag gat gat
391
Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Asp Asp
            105             110             115

gct tat gag tac atg gtt gag tat tca cag acc aac aag ctc gcg ggg
439
Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Asn Lys Leu Ala Gly
            120             125             130

cgg ctg gag aat gtt gtt gga tgg tat cac tct cac cct gga tat gga
487
Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro Gly Tyr Gly
        135             140             145

tgc tgg ctc tcc ggt att gat gtt tct acg cag acg ctt aac caa cag
535
Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Thr Leu Asn Gln Gln
    150             155             160

cat cag gag cca ttt tta gct gtt gtt att gat ccc aca agg act gtt
583
His Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr Arg Thr Val
165             170             175             180

tca gct ggt aag gtt gag att ggt gct ttc aga aca tac tct aaa gga
631
Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr Ser Lys Gly
            185             190             195
```

```
tat aag cct cca gat gaa cct gtt tct gag tat caa act att cct tta
679
Tyr Lys Pro Pro Asp Glu Pro Val Ser Glu Tyr Gln Thr Ile Pro Leu
            200             205             210

aat aag att gag gac ttt ggt gtt cac tgc aaa cag tac tat tca tta
727
Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ser Leu
            215             220             225

gat gtc act tat ttc aag tca tct ctt gat tct cac ctt ctg gat cta
775
Asp Val Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu Leu Asp Leu
            230             235             240

cta tgg aac aag tac tgg gtg aac act ctt tct tct tct cca ctg ctg
823
Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Pro Leu Leu
245             250             255             260

ggt aat gga gac tat gtt gct gga caa ata tca gac tta gct gag aag
871
Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu Ala Glu Lys
            265             270             275

ctt gag caa gcc gag agt cat ctg gtt cag tct cgc ttt gga gga gtt
919
Leu Glu Gln Ala Glu Ser His Leu Val Gln Ser Arg Phe Gly Gly Val
            280             285             290

gtg cca tca tcc ctt cat aag aaa aaa gaa gat gag tct caa cta act
967
Val Pro Ser Ser Leu His Lys Lys Lys Glu Asp Glu Ser Gln Leu Thr
            295             300             305

aag ata act cgg gat agc gca aag ata act gtg gaa cag gtc cat gga
1015
Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu Gln Val His Gly
            310             315             320

cta atg tcg cag gtc ata aaa gat gaa tta ttc aac tca atg cgt cag
1063
Leu Met Ser Gln Val Ile Lys Asp Glu Leu Phe Asn Ser Met Arg Gln
325             330             335             340

tcc aac aac aaa tct ccc act gac tcg tcg gat cca gac cct atg att
1111
Ser Asn Asn Lys Ser Pro Thr Asp Ser Ser Asp Pro Asp Pro Met Ile
            345             350             355

aca tat tga agttgctctt cttttggttt ctatttttgg attgacccat
1160
Thr Tyr

catttgttgt cctttcattt attttctgtt gtgtaaagaa ttataatgtc gtcgcgaatt
1220

cgcggccgct aaaaaaaaac aggaaattga aaaaaattca tccattccaa catctttatt
1280
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696

taatattatc tcctcaatta tataatattc aaacatccct aataacttca tttgaccgtc
1340

cccctccctc ccgtgttgca ttggtgctgg cccc
1374

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378

Met Glu Gly Ser Ser Ser Thr Ile Ala Arg Lys Thr Trp Glu Leu Glu
1   5   10   15

Asn Ser Ile Leu Thr Val Asp Ser Pro Asp Ser Thr Ser Asp Asn Ile
            20   25   30

Phe Tyr Tyr Asp Asp Thr Ser Gln Thr Arg Phe Gln Gln Glu Lys Pro
            35   40   45

Trp Glu Asn Asp Pro His Tyr Phe Lys Arg Val Lys Ile Ser Ala Leu
    50   55   60

Ala Leu Leu Lys Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu
65   70   75   80

Ile Met Gly Leu Met Gln Gly Lys Thr Asp Gly Asp Thr Ile Ile Val
                85   90   95

Met Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn
                100   105   110

Ala Gln Asp Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Asn
            115   120   125

Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His
    130   135   140

Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Thr
145   150   155   160

Leu Asn Gln Gln His Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro
                165   170   175

Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr
            180   185   190

Tyr Ser Lys Gly Tyr Lys Pro Pro Asp Glu Pro Val Ser Glu Tyr Gln
    195   200   205

697

Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln
    210   215   220

Tyr Tyr Ser Leu Asp Val Thr Tyr Phe Lys Ser Ser Leu Asp Ser His
225   230   235   240

Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser
                245   250   255

Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp
                260   265   270

Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser His Leu Val Gln Ser Arg
                275   280   285

Phe Gly Gly Val Val Pro Ser Ser Leu His Lys Lys Lys Glu Asp Glu
    290   295   300

Ser Gln Leu Thr Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu
305   310   315   320

Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Glu Leu Phe Asn
                325   330   335

Ser Met Arg Gln Ser Asn Asn Lys Ser Pro Thr Asp Ser Ser Asp Pro
                340   345   350

Asp Pro Met Ile Thr Tyr
            355

<210> 379 <211> 3174 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(3174) <223> G1243

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atg gcg aga aat tcg aat tcc gat gag gct ttc tcg tca gag gag gaa
48
Met Ala Arg Asn Ser Asn Ser Asp Glu Ala Phe Ser Ser Glu Glu Glu
1   5   10   15

gaa gag cgg gtt aag gat aat gaa gaa gaa gat gag gag gag ctc gag
96
Glu Glu Arg Val Lys Asp Asn Glu Glu Glu Asp Glu Glu Glu Leu Glu
                20   25   30

gct gtt gct cgt tct tct ggc tcc gac gat gac gaa gta gcc gcc gcc
144
Ala Val Ala Arg Ser Ser Gly Ser Asp Asp Asp Glu Val Ala Ala Ala
            35   40   45

```
gac gaa tca cca gtc tcc gac gga gag gct gct ccc gta gaa gat gat
192
Asp Glu Ser Pro Val Ser Asp Gly Glu Ala Ala Pro Val Glu Asp Asp
    50              55              60

tac gag gac gaa gaa gat gag gaa aaa gct gaa atc agc aaa cgt gag
240
Tyr Glu Asp Glu Glu Asp Glu Glu Lys Ala Glu Ile Ser Lys Arg Glu
65              70              75              80

aaa gcc aga ctt aaa gag atg cag aag ttg aag aag cag aag att caa
288
Lys Ala Arg Leu Lys Glu Met Gln Lys Leu Lys Lys Gln Lys Ile Gln
            85              90              95

gag atg ctg gag tcg cag aat gct tcc att gac gcg gat atg aac aat
336
Glu Met Leu Glu Ser Gln Asn Ala Ser Ile Asp Ala Asp Met Asn Asn
            100             105             110

aag gga aaa ggg aga ctg aag tat ctt ctg cag caa act gag tta ttt
384
Lys Gly Lys Gly Arg Leu Lys Tyr Leu Leu Gln Gln Thr Glu Leu Phe
            115             120             125

gcc cac ttt gct aaa agt gat gga tct tct tct cag aag aag gca aaa
432
Ala His Phe Ala Lys Ser Asp Gly Ser Ser Ser Gln Lys Lys Ala Lys
    130             135             140

gga agg gga cgt cat gct tcc aaa ata act gaa gag gag gaa gac gaa
480
Gly Arg Gly Arg His Ala Ser Lys Ile Thr Glu Glu Glu Glu Asp Glu
145             150             155             160

gag tat cta aag gaa gaa gag gat ggc tta act gga tct gga aac aca
528
Glu Tyr Leu Lys Glu Glu Glu Asp Gly Leu Thr Gly Ser Gly Asn Thr
            165             170             175

cgg tta ctc aca cag ccc tct tgt att caa ggg aag atg aga gat tac
576
Arg Leu Leu Thr Gln Pro Ser Cys Ile Gln Gly Lys Met Arg Asp Tyr
            180             185             190

caa tta gct ggt ttg aac tgg ctc att cgt ctt tat gag aat ggc ata
624
Gln Leu Ala Gly Leu Asn Trp Leu Ile Arg Leu Tyr Glu Asn Gly Ile
    195             200             205

aat gga att ctt gct gat gaa atg ggt ctg ggg aag acg ctt caa acg
672
Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly Lys Thr Leu Gln Thr
    210             215             220

att tct ttg ttg gca tat ctt cat gaa tac agg gga atc aat ggt ccc
720
Ile Ser Leu Leu Ala Tyr Leu His Glu Tyr Arg Gly Ile Asn Gly Pro
225             230             235             240
```

699

cat atg gtg gtt gct cca aaa tca aca ctt ggt aat tgg atg aac gaa
768
His Met Val Val Ala Pro Lys Ser Thr Leu Gly Asn Trp Met Asn Glu
            245   250   255

att cgc cgg ttt tgt cct gtc cta cgt gct gtg aag ttc ctt ggt aat
816
Ile Arg Arg Phe Cys Pro Val Leu Arg Ala Val Lys Phe Leu Gly Asn
            260   265   270

cct gag gag agg aga cat att cga gaa gac ctg cta gtt gct ggg aaa
864
Pro Glu Glu Arg Arg His Ile Arg Glu Asp Leu Leu Val Ala Gly Lys
            275   280   285

ttt gat att tgt gtc aca agc ttt gag atg gcc atc aaa gag aag aca
912
Phe Asp Ile Cys Val Thr Ser Phe Glu Met Ala Ile Lys Glu Lys Thr
        290   295   300

gca ctt cgt cgg ttt agc tgg cgt tat att atc att gat gaa gcg cat
960
Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile Ile Ile Asp Glu Ala His
305   310   315   320

cga atc aag aac gag aat tca ctc ctt tct aaa acc atg aga ctt ttt
1008
Arg Ile Lys Asn Glu Asn Ser Leu Leu Ser Lys Thr Met Arg Leu Phe
            325   330   335

agc acc aat tat cgg ctt ctt atc acg ggg acc ccc ctt cag aat aat
1056
Ser Thr Asn Tyr Arg Leu Leu Ile Thr Gly Thr Pro Leu Gln Asn Asn
            340   345   350

ctc cat gaa ctg tgg gct ctt cta aat ttt ctt ctg cct gag att ttt
1104
Leu His Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro Glu Ile Phe
            355   360   365

agt tca gca gag act ttt gat gaa tgg ttt caa att tct ggt gag aat
1152
Ser Ser Ala Glu Thr Phe Asp Glu Trp Phe Gln Ile Ser Gly Glu Asn
        370   375   380

gac cag caa gaa gtt gtg caa caa ctg cac aag gtt ctt cga cca ttt
1200
Asp Gln Gln Glu Val Val Gln Gln Leu His Lys Val Leu Arg Pro Phe
385   390   395   400

ctt ctt cga aga cta aag tca gat gtt gag aaa ggt ttg cca ccg aag
1248
Leu Leu Arg Arg Leu Lys Ser Asp Val Glu Lys Gly Leu Pro Pro Lys
            405   410   415

aag gag acc ata ctt aaa gtt ggt atg tct cag atg caa aag caa tac
1296
Lys Glu Thr Ile Leu Lys Val Gly Met Ser Gln Met Gln Lys Gln Tyr
            420   425   430

700

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tac aag gct tta ctg cag aag gat ctt gaa gcg gtt aat gct ggt gga
1344
Tyr Lys Ala Leu Leu Gln Lys Asp Leu Glu Ala Val Asn Ala Gly Gly
        435                 440                 445

gaa cgc aaa cgt ctg cta aac att gca atg caa ctg cgt aaa tgc tgc
1392
Glu Arg Lys Arg Leu Leu Asn Ile Ala Met Gln Leu Arg Lys Cys Cys
    450                 455                 460

aat cac ccc tat ctc ttc cag ggt gca gaa cct ggt ccc cca tat acc
1440
Asn His Pro Tyr Leu Phe Gln Gly Ala Glu Pro Gly Pro Pro Tyr Thr
465                 470                 475                 480

aca gga gat cac ctt ata aca aat gct ggt aag atg gtt ctc ttg gat
1488
Thr Gly Asp His Leu Ile Thr Asn Ala Gly Lys Met Val Leu Leu Asp
            485                 490                 495

aaa ttg ctt cct aag ttg aaa gaa cgt gat tca agg gtg ctg ata ttt
1536
Lys Leu Leu Pro Lys Leu Lys Glu Arg Asp Ser Arg Val Leu Ile Phe
            500                 505                 510

tct cag atg aca aga ctt ttg gat att ctt gag gac tat tta atg tat
1584
Ser Gln Met Thr Arg Leu Leu Asp Ile Leu Glu Asp Tyr Leu Met Tyr
            515                 520                 525

cgt ggt tac ttg tat tgc cgt att gat gga aac act ggt ggt gac gaa
1632
Arg Gly Tyr Leu Tyr Cys Arg Ile Asp Gly Asn Thr Gly Gly Asp Glu
    530                 535                 540

cga gat gcc tcc ata gaa gcc tac aac aag cca gga agt gag aaa ttt
1680
Arg Asp Ala Ser Ile Glu Ala Tyr Asn Lys Pro Gly Ser Glu Lys Phe
545                 550                 555                 560

gtt ttc ttg tta tct act aga gct gga ggg ctt ggt atc aat ctt gct
1728
Val Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala
            565                 570                 575

act gca gat gtt gtg atc ctt tac gat agt gat tgg aac cca caa gtc
1776
Thr Ala Asp Val Val Ile Leu Tyr Asp Ser Asp Trp Asn Pro Gln Val
            580                 585                 590

gac ttg caa gct cag gat cgt gcc cat agg att ggt caa aaa aaa gaa
1824
Asp Leu Gln Ala Gln Asp Arg Ala His Arg Ile Gly Gln Lys Lys Glu
            595                 600                 605

gtt caa gtg ttt cga ttc tgc act gag tct gct att gag gag aaa gtg
1872
Val Gln Val Phe Arg Phe Cys Thr Glu Ser Ala Ile Glu Glu Lys Val
    610                 615                 620
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701

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att gaa aga gct tac aag aag tta gca ctt gat gct ctg gtt att caa
1920
Ile Glu Arg Ala Tyr Lys Lys Leu Ala Leu Asp Ala Leu Val Ile Gln
625                 630                 635                     640


caa ggg aga ttg gca gaa cag aaa agt aag tct gtc aat aag gat gag
1968
Gln Gly Arg Leu Ala Glu Gln Lys Ser Lys Ser Val Asn Lys Asp Glu
                645                 650                 655


ttg ctt caa atg gta aga tat ggt gct gag atg gtg ttc agt tct aaa
2016
Leu Leu Gln Met Val Arg Tyr Gly Ala Glu Met Val Phe Ser Ser Lys
                660                 665                 670


gat agc aca atc aca gac gag gat att gat aga atc att gcc aaa gga
2064
Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp Arg Ile Ile Ala Lys Gly
            675                 680                 685


gaa gag gca aca gct gaa ctt gat gct aag atg aag aaa ttc aca gaa
2112
Glu Glu Ala Thr Ala Glu Leu Asp Ala Lys Met Lys Lys Phe Thr Glu
        690                 695         -       700


gat gct ata cag ttt aaa atg gat gac agt gct gac ttc tat gat ttt
2160
Asp Ala Ile Gln Phe Lys Met Asp Asp Ser Ala Asp Phe Tyr Asp Phe
705                 710                 715                     720


gat gat gac aat aag gat gaa aac aag ctc gat ttt aaa aag att gta
2208
Asp Asp Asp Asn Lys Asp Glu Asn Lys Leu Asp Phe Lys Lys Ile Val
                725                 730                 735


agc gac aat tgg aat gat ccc ccc aag cgg gag aga aag cgc aac tac
2256
Ser Asp Asn Trp Asn Asp Pro Pro Lys Arg Glu Arg Lys Arg Asn Tyr
                740                 745                 750


tct gaa tct gag tac ttt aag caa aca ttg cgg caa ggt gct cca gct
2304
Ser Glu Ser Glu Tyr Phe Lys Gln Thr Leu Arg Gln Gly Ala Pro Ala
            755                 760                 765


aaa cct aaa gag cct aga att ccg cgc atg ccc cag ttg cac gat ttc
2352
Lys Pro Lys Glu Pro Arg Ile Pro Arg Met Pro Gln Leu His Asp Phe
        770                 775                 780


cag ttc ttt aac att cag aga ttg acc gag ttg tat gaa aag gaa gta
2400
Gln Phe Phe Asn Ile Gln Arg Leu Thr Glu Leu Tyr Glu Lys Glu Val
785                 790                 795                     800


cgt tat ctc atg caa aca cat cag aaa aat cag ttg aaa gac aca att
2448
Arg Tyr Leu Met Gln Thr His Gln Lys Asn Gln Leu Lys Asp Thr Ile
                805                 810                 815
```

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gat gtt gaa gaa cca gaa ggt ggg gat ccc tta act act gaa gaa gta
2496
Asp Val Glu Glu Pro Glu Gly Gly Asp Pro Leu Thr Thr Glu Glu Val
        820             825             830

gaa gaa aag gag gga tta ttg gag gag ggt ttc tca aca tgg agc aga
2544
Glu Glu Lys Glu Gly Leu Leu Glu Glu Gly Phe Ser Thr Trp Ser Arg
    835             840             845

aga gat ttt aat act ttc ctc agg gct tgt gag aag tat ggc cgc aac
2592
Arg Asp Phe Asn Thr Phe Leu Arg Ala Cys Glu Lys Tyr Gly Arg Asn
    850             855             860

gac ata aaa agc att gcc tct gag atg gaa ggg aaa aca gag gaa gaa
2640
Asp Ile Lys Ser Ile Ala Ser Glu Met Glu Gly Lys Thr Glu Glu Glu
865             870             875             880

gtt gaa aga tat gcc aaa gta ttt aaa gag cgg tac aag gag ctg aac
2688
Val Glu Arg Tyr Ala Lys Val Phe Lys Glu Arg Tyr Lys Glu Leu Asn
            885             890             895

gac tat gat aga atc att aag aac att gag agg gga gag gca agg atc
2736
Asp Tyr Asp Arg Ile Ile Lys Asn Ile Glu Arg Gly Glu Ala Arg Ile
        900             905             910

tct agg aaa gac gaa atc atg aag gcc ata ggg aag aaa ctg gat cgc
2784
Ser Arg Lys Asp Glu Ile Met Lys Ala Ile Gly Lys Lys Leu Asp Arg
        915             920             925

tac aga aac cct tgg ctg gaa ctg aag att caa tat ggt cag aac aaa
2832
Tyr Arg Asn Pro Trp Leu Glu Leu Lys Ile Gln Tyr Gly Gln Asn Lys
    930             935             940

ggc aag ctg tac aat gaa gag tgt gac cgt ttc atg atc tgc atg att
2880
Gly Lys Leu Tyr Asn Glu Glu Cys Asp Arg Phe Met Ile Cys Met Ile
945             950             955             960

cac aaa ctt ggt tat ggg aat tgg gat gag cta aag gca gca ttt agg
2928
His Lys Leu Gly Tyr Gly Asn Trp Asp Glu Leu Lys Ala Ala Phe Arg
            965             970             975

aca tcg tct gtg ttc agg ttt gac tgg ttt gtg aaa tcc cgc acg agt
2976
Thr Ser Ser Val Phe Arg Phe Asp Trp Phe Val Lys Ser Arg Thr Ser
            980             985             990

cag gaa ctt gca aga aga tgc gac  act ctg att cga ctg  atc gag aaa
3024
Gln Glu Leu Ala Arg Arg Cys Asp  Thr Leu Ile Arg Leu  Ile Glu Lys
        995             1000            1005
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gag aac  cag gag ttt gat gaa  aga gag agg caa gcc  cgc aaa gag
3069
Glu Asn  Gln Glu Phe Asp Glu  Arg Glu Arg Gln Ala  Arg Lys Glu
    1010                1015                1020


aag aag  ctc gcg aag agt gca  aca cca tca aag cga  cct tta gga
3114
Lys Lys  Leu Ala Lys Ser Ala  Thr Pro Ser Lys Arg  Pro Leu Gly
    1025                1030                1035


aga caa  gca agt gag agt cct  tca tcg acg aag aag  cgg aag cac
3159
Arg Gln  Ala Ser Glu Ser Pro  Ser Ser Thr Lys Lys  Arg Lys His
    1040                1045                1050


ctg tcg  atg aga tga
3174
Leu Ser  Met Arg
    1055
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Met Ala Arg Asn Ser Asn Ser Asp Glu Ala Phe Ser Ser Glu Glu Glu
1               5                   10                  15


Glu Glu Arg Val Lys Asp Asn Glu Glu Glu Asp Glu Glu Glu Leu Glu
            20                  25                  30


Ala Val Ala Arg Ser Ser Gly Ser Asp Asp Asp Glu Val Ala Ala Ala
            35                  40                  45


Asp Glu Ser Pro Val Ser Asp Gly Glu Ala Ala Pro Val Glu Asp Asp
    50                  55                  60


Tyr Glu Asp Glu Glu Asp Glu Glu Lys Ala Glu Ile Ser Lys Arg Glu
65                  70                  75                  80


Lys Ala Arg Leu Lys Glu Met Gln Lys Leu Lys Lys Gln Lys Ile Gln
                85                  90                  95


Glu Met Leu Glu Ser Gln Asn Ala Ser Ile Asp Ala Asp Met Asn Asn
            100                 105                 110


Lys Gly Lys Gly Arg Leu Lys Tyr Leu Leu Gln Gln Thr Glu Leu Phe
            115                 120                 125


Ala His Phe Ala Lys Ser Asp Gly Ser Ser Ser Gln Lys Lys Ala Lys
    130                 135                 140


Gly Arg Gly Arg His Ala Ser Lys Ile Thr Glu Glu Glu Glu Asp Glu
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704

145   150   ·   155   160

Glu Tyr Leu Lys Glu Glu Glu Asp Gly Leu Thr Gly Ser Gly Asn Thr
                165   170   175

Arg Leu Leu Thr Gln Pro Ser Cys Ile Gln Gly Lys Met Arg Asp Tyr
            180   185   190

Gln Leu Ala Gly Leu Asn Trp Leu Ile Arg Leu Tyr Glu Asn Gly Ile
            195   200   205

Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly Lys Thr Leu Gln Thr
    210   215   220

Ile Ser Leu Leu Ala Tyr Leu His Glu Tyr Arg Gly Ile Asn Gly Pro
225   230   235   ·   240

His Met Val Val Ala Pro Lys Ser Thr Leu Gly Asn Trp Met Asn Glu
            245   250   255

Ile Arg Arg Phe Cys Pro Val Leu Arg Ala Val Lys Phe Leu Gly Asn
            260   265   270

Pro Glu Glu Arg Arg His Ile Arg Glu Asp Leu Leu Val Ala Gly Lys
    275   ·   280   285

Phe Asp Ile Cys Val Thr Ser Phe Glu Met Ala Ile Lys Glu Lys Thr
    290   295   300

Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile Ile Ile Asp Glu Ala His
305   310   315   320

Arg Ile Lys Asn Glu Asn Ser Leu Leu Ser Lys Thr Met Arg Leu Phe
            325   ·   330   ·335

Ser Thr Asn Tyr Arg Leu Leu Ile Thr Gly Thr Pro Leu Gln Asn Asn
            340   345   350

Leu His Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro Glu Ile Phe
            355   360   365

Ser Ser Ala Glu Thr Phe Asp Glu Trp Phe Gln Ile Ser Gly Glu Asn
            370   375   380

Asp Gln Gln Glu Val Val Gln Gln Leu His Lys Val Leu Arg Pro Phe
385   390   395   400

Leu Leu Arg Arg Leu Lys Ser Asp Val Glu Lys Gly Leu Pro Pro Lys
            405   410   415

Lys Glu Thr Ile Leu Lys Val Gly Met Ser Gln Met Gln Lys Gln Tyr
            420   425   430

Tyr Lys Ala Leu Leu Gln Lys Asp Leu Glu Ala Val Asn Ala Gly Gly
            435   440   445

Glu Arg Lys Arg Leu Leu Asn Ile Ala Met Gln Leu Arg Lys Cys Cys
    450   455   460

Asn His Pro Tyr Leu Phe Gln Gly Ala Glu Pro Gly Pro Pro Tyr Thr
465   470   475   480

Thr Gly Asp His Leu Ile Thr Asn Ala Gly Lys Met Val Leu Leu Asp
            485   490   495

Lys Leu Leu Pro Lys Leu Lys Glu Arg Asp Ser Arg Val Leu Ile Phe
            500   505   510

Ser Gln Met Thr Arg Leu Leu Asp Ile Leu Glu Asp Tyr Leu Met Tyr
            515   520   525

Arg Gly Tyr Leu Tyr Cys Arg Ile Asp Gly Asn Thr Gly Gly Asp Glu
    530   535   540

Arg Asp Ala Ser Ile Glu Ala Tyr Asn Lys Pro Gly Ser Glu Lys Phe
545   550   555   560

Val Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala
            565   570   575

Thr Ala Asp Val Val Ile Leu Tyr Asp Ser Asp Trp Asn Pro Gln Val
            580   585   590

Asp Leu Gln Ala Gln Asp Arg Ala His Arg Ile Gly Gln Lys Lys Glu
            595   600   605

Val Gln Val Phe Arg Phe Cys Thr Glu Ser Ala Ile Glu Glu Lys Val
    610   615   620

Ile Glu Arg Ala Tyr Lys Lys Leu Ala Leu Asp Ala Leu Val Ile Gln
625   630   635   640

706

Gln Gly Arg Leu Ala Glu Gln Lys Ser Lys Ser Val Asn Lys Asp Glu
            645   650   655

Leu Leu Gln Met Val Arg Tyr Gly Ala Glu Met Val Phe Ser Ser Lys
            660   665   670

Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp Arg Ile Ile Ala Lys Gly
            675   680   685

Glu Glu Ala Thr Ala Glu Leu Asp Ala Lys Met Lys Lys Phe Thr Glu
        690   695   700

Asp Ala Ile Gln Phe Lys Met Asp Asp Ser Ala Asp Phe Tyr Asp Phe
705   710   715   720

Asp Asp Asp Asn Lys Asp Glu Asn Lys Leu Asp Phe Lys Lys Ile Val
                725   730   735

Ser Asp Asn Trp Asn Asp Pro Pro Lys Arg Glu Arg Lys Arg Asn Tyr
              740   745   750

Ser Glu Ser Glu Tyr Phe Lys Gln Thr Leu Arg Gln Gly Ala Pro Ala
            755   760   765

Lys Pro Lys Glu Pro Arg Ile Pro Arg Met Pro Gln Leu His Asp Phe
      770   775   780

Gln Phe Phe Asn Ile Gln Arg Leu Thr Glu Leu Tyr Glu Lys Glu Val
785   790   795   800

Arg Tyr Leu Met Gln Thr His Gln Lys Asn Gln Leu Lys Asp Thr Ile
              805   810   815

Asp Val Glu Glu Pro Glu Gly Gly Asp Pro Leu Thr Thr Glu Glu Val
            820   825   830

Glu Glu Lys Glu Gly Leu Leu Glu Glu Gly Phe Ser Thr Trp Ser Arg
            835   840   845

Arg Asp Phe Asn Thr Phe Leu Arg Ala Cys Glu Lys Tyr Gly Arg Asn
            850   855   860

Asp Ile Lys Ser Ile Ala Ser Glu Met Glu Gly Lys Thr Glu Glu Glu
865   870   875   880

707

Val Glu Arg Tyr Ala Lys Val Phe Lys Glu Arg Tyr Lys Glu Leu Asn
                885   890   895

Asp Tyr Asp Arg Ile Ile Lys Asn Ile Glu Arg Gly Glu Ala Arg Ile
            900   905   910

Ser Arg Lys Asp Glu Ile Met Lys Ala Ile Gly Lys Lys Leu Asp Arg
            915   920   925

Tyr Arg Asn Pro Trp Leu Glu Leu Lys Ile Gln Tyr Gly Gln Asn Lys
        930   935   940

Gly Lys Leu Tyr Asn Glu Glu Cys Asp Arg Phe Met Ile Cys Met Ile
945   950   955   960

His Lys Leu Gly Tyr Gly Asn Trp Asp Glu Leu Lys Ala Ala Phe Arg
            965   970   975

Thr Ser Ser Val Phe Arg Phe Asp Trp Phe Val Lys Ser Arg Thr Ser
            980   985   990

Gln Glu Leu Ala Arg Arg Cys Asp Thr Leu Ile Arg Leu Ile Glu Lys
        995   1000   1005

Glu Asn Gln Glu Phe Asp Glu Arg Glu Arg Gln Ala Arg Lys Glu
    1010   1015   1020

Lys Lys Leu Ala Lys Ser Ala Thr Pro Ser Lys Arg Pro Leu Gly
    1025   1030   1035

Arg Gln Ala Ser Glu Ser Pro Ser Ser Thr Lys Lys Arg Lys His
    1040   1045   1050

Leu Ser Met Arg
    1055

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<221> CDS <222> (54)..(1859) <223> G1290

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56
                                                            Met
                                                            1

atg gcc acc acc acc acc acc acc gct aga ttc tct gat tca tac
104
Met Ala Thr Thr Thr Thr Thr Thr Thr Ala Arg Phe Ser Asp Ser Tyr
            5   10   15

708

```
gag ttc agc aac aca agc ggc aat agc ttc ttc gcc gcc gag tca tct
152
Glu Phe Ser Asn Thr Ser Gly Asn Ser Phe Phe Ala Ala Glu Ser Ser
        20              25              30

ctt gat tat ccg acg gaa ttt ctc acg cca ccg gag gta tca gct ctt
200
Leu Asp Tyr Pro Thr Glu Phe Leu Thr Pro Pro Glu Val Ser Ala Leu
    35              40              45

aaa ctt ctg tct aac tgc ctc gag tct gtt ttc gac tcg ccg gag acg
248
Lys Leu Leu Ser Asn Cys Leu Glu Ser Val Phe Asp Ser Pro Glu Thr
50              55              60              65

ttc tac agc gat gct aag cta gtt ctc gcc ggc ggc cgg gaa gtt tct
296
Phe Tyr Ser Asp Ala Lys Leu Val Leu Ala Gly Gly Arg Glu Val Ser
            70              75              80

ttt cac cgt tgt att ctt tcc gcg aga att cct gtc ttc aaa agc gct
344
Phe His Arg Cys Ile Leu Ser Ala Arg Ile Pro Val Phe Lys Ser Ala
            85              90              95

tta gcc acc gtg aag gaa caa aaa tcc tcc acc acc gtg aag ctc cag
392
Leu Ala Thr Val Lys Glu Gln Lys Ser Ser Thr Thr Val Lys Leu Gln
        100             105             110

ctg aaa gag atc gcc aga gat tac gaa gtc ggc ttt gac tcg gtt gtg
440
Leu Lys Glu Ile Ala Arg Asp Tyr Glu Val Gly Phe Asp Ser Val Val
    115             120             125

gcg gtt ttg gcg tat gtt tac agc ggc aga gtg agg tcc ccg ccg aag
488
Ala Val Leu Ala Tyr Val Tyr Ser Gly Arg Val Arg Ser Pro Pro Lys
130             135             140             145

gga gct tct gct tgc gta gac gac gat tgt tgc cac gtg gct tgc cgg
536
Gly Ala Ser Ala Cys Val Asp Asp Asp Cys Cys His Val Ala Cys Arg
            150             155             160

tca aag gtg gat ttc atg gtg gag gtt ctt tat ctg tct ttc gtt ttc
584
Ser Lys Val Asp Phe Met Val Glu Val Leu Tyr Leu Ser Phe Val Phe
            165             170             175

cag att caa gaa tta gtt act ctg tat gag agg cag ttc ttg gaa att
632
Gln Ile Gln Glu Leu Val Thr Leu Tyr Glu Arg Gln Phe Leu Glu Ile
        180             185             190

gta gac aaa gtt gta gtc gaa gac atc ttg gtt ata ttc aag ctt gat
680
Val Asp Lys Val Val Val Glu Asp Ile Leu Val Ile Phe Lys Leu Asp
    195             200             205
```

709

```
act cta tgt ggt aca aca tac aag aag ctt ttg gat aga tgc ata gaa
728
Thr Leu Cys Gly Thr Thr Tyr Lys Lys Leu Leu Asp Arg Cys Ile Glu
210              215             220                 225

att atc gtg aag tct gat ata gaa cta gtt agt ctt gag aag tct tta
776
Ile Ile Val Lys Ser Asp Ile Glu Leu Val Ser Leu Glu Lys Ser Leu
            230             235                 240

cct caa cac att ttc aag caa atc ata gac atc cgc gaa gcg ctc tgt
824
Pro Gln His Ile Phe Lys Gln Ile Ile Asp Ile Arg Glu Ala Leu Cys
            245             250                 255

cta gag cca cct aaa cta gaa agg cat gtc aag aac ata tac aag gcg
872
Leu Glu Pro Pro Lys Leu Glu Arg His Val Lys Asn Ile Tyr Lys Ala
        260             265             270

cta gac tca gat gat gtt gag ctt gtc aag atg ctt ttg cta gaa gga
920
Leu Asp Ser Asp Asp Val Glu Leu Val Lys Met Leu Leu Leu Glu Gly
        275             280             285

cac acc aat ctc gat gag gcg tat gct ctt cat ttt gct atc gct cac
968
His Thr Asn Leu Asp Glu Ala Tyr Ala Leu His Phe Ala Ile Ala His
290             295             300                 305

tgc gct gtg aag acc gcg tat gat ctc ctc gag ctt gag ctt gcg gat
1016
Cys Ala Val Lys Thr Ala Tyr Asp Leu Leu Glu Leu Glu Leu Ala Asp
                310             315                 320

gtt aac ctt aga aat ccg agg gga tac act gtg ctt cat gtt gct gcg
1064
Val Asn Leu Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala
            325             330             335

atg cgg aag gag ccg aag ttg ata ata tct ttg tta atg aaa ggg gca
1112
Met Arg Lys Glu Pro Lys Leu Ile Ile Ser Leu Leu Met Lys Gly Ala
            340             345             350

aat att tta gac aca aca ttg gat ggt aga acc gct tta gtg att gta
1160
Asn Ile Leu Asp Thr Thr Leu Asp Gly Arg Thr Ala Leu Val Ile Val
    355             360             365

aaa cga ctc act aaa gcg gat gac tac aaa act agt acg gag gac ggt
1208
Lys Arg Leu Thr Lys Ala Asp Asp Tyr Lys Thr Ser Thr Glu Asp Gly
370             375             380                 385

acg cct tct ctg aaa ggc gga tta tgc ata gag gta ctt gag cat gaa
1256
Thr Pro Ser Leu Lys Gly Gly Leu Cys Ile Glu Val Leu Glu His Glu
                390             395                 400
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710

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caa aaa cta gaa tat ttg tcg cct ata gag gct tca ctt tct ctt cca
1304
Gln Lys Leu Glu Tyr Leu Ser Pro Ile Glu Ala Ser Leu Ser Leu Pro
            405             410             415

gta act cca gag gag ttg agg atg agg ttg ctc tat tat gaa aac cga
1352
Val Thr Pro Glu Glu Leu Arg Met Arg Leu Leu Tyr Tyr Glu Asn Arg
        420             425             430

gtt gca ctt gct cga ctt ctc ttt cca gtg gaa act gaa act gta cag
1400
Val Ala Leu Ala Arg Leu Leu Phe Pro Val Glu Thr Glu Thr Val Gln
    435             440             445

ggt att gcc aaa ttg gag gaa aca tgc gag ttt aca gct tct agt ctc
1448
Gly Ile Ala Lys Leu Glu Glu Thr Cys Glu Phe Thr Ala Ser Ser Leu
450             455             460             465

gag cct gat cat cac att ggt gaa aag cgg aca tca cta gac cta aat
1496
Glu Pro Asp His His Ile Gly Glu Lys Arg Thr Ser Leu Asp Leu Asn
            470             475             480

atg gcg ccg ttc caa atc cat gag aag cat ttg agt aga cta aga gca
1544
Met Ala Pro Phe Gln Ile His Glu Lys His Leu Ser Arg Leu Arg Ala
            485             490             495

ctt tgt aaa acc gtg gaa ctg ggg aaa cgc tac ttc aaa cga tgt tcg
1592
Leu Cys Lys Thr Val Glu Leu Gly Lys Arg Tyr Phe Lys Arg Cys Ser
        500             505             510

ctt gat cac ttt atg gat act gag gac ttg aat cat ctt gct agc gta
1640
Leu Asp His Phe Met Asp Thr Glu Asp Leu Asn His Leu Ala Ser Val
    515             520             525

gaa gaa gat act cct gag aaa cgg cta caa aag aag caa agg tac atg
1688
Glu Glu Asp Thr Pro Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met
530             535             540             545

gaa cta caa gag act ctg atg aag acc ttt agt gag gac aag gag gaa
1736
Glu Leu Gln Glu Thr Leu Met Lys Thr Phe Ser Glu Asp Lys Glu Glu
            550             555             560

tgt gga aag tct tcc aca ccg aaa cca acc tct gcg gtg agg tct aat
1784
Cys Gly Lys Ser Ser Thr Pro Lys Pro Thr Ser Ala Val Arg Ser Asn
            565             570             575

aga aaa ctc tct cac cgg cgc cta aaa gtg gac aaa cgg gat ttt ttg
1832
Arg Lys Leu Ser His Arg Arg Leu Lys Val Asp Lys Arg Asp Phe Leu
            580             585             590
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711

aaa cga cct tac ggg aac ggg gat taa ggaatgggaa atcatattcc
1879
Lys Arg Pro Tyr Gly Asn Gly Asp
    595   600

atttcactcc cacaactaaa aatgatgtat gtcctatatc atgatgtttc gtgagtttca
1939   ·

aataaattga aacgtacata tatcagtttt tcatctacgt gactgcgttg tatagttttc
1999

gttcttcact tagcatcatg tgtattctag ctccaagtgc gtttcaaaca aatatagtta
2059

tttttagcca attatatata cggt
2083

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382

Met Met Ala Thr Thr Thr Thr Thr Thr Thr Ala Arg Phe Ser Asp Ser
1   5   10   15

Tyr Glu Phe Ser Asn Thr Ser Gly Asn Ser Phe Phe Ala Ala Glu Ser
          20   25   30   ·

Ser Leu Asp Tyr Pro Thr Glu Phe Leu Thr Pro Pro Glu Val Ser Ala
          35   40   45

Leu Lys Leu Leu Ser Asn Cys Leu Glu Ser Val Phe Asp Ser Pro Glu
    50   55   60

Thr Phe Tyr Ser Asp Ala Lys Leu Val Leu Ala Gly Gly Arg Glu Val
65   70   75   80

Ser Phe His Arg Cys Ile Leu Ser Ala Arg Ile Pro Val Phe Lys Ser
      .   85   90   95

Ala Leu Ala Thr Val Lys Glu Gln Lys Ser Ser Thr Thr Val Lys Leu
          100   105   110   .

Gln Leu Lys Glu Ile Ala Arg Asp Tyr Glu Val Gly Phe Asp Ser Val
          115   120   125

Val Ala Val Leu Ala Tyr Val Tyr Ser Gly Arg Val Arg Ser Pro Pro
    130   135   140

Lys Gly Ala Ser Ala Cys Val Asp Asp Asp Cys Cys His Val Ala Cys
145   150   155   160

Arg Ser Lys Val Asp Phe Met Val Glu Val Leu Tyr Leu Ser Phe Val
            165   170   175

Phe Gln Ile Gln Glu Leu Val Thr Leu Tyr Glu Arg Gln Phe Leu Glu
            180   185   190

Ile Val Asp Lys Val Val Val Glu Asp Ile Leu Val Ile Phe Lys Leu
            195   200   205

Asp Thr Leu Cys Gly Thr Thr Tyr Lys Lys Leu Leu Asp Arg Cys Ile
    210   215   220

Glu Ile Ile Val Lys Ser Asp Ile Glu Leu Val Ser Leu Glu Lys Ser
225   230   235   240

Leu Pro Gln His Ile Phe Lys Gln Ile Ile Asp Ile Arg Glu Ala Leu
            245   250   255

Cys Leu Glu Pro Pro Lys Leu Glu Arg His Val Lys Asn Ile Tyr Lys
            260   265   270

Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Met Leu Leu Leu Glu
            275   280   285

Gly His Thr Asn Leu Asp Glu Ala Tyr Ala Leu His Phe Ala Ile Ala
    290   295   300

His Cys Ala Val Lys Thr Ala Tyr Asp Leu Leu Glu Leu Glu Leu Ala
305   310   315   320

Asp Val Asn Leu Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala
            325   330   335

Ala Met Arg Lys Glu Pro Lys Leu Ile Ile Ser Leu Leu Met Lys Gly
            340   345   350

Ala Asn Ile Leu Asp Thr Thr Leu Asp Gly Arg Thr Ala Leu Val Ile
            355   360   365

Val Lys Arg Leu Thr Lys Ala Asp Asp Tyr Lys Thr Ser Thr Glu Asp
    370   375   380

Gly Thr Pro Ser Leu Lys Gly Gly Leu Cys Ile Glu Val Leu Glu His
385   390   395   400

Glu Gln Lys Leu Glu Tyr Leu Ser Pro Ile Glu Ala Ser Leu Ser Leu

713

          405   410   415

Pro Val Thr Pro Glu Glu Leu Arg Met Arg Leu Leu Tyr Tyr Glu Asn
         420   425   430

Arg Val Ala Leu Ala Arg Leu Leu Phe Pro Val Glu Thr Glu Thr Val
         435   440   445

Gln Gly Ile Ala Lys Leu Glu Glu Thr Cys Glu Phe Thr Ala Ser Ser
    450   455   460

Leu Glu Pro Asp His His Ile Gly Glu Lys Arg Thr Ser Leu Asp Leu
465   470   475   480

Asn Met Ala Pro Phe Gln Ile His Glu Lys His Leu Ser Arg Leu Arg
                  485   490   495

Ala Leu Cys Lys Thr Val Glu Leu Gly Lys Arg Tyr Phe Lys Arg Cys
         500   505   510

Ser Leu Asp His Phe Met Asp Thr Glu Asp Leu Asn His Leu Ala Ser
         515   520   525

Val Glu Glu Asp Thr Pro Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr
    530   535   540

Met Glu Leu Gln Glu Thr Leu Met Lys Thr Phe Ser Glu Asp Lys Glu
545   550   555   560

Glu Cys Gly Lys Ser Ser Thr Pro Lys Pro Thr Ser Ala Val Arg Ser
                  565   570   575

Asn Arg Lys Leu Ser His Arg Arg Leu Lys Val Asp Lys Arg Asp Phe
                  580   585   590

Leu Lys Arg Pro Tyr Gly Asn Gly Asp
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56
                                        Met Met Cys Ser Arg Gly
                                        1   5

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cat tgg aga cct gca gaa gac gag aag cta aga gaa ctc gtc gag caa
104
His Trp Arg Pro Ala Glu Asp Glu Lys Leu Arg Glu Leu Val Glu Gln
            10                  15                  20

ttt ggt cct cat aat tgg aac gcc ata gct cag aag ctc tct ggt cga
152
Phe Gly Pro His Asn Trp Asn Ala Ile Ala Gln Lys Leu Ser Gly Arg
            25                  30                  35

tct ggt aag agt tgt aga ttg aga tgg ttt aat caa ttg gat cct agg
200
Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe Asn Gln Leu Asp Pro Arg
            40                  45                  50

att aac cga aac cct ttc acg gag gaa gaa gaa gaa agg ctt tta gcg
248
Ile Asn Arg Asn Pro Phe Thr Glu Glu Glu Glu Glu Arg Leu Leu Ala
55                  60                  65                  70

cct cat cgg atc cat ggg aac aga tgg tct gtg atc gct aga ttt ttt
296
Pro His Arg Ile His Gly Asn Arg Trp Ser Val Ile Ala Arg Phe Phe
                75                  80                  85

ccc ggt cga act gat aac gct gtt aaa aac cat tgg cac gtc atc atg
344
Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His Trp His Val Ile Met
                90                  95                  100

gct cgt cgt ggc cga gaa cgg tcc aag ctc cgt cca cga ggc ctt ggc
392
Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu Arg Pro Arg Gly Leu Gly
            105                 110                 115

cat gat ggc acg gtg gct gcg act ggg atg att ggt aat tat aaa gac
440
His Asp Gly Thr Val Ala Ala Thr Gly Met Ile Gly Asn Tyr Lys Asp
        120                 125                 130

tgc gat aag gag aga aga ttg gca acc aca acc gct atc aat ttt cct
488
Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr Thr Ala Ile Asn Phe Pro
135                 140                 145                 150

tat caa ttc tct cat att aat cat ttt caa gtc ctc aaa gag tcc ttg
536
Tyr Gln Phe Ser His Ile Asn His Phe Gln Val Leu Lys Glu Ser Leu
                155                 160                 165

acc gga aag atc ggg ttc aga aat agt act act cca ata caa gaa gga
584
Thr Gly Lys Ile Gly Phe Arg Asn Ser Thr Thr Pro Ile Gln Glu Gly
                170                 175                 180

gca ata gac caa act aaa cga ccg atg gag ttc tac aat ttt ctc caa
632
Ala Ile Asp Gln Thr Lys Arg Pro Met Glu Phe Tyr Asn Phe Leu Gln
            185                 190                 195
```

715

```
gta aac acg gat tcg aag ata cac gaa ttg ata gat aat tca aga aaa
680
Val Asn Thr Asp Ser Lys Ile His Glu Leu Ile Asp Asn Ser Arg Lys
    200             205             210

gac gaa gaa gaa gat gtc gat caa aac aac cga att cgt aac gag aat
728
Asp Glu Glu Glu Asp Val Asp Gln Asn Asn Arg Ile Arg Asn Glu Asn
215             220             225             230

tgt gtt cca ttt ttc gac ttt ttg tct gtt gga aac tct gcc tct cag
776
Cys Val Pro Phe Phe Asp Phe Leu Ser Val Gly Asn Ser Ala Ser Gln
            235             240             245

ggt tta tgt taa tttgtccgta ccacatgtac tataaggtgg accatatgtt
828
Gly Leu Cys

aactaaagat aatgtagaaa gtactaatca attagagctc ctgtttgagc caaatgtgaa
888

aattagttaa gacatcccaa acattttctt gtataacaca tataaggttg tactttatc
948

aggtctaatt ttctattttt attttaagga tgtttaatca gacccataac cattcgataa
1008

aaaaaaaaaa aa
1020
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<210> 384 <211> 249 <212> PRT <213> Arabidopsis thaliana <400>
384

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Met Met Cys Ser Arg Gly His Trp Arg Pro Ala Glu Asp Glu Lys Leu
1           5               10              15

Arg Glu Leu Val Glu Gln Phe Gly Pro His Asn Trp Asn Ala Ile Ala
            20              25              30

Gln Lys Leu Ser Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe
        35              40              45

Asn Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe Thr Glu Glu Glu
    50              55              60

Glu Glu Arg Leu Leu Ala Pro His Arg Ile His Gly Asn Arg Trp Ser
65              70              75              80

Val Ile Ala Arg Phe Phe Pro Gly Arg Thr Asp Asn Ala Val Lys Asn
            85              90              95

His Trp His Val Ile Met Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu
```

                100   105   110

Arg Pro Arg Gly Leu Gly His Asp Gly Thr Val Ala Ala Thr Gly Met
        115   120   125

Ile Gly Asn Tyr Lys Asp Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr
    130   135   140

Thr Ala Ile Asn Phe Pro Tyr Gln Phe Ser His Ile Asn His Phe Gln
145   150   155   160

Val Leu Lys Glu Ser Leu Thr Gly Lys Ile Gly Phe Arg Asn Ser Thr
                165   170   175

Thr Pro Ile Gln Glu Gly Ala Ile Asp Gln Thr Lys Arg Pro Met Glu
                180   185   190

Phe Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Lys Ile His Glu Leu
        195   200   205

Ile Asp Asn Ser Arg Lys Asp Glu Glu Glu Asp Val Asp Gln Asn Asn
    210   215   220

Arg Ile Arg Asn Glu Asn Cys Val Pro Phe Phe Asp Phe Leu Ser Val
225   230   235   240

Gly Asn Ser Ala Ser Gln Gly Leu Cys
                245

<210> 385 <211> 925 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (59)..(697) <223> G1329

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ccacgcgtcc gtacctttta caatttgttt atatatttta cgtatctatc tttgttcc
58

atg gag ggt tcg tcc aaa ggg ctg cga aaa ggt gct tgg act act gaa
106
Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Thr Glu
1   5   10   15

gaa gat agt ctc ttg aga cag tgc att aat aag tat gga gaa ggc aaa
154
Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys
            20   25   30

tgg cac caa gtt cct gta aga gct ggg cta aac cgg tgc agg aaa agt
202
Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
        35   40   45

                                717

```
tgt aga tta aga tgg ttg aac tat ttg aag cca agt atc aag aga gga
250
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
    50                  55                  60

aaa ctt agc tct gat gaa gtc gat ctt ctt ctt cgc ctt cat agg ctt
298
Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Arg Leu
65                  70                  75                  80

cta ggg aat agg tgg tct tta att gct gga aga tta cct ggt cgg acc
346
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
                85                  90                  95

gca aat gac gtc aag aat tac tgg aac act cat ctg agt aag aaa cat
394
Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
            100                 105                 110

gaa ccg tgt tgt aag ata aag atg aaa aag aga gac att acg ccc att
442
Glu Pro Cys Cys Lys Ile Lys Met Lys Lys Arg Asp Ile Thr Pro Ile
        115                 120                 125

cct aca aca ccg gca cta aaa aac aat gtt tat aag cct cga cct cga
490
Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg
    130                 135                 140

tcc ttc aca gtt aac aac gac tgc aac cat ctc aat gcc cca cca aaa
538
Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys
145                 150                 155                 160

gtt gac gtt aat cct cca tgc ctt gga ctt aac atc aat aat gtt tgt
586
Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys
                165                 170                 175

gac aat agt atc ata tac aac aaa gat aag aag aaa gac caa cta gtg
634
Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val
            180                 185                 190

aat aat ttg att gat gga gat aat atg tgg tta gag aaa ttc cta agg
682
Asn Asn Leu Ile Asp Gly Asp Asn Met Trp Leu Glu Lys Phe Leu Arg
        195                 200                 205

aaa gcc aag agg tag atattttggt tcctgaagcg acgacaacag aaaaggggga
737
Lys Ala Lys Arg
    210


caccttggct tttgacgttg atcaactttg gagtctttc gatggagaga ctgtgaaatt
797


tgattagtgt ttcgaacatt tgtttgcgtt tgtgtatagg tttgctttca cctttaatt
857
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tgtgtgtttt gataaataag ctaatagttt ttagcatttt aatgaaatat ttcaagtttc
917

cgtgttac
925

<210> 386 <211> 212 <212> PRT <213> Arabidopsis thaliana <400>
386

Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Thr Glu
1   5   10   15

Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys
            20   25   30

Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
        35   40   45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
    50   55   60

Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Arg Leu
65   70   75   80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
                85   90   95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
            100   105   110

Glu Pro Cys Cys Lys Ile Lys Met Lys Lys Arg Asp Ile Thr Pro Ile
        115   120   125

Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg
    130   135   140

Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys
145   150   155   160

Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys
                165   170   175

Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val
            180   185   190

Asn Asn Leu Ile Asp Gly Asp Asn Met Trp Leu Glu Lys Phe Leu Arg
            195   200   205

Lys Ala Lys Arg
    210

<210> 387 <211> 1989 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (8)..(1966) <223> G1455

<400> 387
cgtcgac atg aac caa ata aaa aac aaa act tta ccg gag atg acg acg
49
        Met Asn Gln Ile Lys Asn Lys Thr Leu Pro Glu Met Thr Thr
        1   5   10

gag caa gct ttg ttg tct atg gaa gct tta cct tta ggt ttc aga ttc
97
Glu Gln Ala Leu Leu Ser Met Glu Ala Leu Pro Leu Gly Phe Arg Phe
15   20   25   30

aga cca acg gat gaa gaa ctc atc aat cat tac cta agg tta aaa atc
145
Arg Pro Thr Asp Glu Glu Leu Ile Asn His Tyr Leu Arg Leu Lys Ile
            35   40   45

aac ggc cgt gat tta gag gtt aga gtc atc cct gag atc gat gtt tgc
193
Asn Gly Arg Asp Leu Glu Val Arg Val Ile Pro Glu Ile Asp Val Cys
        50   55   60

aag tgg gaa cca tgg gac tta cct ggg cta tcg gtg ata aag aca gat
241
Lys Trp Glu Pro Trp Asp Leu Pro Gly Leu Ser Val Ile Lys Thr Asp
        65   70   75

gat caa gaa tgg ttc ttt ttt tgt cct cgt gat cga aag tat ccg agt
289
Asp Gln Glu Trp Phe Phe Phe Cys Pro Arg Asp Arg Lys Tyr Pro Ser
    80   85   90

ggt cat cgt tct aat aga gct act gat att ggt tac tgg aaa gct act
337
Gly His Arg Ser Asn Arg Ala Thr Asp Ile Gly Tyr Trp Lys Ala Thr
95   100   105   110

ggg aaa gat cga act att aag tct aag aag atg att att ggt atg aag
385
Gly Lys Asp Arg Thr Ile Lys Ser Lys Lys Met Ile Ile Gly Met Lys
                115   120   125

aag act ctt gtt ttc tat cgt gga aga gct cct aga gga gag cgt act
433
Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Arg Gly Glu Arg Thr
            130   135   140

aat tgg att atg cat gag tat cgt gct aca gac aag gaa cta gat ggt
481
Asn Trp Ile Met His Glu Tyr Arg Ala Thr Asp Lys Glu Leu Asp Gly
        145   150   155

act gga cct ggt cag aat ccg tat gtt ttg tgt cgc ttg ttc cac aag
529

720

```
Thr Gly Pro Gly Gln Asn Pro Tyr Val Leu Cys Arg Leu Phe His Lys
    160             165             170

cct agt gat agt tgt gat cct gca cac tgt gag gaa ata gag aaa gtt
577
Pro Ser Asp Ser Cys Asp Pro Ala His Cys Glu Glu Ile Glu Lys Val
175             180             185             190

aat ttt act cca acc acc acc act aga tgc tct cct gat gac aca tct
625
Asn Phe Thr Pro Thr Thr Thr Thr Arg Cys Ser Pro Asp Asp Thr Ser
            195             200             205

tct gaa atg gtc caa gaa aca gct aca tct ggt gta cat gct cta gat
673
Ser Glu Met Val Gln Glu Thr Ala Thr Ser Gly Val His Ala Leu Asp
            210             215             220

aga tca gat gac act gag agg tgt tta agt gac aag ggc aat aat gat
721
Arg Ser Asp Asp Thr Glu Arg Cys Leu Ser Asp Lys Gly Asn Asn Asp
        225             230             235

gtg aaa cct gat gtt tca gtg ata aac aat act tct gtc aat cac gct
769
Val Lys Pro Asp Val Ser Val Ile Asn Asn Thr Ser Val Asn His Ala
    240             245             250

gaa act tct cgt gcc aaa gac cgt aat ttg ggc aag acg tta gta gag
817
Glu Thr Ser Arg Ala Lys Asp Arg Asn Leu Gly Lys Thr Leu Val Glu
255             260             265             270

gaa aat cca ctt cta agg gac gtt cca act ctt cat gga ccc atc ttg
865
Glu Asn Pro Leu Leu Arg Asp Val Pro Thr Leu His Gly Pro Ile Leu
            275             280             285

agt gag aaa tca tat tat cca gga cag tca agc atc ggt ttt gct aca
913
Ser Glu Lys Ser Tyr Tyr Pro Gly Gln Ser Ser Ile Gly Phe Ala Thr
            290             295             300

tct cac atg gat tct atg tat tct agt gat ttt gga aac tgt gat tat
961
Ser His Met Asp Ser Met Tyr Ser Ser Asp Phe Gly Asn Cys Asp Tyr
        305             310             315

ggg cta cat ttt caa gat ggt gcc tct gaa caa gat gca tct tta aca
1009
Gly Leu His Phe Gln Asp Gly Ala Ser Glu Gln Asp Ala Ser Leu Thr
    320             325             330

gat gtc ttg gat gaa gta ttc cat aac cat aat gaa tcc tct aat gac
1057
Asp Val Leu Asp Glu Val Phe His Asn His Asn Glu Ser Ser Asn Asp
335             340             345             350

agg aaa gac ttt gta ctt ccg aat atg atg cat tgg cct ggt aat aca
1105
Arg Lys Asp Phe Val Leu Pro Asn Met Met His Trp Pro Gly Asn Thr
```

721

```
                    355                    360                    365

aga ctg ttg tct act gag tac cca ttt ctc aaa gat tct gtt gct ttt
1153
Arg Leu Leu Ser Thr Glu Tyr Pro Phe Leu Lys Asp Ser Val Ala Phe
            370                    375                    380

gtt gac ggc agt gct gaa gtt tcc ggc tca cag caa ttt gtt cct gac
1201
Val Asp Gly Ser Ala Glu Val Ser Gly Ser Gln Gln Phe Val Pro Asp
            385                    390                    395

att tta gct tct aga tgg gtc agt gaa cag aac gtt gat agc aag gag
1249
Ile Leu Ala Ser Arg Trp Val Ser Glu Gln Asn Val Asp Ser Lys Glu
        400                    405                    410

gca gta gag att cta tct tca acc ggg tcc tct cgg acc ttg acg cca
1297
Ala Val Glu Ile Leu Ser Ser Thr Gly Ser Ser Arg Thr Leu Thr Pro
415                    420                    425                    430

ctt cat aac aac gtt ttt ggg caa tat gct tca tcg tct tac gca gct
1345
Leu His Asn Asn Val Phe Gly Gln Tyr Ala Ser Ser Ser Tyr Ala Ala
            435                    440                    445

atc gat cca ttt aac tat aat gtc aat cag cct gaa cag tca tcc ttt
1393
Ile Asp Pro Phe Asn Tyr Asn Val Asn Gln Pro Glu Gln Ser Ser Phe
            450                    455                    460

gag caa agc cat gtt gac cgc aac att agt ccc agt aac att ttt gag
1441
Glu Gln Ser His Val Asp Arg Asn Ile Ser Pro Ser Asn Ile Phe Glu
            465                    470                    475

ttc aag gct agg tct cga gag aat cag aga gat ctg gac tct gtt gtg
1489
Phe Lys Ala Arg Ser Arg Glu Asn Gln Arg Asp Leu Asp Ser Val Val
        480                    485                    490

gac caa ggc act gct cct aga aga att cgg ctg cag atc gaa cag cca
1537
Asp Gln Gly Thr Ala Pro Arg Arg Ile Arg Leu Gln Ile Glu Gln Pro
495                    500                    505                    510

ttg acg cca gtt acc aac aag aaa gag aga gat gcg gac aac tat gaa
1585
Leu Thr Pro Val Thr Asn Lys Lys Glu Arg Asp Ala Asp Asn Tyr Glu
            515                    520                    525

gaa gaa gat gaa gta caa tct gcc atg tcc aag gtc gta gag gaa gaa
1633
Glu Glu Asp Glu Val Gln Ser Ala Met Ser Lys Val Val Glu Glu Glu
            530                    535                    540

ccg gct aat tta agt gct cag ggg act gct cag agg aga atc cgc ctg
1681
Pro Ala Asn Leu Ser Ala Gln Gly Thr Ala Gln Arg Arg Ile Arg Leu
        545                    550                    555
```

                                      722

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cag acg aga ttg agg aag cct ctc ata acc cta aac aat aca aaa aga
1729
Gln Thr Arg Leu Arg Lys Pro Leu Ile Thr Leu Asn Asn Thr Lys Arg
    560             565             570

aac tca aat ggc aga gaa gga gaa gca agc cat agg aag tgt gaa atg
1777
Asn Ser Asn Gly Arg Glu Gly Glu Ala Ser His Arg Lys Cys Glu Met
575             580             585             590

cag gaa aaa gaa gat ata tca tca tca tca tca tgg cag aaa cag aag
1825
Gln Glu Lys Glu Asp Ile Ser Ser Ser Ser Ser Trp Gln Lys Gln Lys
            595             600             605

aag agc ttg gtg cag ttt agt agt gtg gtg ata ata gtg gcg gtg ata
1873
Lys Ser Leu Val Gln Phe Ser Ser Val Val Ile Ile Val Ala Val Ile
            610             615             620

gtt gtt tta gta gaa ata tgg aaa gag tca aga gat gcg aaa tgt agc
1921
Val Val Leu Val Glu Ile Trp Lys Glu Ser Arg Asp Ala Lys Cys Ser
            625             630             635

ttc ttg ttt cat caa tta gat tcc ttc aaa ggc atg ttt act tga
1966
Phe Leu Phe His Gln Leu Asp Ser Phe Lys Gly Met Phe Thr
    640             645             650

tgatatattg tgccgcggcc gct
1989


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388

Met Asn Gln Ile Lys Asn Lys Thr Leu Pro Glu Met Thr Thr Glu Gln
1               5               10              15

Ala Leu Leu Ser Met Glu Ala Leu Pro Leu Gly Phe Arg Phe Arg Pro
            20              25              30

Thr Asp Glu Glu Leu Ile Asn His Tyr Leu Arg Leu Lys Ile Asn Gly
            35              40              45

Arg Asp Leu Glu Val Arg Val Ile Pro Glu Ile Asp Val Cys Lys Trp
    50              55              60

Glu Pro Trp Asp Leu Pro Gly Leu Ser Val Ile Lys Thr Asp Asp Gln
65              70              75              80

Glu Trp Phe Phe Phe Cys Pro Arg Asp Arg Lys Tyr Pro Ser Gly His
            85              90              95
```

Arg Ser Asn Arg Ala Thr Asp Ile Gly Tyr Trp Lys Ala Thr Gly Lys
            100   105   110

Asp Arg Thr Ile Lys Ser Lys Lys Met Ile Ile Gly Met Lys Lys Thr
            115   120   125

Leu Val Phe Tyr Arg Gly Arg Ala Pro Arg Gly Glu Arg Thr Asn Trp
        130   135   140

Ile Met His Glu Tyr Arg Ala Thr Asp Lys Glu Leu Asp Gly Thr Gly
145   150   155   160

Pro Gly Gln Asn Pro Tyr Val Leu Cys Arg Leu Phe His Lys Pro Ser
                165   170   175

Asp Ser Cys Asp Pro Ala His Cys Glu Glu Ile Glu Lys Val Asn Phe
            180   185   190

Thr Pro Thr Thr Thr Thr Arg Cys Ser Pro Asp Asp Thr Ser Ser Glu
        195   200   205

Met Val Gln Glu Thr Ala Thr Ser Gly Val His Ala Leu Asp Arg Ser
    210   215   220

Asp Asp Thr Glu Arg Cys Leu Ser Asp Lys Gly Asn Asn Asp Val Lys
225   230   235   240

Pro Asp Val Ser Val Ile Asn Asn Thr Ser Val Asn His Ala Glu Thr
                245   250   255

Ser Arg Ala Lys Asp Arg Asn Leu Gly Lys Thr Leu Val Glu Glu Asn
            260   265   270

Pro Leu Leu Arg Asp Val Pro Thr Leu His Gly Pro Ile Leu Ser Glu
        275   280   285

Lys Ser Tyr Tyr Pro Gly Gln Ser Ser Ile Gly Phe Ala Thr Ser His
    290   295   300

Met Asp Ser Met Tyr Ser Ser Asp Phe Gly Asn Cys Asp Tyr Gly Leu
305   310   315   320

His Phe Gln Asp Gly Ala Ser Glu Gln Asp Ala Ser Leu Thr Asp Val
                325   330   335

724

Leu Asp Glu Val Phe His Asn His Asn Glu Ser Ser Asn Asp Arg Lys
            340   345   350

Asp Phe Val Leu Pro Asn Met Met His Trp Pro Gly Asn Thr Arg Leu
            355   360   365

Leu Ser Thr Glu Tyr Pro Phe Leu Lys Asp Ser Val Ala Phe Val Asp
    370   375   380

Gly Ser Ala Glu Val Ser Gly Ser Gln Gln Phe Val Pro Asp Ile Leu
385   390   395   400

Ala Ser Arg Trp Val Ser Glu Gln Asn Val Asp Ser Lys Glu Ala Val
            405   410   415

Glu Ile Leu Ser Ser Thr Gly Ser Ser Arg Thr Leu Thr Pro Leu His
            420   425   430

Asn Asn Val Phe Gly Gln Tyr Ala Ser Ser Ser Tyr Ala Ala Ile Asp
            435   440   445

Pro Phe Asn Tyr Asn Val Asn Gln Pro Glu Gln Ser Ser Phe Glu Gln
    450   455   460

Ser His Val Asp Arg Asn Ile Ser Pro Ser Asn Ile Phe Glu Phe Lys
465   470   475   480

Ala Arg Ser Arg Glu Asn Gln Arg Asp Leu Asp Ser Val Val Asp Gln
            485   490   495

Gly Thr Ala Pro Arg Arg Ile Arg Leu Gln Ile Glu Gln Pro Leu Thr
            500   505   510

Pro Val Thr Asn Lys Lys Glu Arg Asp Ala Asp Asn Tyr Glu Glu Glu
            515   520   525

Asp Glu Val Gln Ser Ala Met Ser Lys Val Val Glu Glu Glu Pro Ala
    530   535   540

Asn Leu Ser Ala Gln Gly Thr Ala Gln Arg Arg Ile Arg Leu Gln Thr
545   550   555   560

Arg Leu Arg Lys Pro Leu Ile Thr Leu Asn Asn Thr Lys Arg Asn Ser
            565   570   575

Asn Gly Arg Glu Gly Glu Ala Ser His Arg Lys Cys Glu Met Gln Glu

725

```
                580                     585                     590

         Lys Glu Asp Ile Ser Ser Ser Ser Ser Trp Gln Lys Gln Lys Lys Ser
                 595                     600                     605

         Leu Val Gln Phe Ser Ser Val Val Ile Ile Val Ala Val Ile Val Val
             610                     615                     620

         Leu Val Glu Ile Trp Lys Glu Ser Arg Asp Ala Lys Cys Ser Phe Leu
         625                     630                     635                     640

         Phe His Gln Leu Asp Ser Phe Lys Gly Met Phe Thr
                         645                     650


<210>  389 <211>  2178 <212>  DNA <213>  Arabidopsis thaliana <220>
<221>  CDS <222>  (1)..(2178) <223>  G1544

 <400>  389
atg tct cag tca aac atg gta cca gtg gct aac aac gga gac aac aac
48
Met Ser Gln Ser Asn Met Val Pro Val Ala Asn Asn Gly Asp Asn Asn
1                5                  10                  15

aac gac aac gaa aac aac aac aac aac aac aac aat ggt gga act gac
96
Asn Asp Asn Glu Asn Asn Asn Asn Asn Asn Asn Asn Gly Gly Thr Asp
                20                  25                  30

aac act aat gct gga aat gat tct gga gat caa gat ttc gac agt ggg
144
Asn Thr Asn Ala Gly Asn Asp Ser Gly Asp Gln Asp Phe Asp Ser Gly
         35                  40                  45

aat acc tca agt ggc aat cat gga gaa ggg ttg gga aac aat caa gct
192
Asn Thr Ser Ser Gly Asn His Gly Glu Gly Leu Gly Asn Asn Gln Ala
     50                  55                  60

cct cgt cat aag aag aaa aaa tac aat cgt cac acc caa ctt cag att
240
Pro Arg His Lys Lys Lys Lys Tyr Asn Arg His Thr Gln Leu Gln Ile
65                  70                  75                  80

tcg gag atg gaa gct ttc ttc aga gag tgt cct cac cca gat gac aaa
288
Ser Glu Met Glu Ala Phe Phe Arg Glu Cys Pro His Pro Asp Asp Lys
                85                  90                  95

caa agg tac gac ctt agc gct caa ttg gga ttg gac cct gtt cag atc
336
Gln Arg Tyr Asp Leu Ser Ala Gln Leu Gly Leu Asp Pro Val Gln Ile
            100                 105                 110

aaa ttc tgg ttc cag aac aaa cgc act caa aac aag aat caa caa gaa
384
Lys Phe Trp Phe Gln Asn Lys Arg Thr Gln Asn Lys Asn Gln Gln Glu
```

726

```
          115                         120                         125

cgc ttt gag aac tca gaa ctt cgg aat ctg aac aac cac ctt agg tct
432
Arg Phe Glu Asn Ser Glu Leu Arg Asn Leu Asn Asn His Leu Arg Ser
    130                     135                     140

gaa aat cag cgg tta cga gaa gct att cat caa gcc tta tgc cct aag
480
Glu Asn Gln Arg Leu Arg Glu Ala Ile His Gln Ala Leu Cys Pro Lys
145                     150                     155                     160

tgt gga ggc caa act gca att ggc gaa atg acc ttc gaa gag cac cat
528
Cys Gly Gly Gln Thr Ala Ile Gly Glu Met Thr Phe Glu Glu His His
                165                     170                     175

ctt cgc atc ctc aac gct cgt ttg act gaa gag atc aag caa ctt tcc
576
Leu Arg Ile Leu Asn Ala Arg Leu Thr Glu Glu Ile Lys Gln Leu Ser
                180                     185                     190

gtg aca gcg gaa aag ata tca agg ctt acg ggg ata cca gta agg agc
624
Val Thr Ala Glu Lys Ile Ser Arg Leu Thr Gly Ile Pro Val Arg Ser
                195                     200                     205

cat ccc cgt gtg tct cct cct aat cct cct cca aat ttc gag ttc ggg
672
His Pro Arg Val Ser Pro Pro Asn Pro Pro Pro Asn Phe Glu Phe Gly
        210                     215                     220

atg gga tct aag gga aat gtc gga aac cac tcg agg gaa acc act gga
720
Met Gly Ser Lys Gly Asn Val Gly Asn His Ser Arg Glu Thr Thr Gly
225                     230                     235                     240

cct gca gat gct aat acc aag ccg atc atc atg gag ttg gca ttt gga
768
Pro Ala Asp Ala Asn Thr Lys Pro Ile Ile Met Glu Leu Ala Phe Gly
                245                     250                     255

gcc atg gag gag ctc ttg gtg atg gct caa gtg gct gaa cca ctg tgg
816
Ala Met Glu Glu Leu Leu Val Met Ala Gln Val Ala Glu Pro Leu Trp
            260                     265                     270

atg gga gga ttt aat ggc act agc tta gct ttg aac ttg gat gaa tac
864
Met Gly Gly Phe Asn Gly Thr Ser Leu Ala Leu Asn Leu Asp Glu Tyr
            275                     280                     285

gaa aag acg ttt cgc acg ggt ctc ggt cct aga ctt ggc ggg ttt cga
912
Glu Lys Thr Phe Arg Thr Gly Leu Gly Pro Arg Leu Gly Gly Phe Arg
        290                     295                     300

acc gag gca tcc agg gaa act gca ctc gtg gca atg tgt cct act ggc
960
Thr Glu Ala Ser Arg Glu Thr Ala Leu Val Ala Met Cys Pro Thr Gly
305                     310                     315                     320
```

727

att gtt gaa atg ctc atg caa gag aat ctg tgg tca aca atg ttt gcc
1008
Ile Val Glu Met Leu Met Gln Glu Asn Leu Trp Ser Thr Met Phe Ala
            325   330   335

gga att gtt ggt aga gcc agg act·cat gaa cag ata atg gct gat gct
1056
Gly Ile Val Gly Arg Ala Arg Thr His Glu Gln Ile Met Ala Asp Ala
            340   345   350

gct gga aac ttc aat gga aat ctc caa ata atg agt gct gag tac caa
1104
Ala Gly Asn Phe Asn Gly Asn Leu Gln Ile Met Ser Ala Glu Tyr Gln
            355   360   365

gtg ctt tcc ccg cta gtc aca acc cgc gaa agc tac ttc gtc cgc tac
1152
Val Leu Ser Pro Leu Val Thr Thr Arg Glu Ser Tyr Phe Val Arg Tyr
        370   375   380

tgt aag caa caa gga gag ggt ttg tgg gcg gtg gtc gat att tcc atc
1200 ·
Cys Lys Gln Gln Gly Glu Gly Leu Trp Ala Val Val Asp Ile Ser Ile
385   390   395   400

gac cat ctc ctc cca aac atc aac cta aaa tgt cgc cgc cga ccc tct
1248
Asp His Leu Leu Pro Asn Ile Asn Leu Lys Cys Arg Arg Arg Pro Ser
            405   410   415

gga tgt ctg att caa gaa atg cat agt ggt tac tcc aag gtt aca tgg
1296
Gly Cys Leu Ile Gln Glu Met His Ser Gly Tyr Ser Lys Val Thr Trp
            420   425   430

gtg gaa cat gtg gaa gta gat gat gca gga agt tac agc atc ttt gag
1344
Val Glu His Val Glu Val Asp Asp Ala Gly Ser Tyr Ser Ile Phe Glu
            435   440   445

aaa tta atc tgt act ggt caa gct ttt gct gct aac cgc tgg gtt ggt
1392
Lys Leu Ile Cys Thr Gly Gln Ala Phe Ala Ala Asn Arg Trp Val Gly
        450   455   460

aca ttg gta cgc cag tgt gag cgg ata tct agc atc ttg tcg aca gat
1440
Thr Leu Val Arg Gln Cys Glu Arg Ile Ser Ser Ile Leu Ser Thr Asp
465   470   475   480

ttt caa tct gtc gat tcc ggt gat cac ata acg cta act aac cat gga
1488
Phe Gln Ser Val Asp Ser Gly Asp His Ile Thr Leu Thr Asn His Gly
            485   490   495

aag atg agc atg ctg aag ata gct gag cgg att gcg aga acc ttc ttt
1536
Lys Met Ser Met Leu Lys Ile Ala Glu Arg Ile Ala Arg Thr Phe Phe
        500   505   510

gct gga atg acc aat gcg acg ggg tct aca ata ttt tct ggt gtt gaa
1584
Ala Gly Met Thr Asn Ala Thr Gly Ser Thr Ile Phe Ser Gly Val Glu
        515   520   525

gga gaa gat atc aga gtg atg aca atg aag agc gtg aat gat cca gga
1632
Gly Glu Asp Ile Arg Val Met Thr Met Lys Ser Val Asn Asp Pro Gly
    530   535   540

aag cct ccc ggt gtc att att tgt gca gcc act tcc ttt tgg ctt cct
1680
Lys Pro Pro Gly Val Ile Ile Cys Ala Ala Thr Ser Phe Trp Leu Pro
545   550   555   560

gct cct cct aac act gtc ttt gac ttc ctc aga gag gct act cac cga
1728
Ala Pro Pro Asn Thr Val Phe Asp Phe Leu Arg Glu Ala Thr His Arg
                565   570   575

cac aat tgg gat gtt ctc tgc aac gga gag atg atg cac aag ata gca
1776
His Asn Trp Asp Val Leu Cys Asn Gly Glu Met Met His Lys Ile Ala
            580   585   590

gag att acg aat ggg ata gac aaa agg aac tgt gca agt tta ctc cgg
1824
Glu Ile Thr Asn Gly Ile Asp Lys Arg Asn Cys Ala Ser Leu Leu Arg
        595   600   605

cat gga cac act agc aag agc aag atg atg ata gtt caa gag act tct
1872
His Gly His Thr Ser Lys Ser Lys Met Met Ile Val Gln Glu Thr Ser
    610   615   620

act gac cca aca gct tca ttt gtg ctt tat gcg cct gtt gat atg aca
1920
Thr Asp Pro Thr Ala Ser Phe Val Leu Tyr Ala Pro Val Asp Met Thr
625   630   635   640

tca atg gat att act ctc cat gga ggt ggt gat cct gac ttt gtg gtg
1968
Ser Met Asp Ile Thr Leu His Gly Gly Gly Asp Pro Asp Phe Val Val
                645   650   655

atc ctg cct tct ggt ttt gct att ttt cca gat ggt acg ggt aag cct
2016
Ile Leu Pro Ser Gly Phe Ala Ile Phe Pro Asp Gly Thr Gly Lys Pro
            660   665   670

gga gga aaa gaa gga gga tca ctt ttg acc att tcc ttc caa atg ctg
2064
Gly Gly Lys Glu Gly Gly Ser Leu Leu Thr Ile Ser Phe Gln Met Leu
        675   680   685

gtt gag tca ggt cct gag gct agg ctg agt gtt agc tct gtt gca act
2112
Val Glu Ser Gly Pro Glu Ala Arg Leu Ser Val Ser Ser Val Ala Thr
    690   695   700

act gag aat ctg att cgt aca acc gtg cgg agg atc aaa gat ttg ttt
2160
Thr Glu Asn Leu Ile Arg Thr Thr Val Arg Arg Ile Lys Asp Leu Phe
705   710   715   720

cct tgt cag act gct tga
2178
Pro Cys Gln Thr Ala
                725

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390

Met Ser Gln Ser Asn Met Val Pro Val Ala Asn Asn Gly Asp Asn Asn
1   5   10   15

Asn Asp Asn Glu Asn Asn Asn Asn Asn Asn Asn Asn Gly Gly Thr Asp
            20   25   30

Asn Thr Asn Ala Gly Asn Asp Ser Gly Asp Gln Asp Phe Asp Ser Gly
        35   40   45

Asn Thr Ser Ser Gly Asn His Gly Glu Gly Leu Gly Asn Asn Gln Ala
    50   55   60

Pro Arg His Lys Lys Lys Lys Tyr Asn Arg His Thr Gln Leu Gln Ile
65   70   75   80

Ser Glu Met Glu Ala Phe Phe Arg Glu Cys Pro His Pro Asp Asp Lys
            85   90   95

Gln Arg Tyr Asp Leu Ser Ala Gln Leu Gly Leu Asp Pro Val Gln Ile
            100   105   110

Lys Phe Trp Phe Gln Asn Lys Arg Thr Gln Asn Lys Asn Gln Gln Glu
        115   120   125

Arg Phe Glu Asn Ser Glu Leu Arg Asn Leu Asn Asn His Leu Arg Ser
    130   135   140

Glu Asn Gln Arg Leu Arg Glu Ala Ile His Gln Ala Leu Cys Pro Lys
145   150   155   160

Cys Gly Gly Gln Thr Ala Ile Gly Glu Met Thr Phe Glu Glu His His
                165   170   175

Leu Arg Ile Leu Asn Ala Arg Leu Thr Glu Glu Ile Lys Gln Leu Ser
            180   185   190

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Val Thr Ala Glu Lys Ile Ser Arg Leu Thr Gly Ile Pro Val Arg Ser
        195                 200                 205

His Pro Arg Val Ser Pro Pro Asn Pro Pro Pro Asn Phe Glu Phe Gly
    210                 215                 220

Met Gly Ser Lys Gly Asn Val Gly Asn His Ser Arg Glu Thr Thr Gly
225                 230                 235                 240

Pro Ala Asp Ala Asn Thr Lys Pro Ile Ile Met Glu Leu Ala Phe Gly
                245                 250                 255

Ala Met Glu Glu Leu Leu Val Met Ala Gln Val Ala Glu Pro Leu Trp
            260                 265                 270

Met Gly Gly Phe Asn Gly Thr Ser Leu Ala Leu Asn Leu Asp Glu Tyr
            275                 280                 285

Glu Lys Thr Phe Arg Thr Gly Leu Gly Pro Arg Leu Gly Gly Phe Arg
    290                 295                 300

Thr Glu Ala Ser Arg Glu Thr Ala Leu Val Ala Met Cys Pro Thr Gly
305                 310                 315                 320

Ile Val Glu Met Leu Met Gln Glu Asn Leu Trp Ser Thr Met Phe Ala
                325                 330                 335

Gly Ile Val Gly Arg Ala Arg Thr His Glu Gln Ile Met Ala Asp Ala
            340                 345                 350

Ala Gly Asn Phe Asn Gly Asn Leu Gln Ile Met Ser Ala Glu Tyr Gln
    355                 360                 365

Val Leu Ser Pro Leu Val Thr Thr Arg Glu Ser Tyr Phe Val Arg Tyr
370                 375                 380

Cys Lys Gln Gln Gly Glu Gly Leu Trp Ala Val Val Asp Ile Ser Ile
385                 390                 395                 400

Asp His Leu Leu Pro Asn Ile Asn Leu Lys Cys Arg Arg Arg Pro Ser
                405                 410                 415

Gly Cys Leu Ile Gln Glu Met His Ser Gly Tyr Ser Lys Val Thr Trp
            420                 425                 430
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731

Val Glu His Val Glu Val Asp Asp Ala Gly Ser Tyr Ser Ile Phe Glu
        435   440   445

Lys Leu Ile Cys Thr Gly Gln Ala Phe Ala Ala Asn Arg Trp Val Gly
        450   455   460

Thr Leu Val Arg Gln Cys Glu Arg Ile Ser Ser Ile Leu Ser Thr Asp
465   470   475   480

Phe Gln Ser Val Asp Ser Gly Asp His Ile Thr Leu Thr Asn His Gly
                485   490   495

Lys Met Ser Met Leu Lys Ile Ala Glu Arg Ile Ala Arg Thr Phe Phe
            500   505   510

Ala Gly Met Thr Asn Ala Thr Gly Ser Thr Ile Phe Ser Gly Val Glu
        515   520   525

Gly Glu Asp Ile Arg Val Met Thr Met Lys Ser Val Asn Asp Pro Gly
    530   535   540

Lys Pro Pro Gly Val Ile Ile Cys Ala Ala Thr Ser Phe Trp Leu Pro
545   550   555   560

Ala Pro Pro Asn Thr Val Phe Asp Phe Leu Arg Glu Ala Thr His Arg
                565   570   575

His Asn Trp Asp Val Leu Cys Asn Gly Glu Met Met His Lys Ile Ala
            580   585   590

Glu Ile Thr Asn Gly Ile Asp Lys Arg Asn Cys Ala Ser Leu Leu Arg
        595   600   605

His Gly His Thr Ser Lys Ser Lys Met Met Ile Val Gln Glu Thr Ser
    610   615   620

Thr Asp Pro Thr Ala Ser Phe Val Leu Tyr Ala Pro Val Asp Met Thr
625   630   635   640

Ser Met Asp Ile Thr Leu His Gly Gly Gly Asp Pro Asp Phe Val Val
                645   650   655

Ile Leu Pro Ser Gly Phe Ala Ile Phe Pro Asp Gly Thr Gly Lys Pro
            660   665   670

Gly Gly Lys Glu Gly Gly Ser Leu Leu Thr Ile Ser Phe Gln Met Leu

732

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        675                    680                    685


Val Glu Ser Gly Pro Glu Ala Arg Leu Ser Val Ser Ser Val Ala Thr
    690                    695                    700


Thr Glu Asn Leu Ile Arg Thr Thr Val Arg Arg Ile Lys Asp Leu Phe
705                    710                    715                    720


Pro Cys Gln Thr Ala
                725


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48
Met Ser Gln Thr Ser Leu Glu Pro Leu Ile Ile Ser Ile Ile Lys Leu
1               5                   10                  15


caa att ttg caa ctt tgg ttg aaa ttg ata gct gtt ggt tgg aat tta
96
Gln Ile Leu Gln Leu Trp Leu Lys Leu Ile Ala Val Gly Trp Asn Leu
            20                  25                  30


ggg tct aat gat gat gaa ttg tac acg gag cta tgg aaa gct tgt gca
144
Gly Ser Asn Asp Asp Glu Leu Tyr Thr Glu Leu Trp Lys Ala Cys Ala
        35                  40                  45


ggg cca ctt gtg gaa gtt cct cgt tat ggt gaa aga gtt ttc tac ttc
192
Gly Pro Leu Val Glu Val Pro Arg Tyr Gly Glu Arg Val Phe Tyr Phe
    50                  55                  60


cct caa ggt cac atg gaa caa ttg gtt gct tcg act aat caa gga gtt
240
Pro Gln Gly His Met Glu Gln Leu Val Ala Ser Thr Asn Gln Gly Val
65                  70                  75                  80


gtt gat caa gag ata cca gtg ttt aat ctt cct cca aag ata ctt tgt
288
Val Asp Gln Glu Ile Pro Val Phe Asn Leu Pro Pro Lys Ile Leu Cys
                85                  90                  95


cgt gtt ctt agt gtt acg tta aaa gca gaa cat gag acc gat gag gtt
336
Arg Val Leu Ser Val Thr Leu Lys Ala Glu His Glu Thr Asp Glu Val
            100                 105                 110


tac gct cag atc aca tta caa cca gaa gaa gat caa agt gaa cca aca
384
Tyr Ala Gln Ile Thr Leu Gln Pro Glu Glu Asp Gln Ser Glu Pro Thr
            115                 120                 125


agt ctt gac cca cct tta gta gaa cca gct aaa cca acg gtt gat tct
432
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733

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            Ser Leu Asp Pro Pro Leu Val Glu Pro Ala Lys Pro Thr Val Asp Ser
                130             135             140

ttt gtg aag att cta aca gct tca gat aca agc aca cat ggt gga ttc
480
Phe Val Lys Ile Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe
145             150             155             160

tct gtt ctt cgt aaa cac gcc act gag tgt tta cct tca ctt gat atg
528
Ser Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Ser Leu Asp Met
                165             170             175

aca caa cct aca ccg act caa gaa ctt gta gct aga gat ctt cac ggc
576
Thr Gln Pro Thr Pro Thr Gln Glu Leu Val Ala Arg Asp Leu His Gly
                180             185             190

tat gaa tgg agg ttt aag cat ata ttt aga ggg caa ccg agg agg cat
624
Tyr Glu Trp Arg Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His
                195             200             205

tta ctt aca acc ggt tgg agt aca ttt gta acc tcg aaa aga ctt gta
672
Leu Leu Thr Thr Gly Trp Ser Thr Phe Val Thr Ser Lys Arg Leu Val
                210             215             220

gct gga gat gca ttt gtg ttc ttg agg ggt gaa acc ggg gat tta cgg
720
Ala Gly Asp Ala Phe Val Phe Leu Arg Gly Glu Thr Gly Asp Leu Arg
225             230             235             240

gtt ggt gtg agg cgt tta gct aag cag caa agc acg atg ccc gca tcc
768
Val Gly Val Arg Arg Leu Ala Lys Gln Gln Ser Thr Met Pro Ala Ser
                245             250             255

gtt att tcg agt cag agt atg cgt ttg gga gtt ctt gct aca gct tct
816
Val Ile Ser Ser Gln Ser Met Arg Leu Gly Val Leu Ala Thr Ala Ser
                260             265             270

cat gct gtt acc aca aca act ata ttt gtt gtc ttc tat aaa cca agg
864
His Ala Val Thr Thr Thr Thr Ile Phe Val Val Phe Tyr Lys Pro Arg
                275             280             285

ata agc cag ttt ata att agt gtg aac aag tat atg atg gcg atg aag
912
Ile Ser Gln Phe Ile Ile Ser Val Asn Lys Tyr Met Met Ala Met Lys
                290             295             300

aac ggg ttt tct ctc ggt atg cgg tat agg atg aga ttc gaa gga gaa
960
Asn Gly Phe Ser Leu Gly Met Arg Tyr Arg Met Arg Phe Glu Gly Glu
305             310             315             320

gag tct cct gag aga ata ttt aca ggt acc att att ggc agt gga gat
1008
Glu Ser Pro Glu Arg Ile Phe Thr Gly Thr Ile Ile Gly Ser Gly Asp
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                        325   330   335

cta tct tct caa tgg cca gct tcc aaa tgg agg tca ttg cag atc caa
1056
Leu Ser Ser Gln Trp Pro Ala Ser Lys Trp Arg Ser Leu Gln Ile Gln
            340   345   350

tgg gac gag cca tct tct ata cag aga cca aac aag gtc tca ccg tgg
1104
Trp Asp Glu Pro Ser Ser Ile Gln Arg Pro Asn Lys Val Ser Pro Trp
            355   360   365

gag atc gag cct ttc tca cca tcc gcg ctt aca cca acc cct act caa
1152
Glu Ile Glu Pro Phe Ser Pro Ser Ala Leu Thr Pro Thr Pro Thr Gln
    370   375   380

caa caa tca aag tcc aaa cgg tcc aga cca atc tca gaa atc aca ggg
1200
Gln Gln Ser Lys Ser Lys Arg Ser Arg Pro Ile Ser Glu Ile Thr Gly
385   390   395   400

agt cct gta gct tct agt ttc ttg agt agt ttc tcg cag agc cac gag
1248
Ser Pro Val Ala Ser Ser Phe Leu Ser Ser Phe Ser Gln Ser His Glu
                405   410   415

tct aat cca tcg gtc aaa ctg ttg ttt caa gat cca gca acc gag aga
1296
Ser Asn Pro Ser Val Lys Leu Leu Phe Gln Asp Pro Ala Thr Glu Arg
            420   425   430

aac tca aac aaa tca gtg ttt tca agt gga tta caa tgc aag ata acc
1344
Asn Ser Asn Lys Ser Val Phe Ser Ser Gly Leu Gln Cys Lys Ile Thr
            435   440   445

gag gct ccg gtc aca agt agt tgt agg tta ttc gga ttc gat ctc acg
1392
Glu Ala Pro Val Thr Ser Ser Cys Arg Leu Phe Gly Phe Asp Leu Thr
    450   455   460

agc aag cct gct tct gct aca att cct cat gac aag cag cta ata agt
1440
Ser Lys Pro Ala Ser Ala Thr Ile Pro His Asp Lys Gln Leu Ile Ser
465   470   475   480

gtg gat tca aat ata tct gat tct acc acc aag tgt caa gat cct aac
1488
Val Asp Ser Asn Ile Ser Asp Ser Thr Thr Lys Cys Gln Asp Pro Asn
                485   490   495

tct tca aac tca cca aaa gag cag aaa caa caa aca tcc aca aga agc
1536
Ser Ser Asn Ser Pro Lys Glu Gln Lys Gln Gln Thr Ser Thr Arg Ser
            500   505   510

cga atc aag gtg caa atg caa gga aca gcg gtt gga cgc gcg gtt gat
1584
Arg Ile Lys Val Gln Met Gln Gly Thr Ala Val Gly Arg Ala Val Asp
            515   520   525

tta aca ttg ttg aga tca tac gat gaa cta ata aaa gag cta gag aaa
1632
Leu Thr Leu Leu Arg Ser Tyr Asp Glu Leu Ile Lys Glu Leu Glu Lys
    530   535   540

atg ttt gag att gaa gga gaa ctt agt cct aaa gac aaa tgg gct atc
1680
Met Phe Glu Ile Glu Gly Glu Leu Ser Pro Lys Asp Lys Trp Ala Ile
545   550   555   560

gtg ttt aca gac gat gaa gga gat agg atg ctt gta gga gat gat cca
1728
Val Phe Thr Asp Asp Glu Gly Asp Arg Met Leu Val Gly Asp Asp Pro
              565   570   575

tgg aat gag ttc tgt aaa atg gca aag aag tta ttc ata tat ccg agt
1776
Trp Asn Glu Phe Cys Lys Met Ala Lys Lys Leu Phe Ile Tyr Pro Ser
              580   585   590

gat gag gtc aag aaa atg agg tcg aag tcg ttg ttg ggt gat aaa ggt
1824
Asp Glu Val Lys Lys Met Arg Ser Lys Ser Leu Leu Gly Asp Lys Gly
          595   600   605

acg atc gta aat ctt gaa tca gat cag agg aca gtt cac gtt taa
1869
Thr Ile Val Asn Leu Glu Ser Asp Gln Arg Thr Val His Val
    610   615   620

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Met Ser Gln Thr Ser Leu Glu Pro Leu Ile Ile Ser Ile Ile Lys Leu
1   5   10   15

Gln Ile Leu Gln Leu Trp Leu Lys Leu Ile Ala Val Gly Trp Asn Leu
          20   25   30

Gly Ser Asn Asp Asp Glu Leu Tyr Thr Glu Leu Trp Lys Ala Cys Ala
          35   40   45

Gly Pro Leu Val Glu Val Pro Arg Tyr Gly Glu Arg Val Phe Tyr Phe
    50   55   60

Pro Gln Gly His Met Glu Gln Leu Val Ala Ser Thr Asn Gln Gly Val
65   70   75   80

Val Asp Gln Glu Ile Pro Val Phe Asn Leu Pro Pro Lys Ile Leu Cys
              85   90   95

Arg Val Leu Ser Val Thr Leu Lys Ala Glu His Glu Thr Asp Glu Val
          100   105   110

736

Tyr Ala Gln Ile Thr Leu Gln Pro Glu Glu Asp Gln Ser Glu Pro Thr
        115   120   125

Ser Leu Asp Pro Pro Leu Val Glu Pro Ala Lys Pro Thr Val Asp Ser
        130   135   140

Phe Val Lys Ile Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe
145   150   155   160

Ser Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Ser Leu Asp Met
                165   170   175

Thr Gln Pro Thr Pro Thr Gln Glu Leu Val Ala Arg Asp Leu His Gly
            180   185   190

Tyr Glu Trp Arg Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His
            195   200   205

Leu Leu Thr Thr Gly Trp Ser Thr Phe Val Thr Ser Lys Arg Leu Val
        210   215   220

Ala Gly Asp Ala Phe Val Phe Leu Arg Gly Glu Thr Gly Asp Leu Arg
225   230   235   240

Val Gly Val Arg Arg Leu Ala Lys Gln Gln Ser Thr Met Pro Ala Ser
                245   250   255

Val Ile Ser Ser Gln Ser Met Arg Leu Gly Val Leu Ala Thr Ala Ser
                260   265   270

His Ala Val Thr Thr Thr Thr Ile Phe Val Val Phe Tyr Lys Pro Arg
        275   280   285

Ile Ser Gln Phe Ile Ile Ser Val Asn Lys Tyr Met Met Ala Met Lys
        290   295   300

Asn Gly Phe Ser Leu Gly Met Arg Tyr Arg Met Arg Phe Glu Gly Glu
305   310   315   320

Glu Ser Pro Glu Arg Ile Phe Thr Gly Thr Ile Ile Gly Ser Gly Asp
                325   330   335

Leu Ser Ser Gln Trp Pro Ala Ser Lys Trp Arg Ser Leu Gln Ile Gln
            340   345   350

737

Trp Asp Glu Pro Ser Ser Ile Gln Arg Pro Asn Lys Val Ser Pro Trp
    355   360   365

Glu Ile Glu Pro Phe Ser Pro Ser Ala Leu Thr Pro Thr Pro Thr Gln
    370   375   380

Gln Gln Ser Lys Ser Lys Arg Ser Arg Pro Ile Ser Glu Ile Thr Gly
385   390   395   400

Ser Pro Val Ala Ser Ser Phe Leu Ser Ser Phe Ser Gln Ser His Glu
              405   410   415

Ser Asn Pro Ser Val Lys Leu Leu Phe Gln Asp Pro Ala Thr Glu Arg
              420   425   430

Asn Ser Asn Lys Ser Val Phe Ser Ser Gly Leu Gln Cys Lys Ile Thr
              435   440   445

Glu Ala Pro Val Thr Ser Ser Cys Arg Leu Phe Gly Phe Asp Leu Thr
    450   455   460

Ser Lys Pro Ala Ser Ala Thr Ile Pro His Asp Lys Gln Leu Ile Ser
465   470   475   480

Val Asp Ser Asn Ile Ser Asp Ser Thr Thr Lys Cys Gln Asp Pro Asn
              485   490   495

Ser Ser Asn Ser Pro Lys Glu Gln Lys Gln Gln Thr Ser Thr Arg Ser
              500   505   510

Arg Ile Lys Val Gln Met Gln Gly Thr Ala Val Gly Arg Ala Val Asp
          515   520   525

Leu Thr Leu Leu Arg Ser Tyr Asp Glu Leu Ile Lys Glu Leu Glu Lys
    530   535   540

Met Phe Glu Ile Glu Gly Glu Leu Ser Pro Lys Asp Lys Trp Ala Ile
545   550   555   560

Val Phe Thr Asp Asp Glu Gly Asp Arg Met Leu Val Gly Asp Asp Pro
              565   570   575

Trp Asn Glu Phe Cys Lys Met Ala Lys Lys Leu Phe Ile Tyr Pro Ser
          580   585   590

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Asp Glu Val Lys Lys Met Arg Ser Lys Ser Leu Leu Gly Asp Lys Gly
        595                 600                 605

Thr Ile Val Asn Leu Glu Ser Asp Gln Arg Thr Val His Val
        610                 615                 620
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48
Met Tyr His Pro Asn Met Phe Glu Ser His His Met Phe Asp Met Thr
1               5               10              15

cca aag agt acc tct gat aac gac ttg gga atc acc ggt agc cga gaa
96
Pro Lys Ser Thr Ser Asp Asn Asp Leu Gly Ile Thr Gly Ser Arg Glu
            20              25              30

gat gac ttt gag acc aag tca ggt acc gaa gtc act act gag aat cct
144
Asp Asp Phe Glu Thr Lys Ser Gly Thr Glu Val Thr Thr Glu Asn Pro
        35              40              45

tct ggt gaa gag ctt caa gat cct agc caa cgt ccc aac aaa aag aag
192
Ser Gly Glu Glu Leu Gln Asp Pro Ser Gln Arg Pro Asn Lys Lys Lys
    50              55              60

cgt tac cat cgc cac acg caa cgc caa att caa gag ctc gaa tca ttc
240
Arg Tyr His Arg His Thr Gln Arg Gln Ile Gln Glu Leu Glu Ser Phe
65              70              75              80

ttt aag gaa tgt cct cat cca gat gat aag caa cga aaa gag ttg agc
288
Phe Lys Glu Cys Pro His Pro Asp Asp Lys Gln Arg Lys Glu Leu Ser
                85              90              95

cgt gat ctc aat tta gag cct ctt caa gtt aag ttt tgg ttc caa aac
336
Arg Asp Leu Asn Leu Glu Pro Leu Gln Val Lys Phe Trp Phe Gln Asn
            100             105             110

aaa cgc aca cag atg aag gca caa agt gag agg cat gag aac cag att
384
Lys Arg Thr Gln Met Lys Ala Gln Ser Glu Arg His Glu Asn Gln Ile
        115             120             125

cta aag tca gac aat gac aag ctc aga gca gag aac aat aga tac aaa
432
Leu Lys Ser Asp Asn Asp Lys Leu Arg Ala Glu Asn Asn Arg Tyr Lys
    130             135             140

gaa gct cta agc aat gct aca tgc cct aac tgt ggc ggt cca gct gct
480
Glu Ala Leu Ser Asn Ala Thr Cys Pro Asn Cys Gly Gly Pro Ala Ala
145             150             155             160
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att gga gaa atg tct ttt gac gaa caa cat ctc agg atc gaa aat gct
528
Ile Gly Glu Met Ser Phe Asp Glu Gln His Leu Arg Ile Glu Asn Ala
                165   170   175

cgg ctc cgc gaa gag att gat agg atc tct gct att gct gcg aaa tac
576
Arg Leu Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala Lys Tyr
            180   185   190

gtt ggg aag ccg tta gga tcg tct ttc gct cca cta gcg atc cac gcg
624
Val Gly Lys Pro Leu Gly Ser Ser Phe Ala Pro Leu Ala Ile His Ala
            195   200   205

cct tct cgt tcg ctt gat ctt gaa gtt gga aac ttt ggg aac cag aca
672
Pro Ser Arg Ser Leu Asp Leu Glu Val Gly Asn Phe Gly Asn Gln Thr
        210   215   220

ggc ttt gta gga gaa atg tat gga aca ggg gac att ttg agg tca gtt
720
Gly Phe Val Gly Glu Met Tyr Gly Thr Gly Asp Ile Leu Arg Ser Val
225   230   235   240

tcg att cct tct gag act gat aag cct ata atc gtg gag cta gcg gtt
768
Ser Ile Pro Ser Glu Thr Asp Lys Pro Ile Ile Val Glu Leu Ala Val
                245   250   255

gca gct atg gag gaa ctc gtg aga atg gct caa act gga gat cct tta
816
Ala Ala Met Glu Glu Leu Val Arg Met Ala Gln Thr Gly Asp Pro Leu
                260   265   270

tgg ctt tca acc gat aat tca gtc gag att ctc aac gaa gaa gag tat
864
Trp Leu Ser Thr Asp Asn Ser Val Glu Ile Leu Asn Glu Glu Glu Tyr
            275   280   285

ttc aga acg ttt ccg aga gga att gga cca aag cca tta gga tta aga
912
Phe Arg Thr Phe Pro Arg Gly Ile Gly Pro Lys Pro Leu Gly Leu Arg
        290   295   300

tca gag gcg tca aga caa tct gca gtt gtt ata atg aat cac atc aat
960
Ser Glu Ala Ser Arg Gln Ser Ala Val Val Ile Met Asn His Ile Asn
305   310   315   320

ctc gtt gag att ctc atg gat gtg aat caa tgg tct tgt gtt ttc tct
1008
Leu Val Glu Ile Leu Met Asp Val Asn Gln Trp Ser Cys Val Phe Ser
                325   330   335

ggg att gtg tca aga gcc ttg aca ctt gaa gtt ctt tca act gga gtt
1056
Gly Ile Val Ser Arg Ala Leu Thr Leu Glu Val Leu Ser Thr Gly Val
            340   345   350

740

gct ggg aac tac aac ggt gct tta caa gtg atg aca gct gag ttt caa
1104
Ala Gly Asn Tyr Asn Gly Ala Leu Gln Val Met Thr Ala Glu Phe Gln
        355   360   365

gtt cca tca ccc cta gtc cca acg cgt gag aac tac ttt gtg aga tac
1152
Val Pro Ser Pro Leu Val Pro Thr Arg Glu Asn Tyr Phe Val Arg Tyr
    370   375   380

tgc aaa caa cac agt gac ggc tct tgg gct gtg gtt gat gtc tct ttg
1200
Cys Lys Gln His Ser Asp Gly Ser Trp Ala Val Val Asp Val Ser Leu
385   390   395   400

gac agc ctt aga cca agt act cca atc tta aga act aga aga agg cct
1248
Asp Ser Leu Arg Pro Ser Thr Pro Ile Leu Arg Thr Arg Arg Arg Pro
            405   410   415

tca ggt tgt ctg att caa gaa ttg cct aat ggt tat tct aag gtt aca
1296
Ser Gly Cys Leu Ile Gln Glu Leu Pro Asn Gly Tyr Ser Lys Val Thr
        420   425   430

tgg ata gag cat atg gag gta gat gat aga tca gtt cac aac atg tat
1344
Trp Ile Glu His Met Glu Val Asp Asp Arg Ser Val His Asn Met Tyr
        435   440   445

aaa ccg ttg gtt cag tcc ggt tta gct ttc ggt gcg aaa cgt tgg gtg
1392
Lys Pro Leu Val Gln Ser Gly Leu Ala Phe Gly Ala Lys Arg Trp Val
    450   455   460

gct aca ctc gaa cga caa tgc gag cgg ctt gct agc tcc atg gcc agc
1440
Ala Thr Leu Glu Arg Gln Cys Glu Arg Leu Ala Ser Ser Met Ala Ser
465   470   475   480

aac att cct ggt gat ctt tcc gtg ata acg agt cct gaa gga agg aag
1488
Asn Ile Pro Gly Asp Leu Ser Val Ile Thr Ser Pro Glu Gly Arg Lys
            485   490   495

agt atg ttg aag cta gct gag aga atg gtt atg agt ttc tgc agt ggt
1536
Ser Met Leu Lys Leu Ala Glu Arg Met Val Met Ser Phe Cys Ser Gly
        500   505   510

gtt ggc gcg tcg act gca cac gct tgg aca aca atg tcg aca aca gga
1584
Val Gly Ala Ser Thr Ala His Ala Trp Thr Thr Met Ser Thr Thr Gly
        515   520   525

tcc gat gat gtt cgg gtc atg acc cgc aag agt atg gat gat cca gga
1632
Ser Asp Asp Val Arg Val Met Thr Arg Lys Ser Met Asp Asp Pro Gly
    530   535   540

741

```
aga cct ccg ggt att gtt ctt agt gca gct act tca ttc tgg atc cca
1680
Arg Pro Pro Gly Ile Val Leu Ser Ala Ala Thr Ser Phe Trp Ile Pro
545                 550                 555                 560

gtt gct ccc aaa cgt gtt ttt gat ttc ctc cgt gac gaa aat tca aga
1728
Val Ala Pro Lys Arg Val Phe Asp Phe Leu Arg Asp Glu Asn Ser Arg
                565                 570                 575

aaa gag tgg gat att ctg tca aat gga ggt atg gtt cag gaa atg gct
1776
Lys Glu Trp Asp Ile Leu Ser Asn Gly Gly Met Val Gln Glu Met Ala
                580                 585                 590

cat ata gcc aat ggt cat gaa cct gga aac tgt gtc tcc ttg ctc cga
1824
His Ile Ala Asn Gly His Glu Pro Gly Asn Cys Val Ser Leu Leu Arg
            595                 600                 605

gtc aat agt gga aac tcg agc cag agc aac atg ttg att cta caa gag
1872
Val Asn Ser Gly Asn Ser Ser Gln Ser Asn Met Leu Ile Leu Gln Glu
        610                 615                 620

agc tgt aca gat gca tca gga tcg tat gtg att tac gcg cca gtg gat
1920
Ser Cys Thr Asp Ala Ser Gly Ser Tyr Val Ile Tyr Ala Pro Val Asp
625                 630                 635                 640

ata gtg gcg atg aat gtg gtt cta agc ggt gga gat cct gat tac gtg
1968
Ile Val Ala Met Asn Val Val Leu Ser Gly Gly Asp Pro Asp Tyr Val
                645                 650                 655

gcg ttg ttg ccg tct ggt ttt gct att tta ccg gat ggt tcg gtt gga
2016
Ala Leu Leu Pro Ser Gly Phe Ala Ile Leu Pro Asp Gly Ser Val Gly
                660                 665                 670

gga gga gat ggg aat cag cat cag gaa atg gtt tct act act tct tct
2064
Gly Gly Asp Gly Asn Gln His Gln Glu Met Val Ser Thr Thr Ser Ser
                675                 680                 685

ggg agt tgt ggt ggt tcg ctt tta acc gtt gcg ttt cag att ctt gtt
2112
Gly Ser Cys Gly Gly Ser Leu Leu Thr Val Ala Phe Gln Ile Leu Val
        690                 695                 700

gac tct gtt cct aca gct aaa ctc tca ctt ggc tcg gtg gct acg gtt
2160
Asp Ser Val Pro Thr Ala Lys Leu Ser Leu Gly Ser Val Ala Thr Val
705                 710                 715                 720

aat agt ctg atc aaa tgt acg gtg gag agg att aaa gct gct gtt tct
2208
Asn Ser Leu Ile Lys Cys Thr Val Glu Arg Ile Lys Ala Ala Val Ser
                725                 730                 735
```

742

```
tgt gat gtt gga gga gga gcg tag
2232
Cys Asp Val Gly Gly Gly Ala
            740
```

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394

```
Met Tyr His Pro Asn Met Phe Glu Ser His His Met Phe Asp Met Thr
1               5               10              15
```

```
Pro Lys Ser Thr Ser Asp Asn Asp Leu Gly Ile Thr Gly Ser Arg Glu
            20              25              30
```

```
Asp Asp Phe Glu Thr Lys Ser Gly Thr Glu Val Thr Thr Glu Asn Pro
            35              40              45
```

```
Ser Gly Glu Glu Leu Gln Asp Pro Ser Gln Arg Pro Asn Lys Lys Lys
    50              55              60
```

```
Arg Tyr His Arg His Thr Gln Arg Gln Ile Gln Glu Leu Glu Ser Phe
65              70              75              80
```

```
Phe Lys Glu Cys Pro His Pro Asp Asp Lys Gln Arg Lys Glu Leu Ser
            85              90              95
```

```
Arg Asp Leu Asn Leu Glu Pro Leu Gln Val Lys Phe Trp Phe Gln Asn
            100             105             110
```

```
Lys Arg Thr Gln Met Lys Ala Gln Ser Glu Arg His Glu Asn Gln Ile
        115             120             125
```

```
Leu Lys Ser Asp Asn Asp Lys Leu Arg Ala Glu Asn Asn Arg Tyr Lys
    130             135             140
```

```
Glu Ala Leu Ser Asn Ala Thr Cys Pro Asn Cys Gly Gly Pro Ala Ala
145             150             155             160
```

```
Ile Gly Glu Met Ser Phe Asp Glu Gln His Leu Arg Ile Glu Asn Ala
            165             170             175
```

```
Arg Leu Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala Lys Tyr
        180             185             190
```

```
Val Gly Lys Pro Leu Gly Ser Ser Phe Ala Pro Leu Ala Ile His Ala
        195             200             205
```

Pro Ser Arg Ser Leu Asp Leu Glu Val Gly Asn Phe Gly Asn Gln Thr
    210   215   220

Gly Phe Val Gly Glu Met Tyr Gly Thr Gly Asp Ile Leu Arg Ser Val
225   230   235   240

Ser Ile Pro Ser Glu Thr Asp Lys Pro Ile Ile Val Glu Leu Ala Val
                245   250   255

Ala Ala Met Glu Glu Leu Val Arg Met Ala Gln Thr Gly Asp Pro Leu
            260   265   270

Trp Leu Ser Thr Asp Asn Ser Val Glu Ile Leu Asn Glu Glu Glu Tyr
        275   280   285

Phe Arg Thr Phe Pro Arg Gly Ile Gly Pro Lys Pro Leu Gly Leu Arg
    290   295   300

Ser Glu Ala Ser Arg Gln Ser Ala Val Val Ile Met Asn His Ile Asn
305   310   315   320

Leu Val Glu Ile Leu Met Asp Val Asn Gln Trp Ser Cys Val Phe Ser
                325   330   335

Gly Ile Val Ser Arg Ala Leu Thr Leu Glu Val Leu Ser Thr Gly Val
            340   345   350

Ala Gly Asn Tyr Asn Gly Ala Leu Gln Val Met Thr Ala Glu Phe Gln
        355   360   365

Val Pro Ser Pro Leu Val Pro Thr Arg Glu Asn Tyr Phe Val Arg Tyr
    370   375   380

Cys Lys Gln His Ser Asp Gly Ser Trp Ala Val Val Asp Val Ser Leu
385   390   395   400

Asp Ser Leu Arg Pro Ser Thr Pro Ile Leu Arg Thr Arg Arg Arg Pro
                405   410   415

Ser Gly Cys Leu Ile Gln Glu Leu Pro Asn Gly Tyr Ser Lys Val Thr
            420   425   430

Trp Ile Glu His Met Glu Val Asp Asp Arg Ser Val His Asn Met Tyr
        435   440   445

Lys Pro Leu Val Gln Ser Gly Leu Ala Phe Gly Ala Lys Arg Trp Val

744

```
            450                   455                    460
```

Ala Thr Leu Glu Arg Gln Cys Glu Arg Leu Ala Ser Ser Met Ala Ser
465   470   475   480

Asn Ile Pro Gly Asp Leu Ser Val Ile Thr Ser Pro Glu Gly Arg Lys
                485   490   495

Ser Met Leu Lys Leu Ala Glu Arg Met Val Met Ser Phe Cys Ser Gly
                500   505   510

Val Gly Ala Ser Thr Ala His Ala Trp Thr Thr Met Ser Thr Thr Gly
            515   520   525

Ser Asp Asp Val Arg Val Met Thr Arg Lys Ser Met Asp Asp Pro Gly
        530   535   540

Arg Pro Pro Gly Ile Val Leu Ser Ala Ala Thr Ser Phe Trp Ile Pro
545   550   555   560

Val Ala Pro Lys Arg Val Phe Asp Phe Leu Arg Asp Glu Asn Ser Arg
                565   570   575

Lys Glu Trp Asp Ile Leu Ser Asn Gly Gly Met Val Gln Glu Met Ala
                580   585   590

His Ile Ala Asn Gly His Glu Pro Gly Asn Cys Val Ser Leu Leu Arg
            595   600   605

Val Asn Ser Gly Asn Ser Ser Gln Ser Asn Met Leu Ile Leu Gln Glu
        610   615   620

Ser Cys Thr Asp Ala Ser Gly Ser Tyr Val Ile Tyr Ala Pro Val Asp
625   630   635   640

Ile Val Ala Met Asn Val Val Leu Ser Gly Gly Asp Pro Asp Tyr Val
                645   650   655

Ala Leu Leu Pro Ser Gly Phe Ala Ile Leu Pro Asp Gly Ser Val Gly
            660   665   670

Gly Gly Asp Gly Asn Gln His Gln Glu Met Val Ser Thr Thr Ser Ser
            675   680   685

Gly Ser Cys Gly Gly Ser Leu Leu Thr Val Ala Phe Gln Ile Leu Val
    690   695   700

```
                                745
```

Asp Ser Val Pro Thr Ala, Lys Leu Ser Leu Gly Ser Val Ala Thr Val
705   710   715   720

Asn Ser Leu Ile Lys Cys Thr Val Glu Arg Ile Lys Ala Ala Val Ser
            725   730   735

Cys Asp Val Gly Gly Gly Ala
            740

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60

tcaccagaat ctctctgttt aaaataatag gtg atg atg atg gat gag ttt atg
114
                                    Met Met Met Asp Glu Phe Met
                                    1   5

gat ctt aga cca gtg aag tac aca gag cac aag aot gtt atc aga aag
162
Asp Leu Arg Pro Val Lys Tyr Thr Glu His Lys Thr Val Ile Arg Lys
        10   15   20

tac act aaa aag tcg tct atg gag agg aag acc agt gtt cgt gac tcg
210
Tyr Thr Lys Lys Ser Ser Met Glu Arg Lys Thr Ser Val Arg Asp Ser
    25   30   35

gcc agg ttg gtt cgg gtc tca atg acg gat cgt gac gcc act gat tca
258
Ala Arg Leu Val Arg Val Ser Met Thr Asp Arg Asp Ala Thr Asp Ser
40   45   50   55

tca agc gac gag gaa gag ttt ctg ttc cct cga aga cgt gtc aag aga
306
Ser Ser Asp Glu Glu Glu Phe Leu Phe Pro Arg Arg Arg Val Lys Arg
            60   65   70

ttg att aac gag atc.aga gtc gag cct agc agc tct tcc acc ggc gac
354
Leu Ile Asn Glu Ile Arg Val Glu Pro Ser Ser Ser Ser Thr Gly Asp
            75   80   85

gtc tct gct tct ccg acg aag gac cgg aaa aga atc aac gtt gat tct
402
Val Ser Ala Ser Pro Thr Lys Asp Arg Lys Arg Ile Asn Val Asp Ser
        90   95   100

acg gtt caa aag ccc tct gtt tcc ggc caa aac cag aag aag tac cgc
450
Thr Val Gln Lys Pro Ser Val Ser Gly Gln Asn Gln Lys Lys Tyr Arg
    105   110   115

ggc gtg aga cag cga cca tgg gga aaa tgg gcg gcg gag att cgt gat
498
Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp
120   125   130   135

cct gag caa cgc cgg aga atc tgg ctc ggt act ttt gca acg gcg gag
546
Pro Glu Gln Arg Arg Arg Ile Trp Leu Gly Thr Phe Ala Thr Ala Glu
            140   145   150

gaa gct gcc atc gtc tac gac aac gca gca atc aaa ctt cgt ggc cct
594
Glu Ala Ala Ile Val Tyr Asp Asn Ala Ala Ile Lys Leu Arg Gly Pro
            155   160   165

gat gct ctt acc aac ttc acc gta caa cca gaa cca gaa ccg gta caa
642
Asp Ala Leu Thr Asn Phe Thr Val Gln Pro Glu Pro Glu Pro Val. Gln
            170   175   180

gaa caa gaa caa gaa ccg gag agc aac atg tcg gtt tcg ata tca gaa
690
Glu Gln Glu Gln Glu Pro Glu Ser Asn Met Ser Val Ser Ile Ser Glu
            185   190   195

tca atg gac gat tct caa cat cta tca tct ccg aca tcg gtt ctc aac
738
Ser Met Asp Asp Ser Gln His Leu Ser Ser Pro Thr Ser Val Leu Asn
200   205   210   215·

tac caa aca tat gtc tcg gag gaa cca atc gat agt ctt atc aaa ccg
786
Tyr Gln Thr Tyr ·Val Ser Glu Glu Pro Ile Asp Ser Leu Ile Lys Pro
            220   225   230

gtt aaa caa gag ttt ctt gaa cca gaa caa gag cca ata agc tgg cat
834
Val Lys Gln Glu Phe Leu Glu Pro Glu Gln Glu Pro Ile Ser Trp His
            235   240   245

ctt gga gaa ggt aat act aat act aat gat gat tca ttt cca ttg gac
882
Leu Gly Glu Gly Asn Thr Asn Thr Asn Asp Asp Ser Phe Pro Leu Asp
            250   255   260

att aca ttt ctc gac aac tat ttc aat gaa tca tta cca gac atc tcc
930
Ile Thr Phe Leu Asp Asn Tyr Phe Asn Glu Ser Leu Pro Asp Ile Ser
            265   270   275

atc ttc gat caa cct atg tct cct att caa cca aca gag aat gat ttc
978
Ile Phe Asp Gln Pro Met Ser Pro Ile Gln Pro Thr Glu Asn Asp Phe
280   285   290   295

ttc aac gac ctt atg tta ttc gat agc aac gca gaa gaa tac tac tcc
1026
Phe Asn Asp Leu Met Leu Phe Asp Ser Asn Ala Glu Glu Tyr Tyr Ser
            300   305   310

747

```
tcc gag atc aaa gag att ggt tca tcg ttc aac gat ctt gat gat tct
1074
Ser Glu Ile Lys Glu Ile Gly Ser Ser Phe Asn Asp Leu Asp Asp Ser
          315             320             325


ttg ata tcc gat ctc tta ctt gtg tga tatttttgcc attaaccaaa
1121
Leu Ile Ser Asp Leu Leu Leu Val
          330             335


caccggtttg gttgc
1136
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<210> 396 <211> 335 <212> PRT <213> Arabidopsis thaliana <400> 396

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Met Met Met Asp Glu Phe Met Asp Leu Arg Pro Val Lys Tyr Thr Glu
1               5               10              15


His Lys Thr Val Ile Arg Lys Tyr Thr Lys Lys Ser Ser Met Glu Arg
          20              25              30


Lys Thr Ser Val Arg Asp Ser Ala Arg Leu Val Arg Val Ser Met Thr
          35              40              45


Asp Arg Asp Ala Thr Asp Ser Ser Ser Asp Glu Glu Glu Phe Leu Phe
     50              55              60


Pro Arg Arg Arg Val Lys Arg Leu Ile Asn Glu Ile Arg Val Glu Pro
65              70              75              80


Ser Ser Ser Ser Thr Gly Asp Val Ser Ala Ser Pro Thr Lys Asp Arg
               85               90              95


Lys Arg Ile Asn Val Asp Ser Thr Val Gln Lys Pro Ser Val Ser Gly
          100             105             110


Gln Asn Gln Lys Lys Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys
          115             120             125


Trp Ala Ala Glu Ile Arg Asp Pro Glu Gln Arg Arg Arg Ile Trp Leu
          130             135             140


Gly Thr Phe Ala Thr Ala Glu Glu Ala Ala Ile Val Tyr Asp Asn Ala
145             150             155             160


Ala Ile Lys Leu Arg Gly Pro Asp Ala Leu Thr Asn Phe Thr Val Gln
               165             170             175
```

748

Pro Glu Pro Glu Pro Val Gln Glu Gln Glu Gln Glu Pro Glu Ser Asn
            180   185   190

Met Ser Val Ser Ile Ser Glu Ser Met Asp Asp Ser Gln His Leu Ser
            195   200   205

Ser Pro Thr Ser Val Leu Asn Tyr Gln Thr Tyr Val Ser Glu Glu Pro
            210   215   220

Ile Asp Ser Leu Ile Lys Pro Val Lys Gln Glu Phe Leu Glu Pro Glu
225   230   235   240

Gln Glu Pro Ile Ser Trp His Leu Gly Glu Gly Asn Thr Asn Thr Asn
                245   250   255

Asp Asp Ser Phe Pro Leu Asp Ile Thr Phe Leu Asp Asn Tyr Phe Asn
            260   265   270

Glu Ser Leu Pro Asp Ile Ser Ile Phe Asp Gln Pro Met Ser Pro Ile
            275   280   285

Gln Pro Thr Glu Asn Asp Phe Phe Asn Asp Leu Met Leu Phe Asp Ser
            290   295   300

Asn Ala Glu Glu Tyr Tyr Ser Ser Glu Ile Lys Glu Ile Gly Ser Ser
305   310   315   320

Phe Asn Asp Leu Asp Asp Ser Leu Ile Ser Asp Leu Leu Leu Val
                325   330   335

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<221> CDS <222> (66)..(2393) <223> G1805

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tacaa atg ggt tgt gct caa tct agg gtt gat aac gaa gaa gca gta gct
110
       Met Gly Cys Ala Gln Ser Arg Val Asp Asn Glu Glu Ala Val Ala
        1   5   10   15

aga tgc aaa gaa cga cga aac gta atc aaa gaa gca gtt tcc gca agc
158
Arg Cys Lys Glu Arg Arg Asn Val Ile Lys Glu Ala Val Ser Ala Ser
                20   25   30

aaa gca ttc gcc gcc ggt cat ttc gct tac gct att gct ttg aaa aac
206
Lys Ala Phe Ala Ala Gly His Phe Ala Tyr Ala Ile Ala Leu Lys Asn
            35   40   45

749

act ggt gct gct tta agt gac tat ggc cat ggc gaa tct gat caa aaa
254
Thr Gly Ala Ala Leu Ser Asp Tyr Gly His Gly Glu Ser Asp Gln Lys
        50   55   60

gct tta gac gat gtg ttg tta gat caa caa cat tac gag aaa cag agt
302
Ala Leu Asp Asp Val Leu Leu Asp Gln Gln His Tyr Glu Lys Gln Ser
    65   70   75

cgt aac aat gta gat ccg gct tct cct cag cca cct cct cca ccg cct
350
Arg Asn Asn Val Asp Pro Ala Ser Pro Gln Pro Pro Pro Pro Pro Pro
80   85   90   95

att gag aat ctt cct cct ccg cct cct cct ttg cct aaa ttc tct cct
398
Ile Glu Asn Leu Pro Pro Pro Pro Pro Pro Leu Pro Lys Phe Ser Pro
                100   105   110

tct ccg att aaa cgt gcg att agt ttg cct tct atg gcg gtt aga ggt
446
Ser Pro Ile Lys Arg Ala Ile Ser Leu Pro Ser Met Ala Val Arg Gly
            115   120   125

cga aag gtt cag act tta gat ggt atg gcg att gag gaa gag gaa gaa
494
Arg Lys Val Gln Thr Leu Asp Gly Met Ala Ile Glu Glu Glu Glu Glu
        130   135   140

gat gaa gag gag gaa gag gaa gtt aag ggt agt ggt aga gac act gct
542
Asp Glu Glu Glu Glu Glu Glu Val Lys Gly Ser Gly Arg Asp Thr Ala
    145   150   155

cag gag gag gag gaa ccg aga acg ccg gag aat gtt ggg aag agt aat
590
Gln Glu Glu Glu Glu Pro Arg Thr Pro Glu Asn Val Gly Lys Ser Asn
160   165   170   175

ggg agg aag aga ttg gag aaa aca acg ccg gag att gtg agt gct tct
638
Gly Arg Lys Arg Leu Glu Lys Thr Thr Pro Glu Ile Val Ser Ala Ser
            180   185   190

ccg gca aat agt atg gct tgg gat tat ttt ttc atg gtg gag aat atg
686
Pro Ala Asn Ser Met Ala Trp Asp Tyr Phe Phe Met Val Glu Asn Met
            195   200   205

cct gga cct aat tta gat gat aga gag gtt agg aat ggt tat gag aat
734
Pro Gly Pro Asn Leu Asp Asp Arg Glu Val Arg Asn Gly Tyr Glu Asn
            210   215   220

cag agt agt cat ttt cag ttt aat gaa gag gat gat gaa gaa gaa gag
782
Gln Ser Ser His Phe Gln Phe Asn Glu Glu Asp Asp Glu Glu Glu Glu
    225   230   235

750

gaa gag gaa aga tct ggg ata tat cgg aag aag tct ggt tct ggt aaa
830
Glu Glu Glu Arg Ser Gly Ile Tyr Arg Lys Lys Ser Gly Ser Gly Lys
240   245   250   255

gta gtt gag gag atg gag cct aag acg ccg gag aaa gtt gaa gaa gaa
878
Val Val Glu Glu Met Glu Pro Lys Thr Pro Glu Lys Val Glu Glu Glu
                260   265   270

gag gag gaa gat gag gaa gag gat gag gaa gag gaa gag gag gag gaa
926
Glu Glu Glu Asp Glu Glu Glu Asp Glu Glu Glu Glu Glu Glu Glu
                275   280   285

gaa gaa gtg gtg gtg gag gta aag aag aag aag aaa ggg aaa gct aag
974
Glu Glu Val Val Val Glu Val Lys Lys Lys Lys Lys Gly Lys Ala Lys
                290   295   300

·att gag cat tcg agt act gct cca ccg gag ttt cgg cgt gcg gtt gct
1022
Ile Glu His Ser Ser Thr Ala Pro Pro Glu Phe Arg Arg Ala Val Ala
        305   310   315

aag act agt gct gct gca tca tca agt gtg aat ttg atg aag att ctt
1070
Lys Thr Ser Ala Ala Ala Ser Ser Ser Val Asn Leu Met Lys Ile Leu
320   325   330   335

gat gag att gat gat aga ttc ctt aag gct tca gaa tgt gct caa gag
1118
Asp Glu Ile Asp Asp Arg Phe Leu Lys Ala Ser Glu Cys Ala Gln Glu
                340   345   350

gtt tct aag atg ctt gaa gct aca agg tta cat tac cac tcg aat ttt
1166
Val Ser Lys Met Leu Glu Ala Thr Arg Leu His Tyr His Ser Asn Phe
            355   360   365

gca gat aac cga gga tat gtt gat cat tca gct aga gta atg cgg gtt
1214
Ala Asp Asn Arg Gly Tyr Val Asp His Ser Ala Arg Val Met Arg Val
            370   375   380

ata act tgg aat aaa tcg tta aga ggc att tcg aat gga gaa ggt gga
1262
Ile Thr Trp Asn Lys Ser Leu Arg Gly Ile Ser Asn Gly Glu Gly Gly
        385   390   395

aaa gat gat caa gaa tca gat gag cat gaa act cat gct acg gtg ttg
1310
Lys Asp Asp Gln Glu Ser Asp Glu His Glu Thr His Ala Thr Val Leu
400   405   410   415

gat aaa ttg tta gca tgg gag aag aaa ctc tat gat gaa gtg aag caa
1358
Asp Lys Leu Leu Ala Trp Glu Lys Lys Leu Tyr Asp Glu Val Lys Gln
                420   425   430

```
ggt gag ctt atg aag ata gag tat cag aag aag gta tct tta ctc aac
1406
Gly Glu Leu Met Lys Ile Glu Tyr Gln Lys Lys Val Ser Leu Leu Asn
            435             440             445

agg cat aag aaa cga ggt gcg agt gca gag acc gtg gag aaa aca aag
1454
Arg His Lys Lys Arg Gly Ala Ser Ala Glu Thr Val Glu Lys Thr Lys
        450             455             460

gcg gct gta agt cat cta cac aca aga tat att gtt gac atg caa tcc
1502
Ala Ala Val Ser His Leu His Thr Arg Tyr Ile Val Asp Met Gln Ser
    465             470             475

atg gat tca acg gtt tct gaa gta aac cgt tta agg gat gat caa ttg
1550
Met Asp Ser Thr Val Ser Glu Val Asn Arg Leu Arg Asp Asp Gln Leu
480             485             490             495

tat cca aga ctt gtt gcc tta gtt gaa ggg atg gcg aag atg tgg aca
1598
Tyr Pro Arg Leu Val Ala Leu Val Glu Gly Met Ala Lys Met Trp Thr
            500             505             510

aac atg tgt ata cac cac gac acc caa cta ggt att gtt gga gag cta
1646
Asn Met Cys Ile His His Asp Thr Gln Leu Gly Ile Val Gly Glu Leu
            515             520             525

aag gcc ctt gaa atc tca act tct ctc aaa gaa acc aca aaa cag cat
1694
Lys Ala Leu Glu Ile Ser Thr Ser Leu Lys Glu Thr Thr Lys Gln His
        530             535             540

cac cat cag act cgc cag ttc tgc acc gtc ttg gaa gaa tgg cat gtt
1742
His His Gln Thr Arg Gln Phe Cys Thr Val Leu Glu Glu Trp His Val
    545             550             555

cag ttc gat aca ctt gtc acc cat cag aag cag tac att aac tct ctc
1790
Gln Phe Asp Thr Leu Val Thr His Gln Lys Gln Tyr Ile Asn Ser Leu
560             565             570             575

aac aac tgg ctg aag cta aat cta atc ccc atc gag agt agt ctt aaa
1838
Asn Asn Trp Leu Lys Leu Asn Leu Ile Pro Ile Glu Ser Ser Leu Lys
            580             585             590

gag aaa gtt tca tca cct cca agg cct cag cgc ccg cca atc caa gct
1886
Glu Lys Val Ser Ser Pro Pro Arg Pro Gln Arg Pro Pro Ile Gln Ala
            595             600             605

ctt ctc cac tca tgg cat gac cgt ctt gag aaa ctt ccc gat gaa gtc
1934
Leu Leu His Ser Trp His Asp Arg Leu Glu Lys Leu Pro Asp Glu Val
            610             615             620
```

gcc aaa tca gct atc tcc tct ttc gcg gca gtc atc aaa acc atc ttg
1982
Ala Lys Ser Ala Ile Ser Ser Phe Ala Ala Val Ile Lys Thr Ile Leu
    625   630   635

ctg cac cag gaa gag gag atg aaa ctg aaa gag aaa tgc gaa gaa aca
2030
Leu His Gln Glu Glu Glu Met Lys Leu Lys Glu Lys Cys Glu Glu Thr
640   645   650   655

cga aga gag ttt ata cgg aag aag caa ggt ttt gag gat tgg tat caa
2078
Arg Arg Glu Phe Ile Arg Lys Lys Gln Gly Phe Glu Asp Trp Tyr Gln
            660   665   670

aaa cat ttg caa aag aga ggg cca aca gag gaa gct gaa ggc ggg gac
2126
Lys His Leu Gln Lys Arg Gly Pro Thr Glu Glu Ala Glu Gly Gly Asp
            675   680   685

gac gca aca aca agc tcc aga gat cat gtc aca gag agg aga att gct
2174
Asp Ala Thr Thr Ser Ser Arg Asp His Val Thr Glu Arg Arg Ile Ala
        690   695   700

gtg gag aca ctg aag aaa agg ctt gaa gaa gaa gaa gaa gct cac cag
2222
Val Glu Thr Leu Lys Lys Arg Leu Glu Glu Glu Glu Glu Ala His Gln
    705   710   715

aga cat tgt gtt cag gtg agg gag aaa tct cta aac agt ttg aag atc
2270
Arg His Cys Val Gln Val Arg Glu Lys Ser Leu Asn Ser Leu Lys Ile
720   725   730   735

aga ttg cct gag atc ttc agg gca ctg tct gat tat gct cac gct tgt
2318
Arg Leu Pro Glu Ile Phe Arg Ala Leu Ser Asp Tyr Ala His Ala Cys
            740   745   750

gct gac tca tat gag aag ctc aga atc ata tcg cag agt cag aaa tca
2366
Ala Asp Ser Tyr Glu Lys Leu Arg Ile Ile Ser Gln Ser Gln Lys Ser
            755   760   765

aac ggt gga gcc act gaa tct tct tga accagtttta gttctattta
2413
Asn Gly Gly Ala Thr Glu Ser Ser
            770   775

acctatgtaa tatgttgtat tatgatggga acattaagca tagttttgtg accagattct
2473

gta
2476

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398

Met Gly Cys Ala Gln Ser Arg Val Asp Asn Glu Glu Ala Val Ala Arg

753

1   5   10   15

Cys Lys Glu Arg Arg Asn Val Ile Lys Glu Ala Val Ser Ala Ser Lys
        20   25   30

Ala Phe Ala Ala Gly His Phe Ala Tyr Ala Ile Ala Leu Lys Asn Thr
        35   40   45

Gly Ala Ala Leu Ser Asp Tyr Gly His Gly Glu Ser Asp Gln Lys Ala
    50   55   60

Leu Asp Asp Val Leu Leu Asp Gln Gln His Tyr Glu Lys Gln Ser Arg
65   70   75   80

Asn Asn Val Asp Pro Ala Ser Pro Gln Pro Pro Pro Pro Pro Pro Ile
            85   90   95

Glu Asn Leu Pro Pro Pro Pro Pro Pro Leu Pro Lys Phe Ser Pro Ser
            100   105   110

Pro Ile Lys Arg Ala Ile Ser Leu Pro Ser Met Ala Val Arg Gly Arg
            115   120   125

Lys Val Gln Thr Leu Asp Gly Met Ala Ile Glu Glu Glu Glu Glu Asp
    130   135   140

Glu Glu Glu Glu Glu Glu Val Lys Gly Ser Gly Arg Asp Thr Ala Gln
145   150   155   160

Glu Glu Glu Glu Pro Arg Thr Pro Glu Asn Val Gly Lys Ser Asn Gly
                165   170   175

Arg Lys Arg Leu Glu Lys Thr Thr Pro Glu Ile Val Ser Ala Ser Pro
            180   185   190

Ala Asn Ser Met Ala Trp Asp Tyr Phe Phe Met Val Glu Asn Met Pro
        195   200   205

Gly Pro Asn Leu Asp Asp Arg Glu Val Arg Asn Gly Tyr Glu Asn Gln
    210   215   220

Ser Ser His Phe Gln Phe Asn Glu Glu Asp Asp Glu Glu Glu Glu Glu
225   230   235   240

Glu Glu Arg Ser Gly Ile Tyr Arg Lys Lys Ser Gly Ser Gly Lys Val
            245   250   255

754

```
Val Glu Glu Met Glu Pro Lys Thr Pro Glu Lys Val Glu Glu Glu Glu
            260             265             270

Glu Glu Asp Glu Glu Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu
        275             280             285

Glu Val Val Val Glu Val Lys Lys Lys Lys Gly Lys Ala Lys Ile
    290             295             300

Glu His Ser Ser Thr Ala Pro Pro Glu Phe Arg Arg Ala Val Ala Lys
305             310             315             320

Thr Ser Ala Ala Ala Ser Ser Ser Val Asn Leu Met Lys Ile Leu Asp
            325             330             335

Glu Ile Asp Asp Arg Phe Leu Lys Ala Ser Glu Cys Ala Gln Glu Val
            340             345             350

Ser Lys Met Leu Glu Ala Thr Arg Leu His Tyr His Ser Asn Phe Ala
            355             360             365

Asp Asn Arg Gly Tyr Val Asp His Ser Ala Arg Val Met Arg Val Ile
    370             375             380

Thr Trp Asn Lys Ser Leu Arg Gly Ile Ser Asn Gly Glu Gly Gly Lys
385             390             395             400

Asp Asp Gln Glu Ser Asp Glu His Glu Thr His Ala Thr Val Leu Asp
            405             410             415

Lys Leu Leu Ala Trp Glu Lys Lys Leu Tyr Asp Glu Val Lys Gln Gly
            420             425             430

Glu Leu Met Lys Ile Glu Tyr Gln Lys Lys Val Ser Leu Leu Asn Arg
            435             440             445

His Lys Lys Arg Gly Ala Ser Ala Glu Thr Val Glu Lys Thr Lys Ala
    450             455             460

Ala Val Ser His Leu His Thr Arg Tyr Ile Val Asp Met Gln Ser Met
465             470             475             480

Asp Ser Thr Val Ser Glu Val Asn Arg Leu Arg Asp Asp Gln Leu Tyr
            485             490             495
```

Pro Arg Leu Val Ala Leu Val Glu Gly Met Ala Lys Met Trp Thr Asn
            500   505   510

Met Cys Ile His His Asp Thr Gln Leu Gly Ile Val Gly Glu Leu Lys
            515   520   525

Ala Leu Glu Ile Ser Thr Ser Leu Lys Glu Thr Thr Lys Gln His His
    530   535   540

His Gln Thr Arg Gln Phe Cys Thr Val Leu Glu Glu Trp His Val Gln
545   .   550   555   560

Phe Asp Thr Leu Val Thr His Gln Lys Gln Tyr Ile Asn Ser Leu Asn
                565   570   575

Asn Trp Leu Lys Leu Asn Leu Ile Pro Ile Glu Ser Ser Leu Lys Glu
            580   585   590

Lys Val Ser Ser Pro Pro Arg Pro Gln Arg Pro Pro Ile Gln Ala Leu
            595   600   605

Leu His Ser Trp His Asp Arg Leu Glu Lys Leu Pro Asp Glu Val Ala
    610   615   620

Lys Ser Ala Ile Ser Ser Phe Ala Ala Val Ile Lys Thr Ile Leu Leu
625   630   635   640

His Gln Glu Glu Glu Met Lys Leu Lys Glu Lys Cys Glu Glu Thr Arg
                645   650   655

Arg Glu Phe Ile Arg Lys Lys Gln Gly Phe Glu Asp Trp Tyr Gln Lys
                660   665   670

His Leu Gln Lys Arg Gly Pro Thr Glu Glu Ala Glu Gly Gly Asp Asp
    675   680   685

Ala Thr Thr Ser Ser Arg Asp His Val Thr Glu Arg Arg Ile Ala Val
    690   695   700

Glu Thr Leu Lys Lys Arg Leu Glu Glu Glu Glu Glu Ala His Gln Arg
705   710   715   720

His Cys Val Gln Val Arg Glu Lys Ser Leu Asn Ser Leu Lys Ile Arg
                725   730   735

```
Leu Pro Glu Ile Phe Arg Ala Leu Ser Asp Tyr Ala His Ala Cys Ala
            740             745             750

Asp Ser Tyr Glu Lys Leu Arg Ile Ile Ser Gln Ser Gln Lys Ser Asn
            755             760             765

Gly Gly Ala Thr Glu Ser Ser
        770             775
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60

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tt atg ttg tcc act gca ccg gcc ttt tca ttc tcc gaa ccg ggt ttg
107
   Met Leu Ser Thr Ala Pro Ala Phe Ser Phe Ser Glu Pro Gly Leu
   1               5                  10                  15

gtt aat caa ttc tcg ggt ttc caa acc ggg ttc act cct tgg gaa tgg
155
Val Asn Gln Phe Ser Gly Phe Gln Thr Gly Phe Thr Pro Trp Glu Trp
            20                  25                  30

gat tgc tct gat ctc ttt ttc gtg gac caa atg tct ctt gaa ccg gcc
203
Asp Cys Ser Asp Leu Phe Phe Val Asp Gln Met Ser Leu Glu Pro Ala
            35                  40                  45

atc cct agt cct tgt tat ggt gaa tcc gac act ggt tcc gtc aaa att
251
Ile Pro Ser Pro Cys Tyr Gly Glu Ser Asp Thr Gly Ser Val Lys Ile
        50                  55                  60

aat tcc ggt tct cat gac atg aaa acc ggt tct gac gaa tct tgt gcc
299
Asn Ser Gly Ser His Asp Met Lys Thr Gly Ser Asp Glu Ser Cys Ala
    65                  70                  75

ggt ttc gtc aaa att aat cct cgt tgt gac gac gcc gac ata tca aac
347
Gly Phe Val Lys Ile Asn Pro Arg Cys Asp Asp Ala Asp Ile Ser Asn
80                  85                  90                  95

gat cta ccg tgc tct caa gca gat gaa ccg gac tcg gac gac aca aaa
395
Asp Leu Pro Cys Ser Gln Ala Asp Glu Pro Asp Ser Asp Asp Thr Lys
            100                 105                 110

caa ttg aca gcc atc aca aat ttc ggt tcg gga gag aat aac cat aac
443
Gln Leu Thr Ala Ile Thr Asn Phe Gly Ser Gly Glu Asn Asn His Asn
            115                 120                 125

cgg aaa aaa atg atc caa ccg gag atg acc gac gag cgg aag agg aag
491
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Arg Lys Lys Met Ile Gln Pro Glu Met Thr Asp Glu Arg Lys Arg Lys
        130   135   140

agg atg gag tca aac cgg gaa tca gcg aaa cgg tca aga atg cgt aaa
539
Arg Met Glu Ser Asn Arg Glu Ser Ala Lys Arg Ser Arg Met Arg Lys
        145   150   155

caa agt cac att gat aac tta cga gag caa gta aac cgg ttg gat tta
587
Gln Ser His Ile Asp Asn Leu Arg Glu Gln Val Asn Arg Leu Asp Leu
160   165   170   175

gaa aac cgt gag ctc ggg aac cga ctc cgg tta gtt tta cac cag ctt
635
Glu Asn Arg Glu Leu Gly Asn Arg Leu Arg Leu Val Leu His Gln Leu
                180   185   190

caa cga gtg aat tcc gac aat aac cgg ctc gtg aca gaa caa gag ata
683
Gln Arg Val Asn Ser Asp Asn Asn Arg Leu Val Thr Glu Gln Glu Ile
                195   200   205

ctc cgg cta aga ttg tcg gag atg cgt cgg att ctg atc att aga caa
731
Leu Arg Leu Arg Leu Ser Glu Met Arg Arg Ile Leu Ile Ile Arg Gln
        210   215   220

ctt caa caa cag caa caa tgg gaa cta cat aac cgg aga atg atc atg
779
Leu Gln Gln Gln Gln Gln Trp Glu Leu His Asn Arg Arg Met Ile Met
        225   230   235

act gaa caa aac cac cct cat ctt caa tga tagatcaaaa tatttaagaa
829
Thr Glu Gln Asn His Pro His Leu Gln
240   245

gaaaaaatat cgaaaaactt agaacaataa ccaaaaaaaa aaagcaaagc aaaaaagaaa
889

ctctcgctat gtctctctat ctctctatgt aaatgaaatg aaggttagga agagaaaatg
949

atagttttct aattttcctt tccacttt
977

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Met Leu Ser Thr Ala Pro Ala Phe Ser Phe Ser Glu Pro Gly Leu Val
1   5   10   15

Asn Gln Phe Ser Gly Phe Gln Thr Gly Phe Thr Pro Trp Glu Trp Asp
                20   25   30

Cys Ser Asp Leu Phe Phe Val Asp Gln Met Ser Leu Glu Pro Ala Ile
        35   40   45

758

Pro Ser Pro Cys Tyr Gly Glu Ser Asp Thr Gly Ser Val Lys Ile Asn
    50   55   60

Ser Gly Ser His Asp Met Lys Thr Gly Ser Asp Glu Ser Cys Ala Gly
65   70   75   80

Phe Val Lys Ile Asn Pro Arg Cys Asp Asp Ala Asp Ile Ser Asn Asp
                85   90   95

Leu Pro Cys Ser Gln Ala Asp Glu Pro Asp Ser Asp Asp Thr Lys Gln
            100   105   110

Leu Thr Ala Ile Thr Asn Phe Gly Ser Gly Glu Asn Asn His Asn Arg
        115   120   125

Lys Lys Met Ile Gln Pro Glu Met Thr Asp Glu Arg Lys Arg Lys Arg
    130   135   140

Met Glu Ser Asn Arg Glu Ser Ala Lys Arg Ser Arg Met Arg Lys Gln
145   150   155   160

Ser His Ile Asp Asn Leu Arg Glu Gln Val Asn Arg Leu Asp Leu Glu
            165   170   175

Asn Arg Glu Leu Gly Asn Arg Leu Arg Leu Val Leu His Gln Leu Gln
            180   185   190

Arg Val Asn Ser Asp Asn Asn Arg Leu Val Thr Glu Gln Glu Ile Leu
        195   200   205

Arg Leu Arg Leu Ser Glu Met Arg Arg Ile Leu Ile Ile Arg Gln Leu
    210   215   220

Gln Gln Gln Gln Gln Trp Glu Leu His Asn Arg Arg Met Ile Met Thr
225   230   235   240

Glu Gln Asn His Pro His Leu Gln
                245

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<221> CDS <222> (601)..(1161) <223> G1818

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60

tgtactttgt acattcatat attattgtta tatatcgttt catacattaa tttgaaccaa
120

tgtaaattaa gtaaaattca atttaacatc atgagcaaat tcttattaaa attctcttaa
180

aattttgagc aaattatgct ttcacattta acatttgaaa acatcatttt taacaagata
240

ttcaaaacta agttttgtac agcaaaattt taactttcaa ttttatagag aaaaaggtat
300

tttttttttt gtttcatttt tataagacta ttatttggta tataatatac actttaagta
360

aaaacaaatc tctttctttt ttcttcttat aataccaacc acaagtctgt cagtcacaca
420

catacagtta ataacattaa atattcttaa caaactacta aataggttga gattcatata
480

tgtaaagaga tcacttctta atcttatcct accatatctt atatacgctt aattttcctt
540

tatatatgca aacctccaca taaaaatatc tcaaacccaa acacttcaaa caaaaaaaaa
600

atg gag aac aac aac aac aac cac caa cag cca ccg aaa gat aac gag
648
Met Glu Asn Asn Asn Asn Asn His Gln Gln Pro Pro Lys Asp Asn Glu
1   5   10   15

caa cta aag agt ttc tgg tca aag ggg atg gaa ggt gac ttg aat gtc
696
Gln Leu Lys Ser Phe Trp Ser Lys Gly Met Glu Gly Asp Leu Asn Val
            20   25   30

aag aat cac gag ttc ccc atc tct cgt atc aag agg ata atg aag ttt
744
Lys Asn His Glu Phe Pro Ile Ser Arg Ile Lys Arg Ile Met Lys Phe
        35   40   45

gat ccg gat gtg agt atg atc gct gct gag gct cca aat ctc tta tct
792
Asp Pro Asp Val Ser Met Ile Ala Ala Glu Ala Pro Asn Leu Leu Ser
    50   55   60

aag gct tgt gaa atg ttt gtc atg gac ctc acg atg cgt tca tgg ctc
840
Lys Ala Cys Glu Met Phe Val Met Asp Leu Thr Met Arg Ser Trp Leu
65   70   75   80

cat gct caa gag agc aac cga ctc acg ata cgg aaa tct gat gtt gat
888
His Ala Gln Glu Ser Asn Arg Leu Thr Ile Arg Lys Ser Asp Val Asp
                85   90   95

gcc gta gtg tct caa acc gtc atc ttt gat ttc ttg cgt gat gat gtc
936
Ala Val Val Ser Gln Thr Val Ile Phe Asp Phe Leu Arg Asp Asp Val
            100   105   110

760

```
cct aag gac gag gga gag ccc gtt gtc gcc gct gct gat cct gtg gac
984
Pro Lys Asp Glu Gly Glu Pro Val Val Ala Ala Ala Asp Pro Val Asp
         115                 120                 125

gat gtt gct gat cat gtg gct gtg cca gat ctt aac aat gaa gaa ctg
1032
Asp Val Ala Asp His Val Ala Val Pro Asp Leu Asn Asn Glu Glu Leu
   130                 135                 140

ccg ccg gga acg gtg ata gga act ccg gtt tgt tac ggt tta gga ata
1080
Pro Pro Gly Thr Val Ile Gly Thr Pro Val Cys Tyr Gly Leu Gly Ile
145                 150                 155                 160

cac gcg cca cac ccg cag atg cct gga gct tgg acc gag gag gat gcg
1128
His Ala Pro His Pro Gln Met Pro Gly Ala Trp Thr Glu Glu Asp Ala
              165                 170                 175

act ggg gca aat gga gga aac ggt ggg aat taa tatttggatt gggttttgta
1181
Thr Gly Ala Asn Gly Gly Asn Gly Gly Asn
              180                 185

accgctgttg tgagaacttg aatttctttt tgagttctgc ttatgttttc aatgttatgt
1241

tttttagttg ttgaatgtat ttctgttgtt ttgtccaaaa aaaaaaaaga atgtatttct
1301

gttgttgtct ttcaaatgaa tctaatggtt tatgaatatt ggctttagat taatttatgc
1361

atacaaaaac acaaggatta cggataaaaa agtcctcagt ttacccatgg aaacataatc
1421

ttctagtgat tccttatgag agtagaaaag aatcatatat tataatctat ttcataagag
1481

atagggtact gtaaacaagg atgtttattc ggctatttct tttttttta atcactttta
1541

cttgtcaaga ctcttttgtg tttgcagctt tttgttagat tacattctag aggcaacaag
1601

atccagagat ctagcaaaaa aaacttattt tgaaacctga atctatttta aaaattttcc
1661

aactcatttt tcgttcttat tctttgtttt ccaacggaat ttggcgcaca aacgatttat
1721

ttgaattttg tctttcaag
1740


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402

Met Glu Asn Asn Asn Asn Asn His Gln Gln Pro Pro Lys Asp Asn Glu
```

```
1                5                    10                    15


Gln Leu Lys Ser Phe Trp Ser Lys Gly Met Glu Gly Asp Leu Asn Val
         20              25              30


Lys Asn His Glu Phe Pro Ile Ser Arg Ile Lys Arg Ile Met Lys Phe
         35              40              45


Asp Pro Asp Val Ser Met Ile Ala Ala Glu Ala Pro Asn Leu Leu Ser
     50              55              60


Lys Ala Cys Glu Met Phe Val Met Asp Leu Thr Met Arg Ser Trp Leu
65              70              75              80


His Ala Gln Glu Ser Asn Arg Leu Thr Ile Arg Lys Ser Asp Val Asp
             85              90              95


Ala Val Val Ser Gln Thr Val Ile Phe Asp Phe Leu Arg Asp Asp Val
             100             105             110


Pro Lys Asp Glu Gly Glu Pro Val Val Ala Ala Ala Asp Pro Val Asp
         115             120             125


Asp Val Ala Asp His Val Ala Val Pro Asp Leu Asn Asn Glu Glu Leu
     130             135             140


Pro Pro Gly Thr Val Ile Gly Thr Pro Val Cys Tyr Gly Leu Gly Ile
145             150             155             160


His Ala Pro His Pro Gln Met Pro Gly Ala Trp Thr Glu Glu Asp Ala
             165             170             175


Thr Gly Ala Asn Gly Gly Asn Gly Gly Asn
             180             185
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atg gaa gag aac aac ggc aac aac aac cac tac ctg ccg caa cca tcg
48
Met Glu Glu Asn Asn Gly Asn Asn Asn His Tyr Leu Pro Gln Pro Ser
1             5                   10                  15


tct tcc caa ctg ccg ccg cca cca ttg tat tat caa tca atg ccg ttg
96
Ser Ser Gln Leu Pro Pro Pro Pro Leu Tyr Tyr Gln Ser Met Pro Leu
             20              25              30
```

```
ccg tca tat tca ctg ccg ctg ccg tac tca ccg cag atg cgg aat tat
144
Pro Ser Tyr Ser Leu Pro Leu Pro Tyr Ser Pro Gln Met Arg Asn Tyr
        35              40              45

tgg att gcg cag atg gga aac gca act gat gtt aag cat cat gcg ttt
192
Trp Ile Ala Gln Met Gly Asn Ala Thr Asp Val Lys His His Ala Phe
    50              55              60

cca cta acc agg ata aag aaa atc atg aag tcc aac ccg gaa gtg aac
240
Pro Leu Thr Arg Ile Lys Lys Ile Met Lys Ser Asn Pro Glu Val Asn
65              70              75              80

atg gtc act gca gag gct ccg gtc ctt ata tcg aag gcc tgt gag atg
288
Met Val Thr Ala Glu Ala Pro Val Leu Ile Ser Lys Ala Cys Glu Met
            85              90              95

ctc att ctt gat ctc aca atg cga tcg tgg ctt cat acc gtg gag ggc
336
Leu Ile Leu Asp Leu Thr Met Arg Ser Trp Leu His Thr Val Glu Gly
            100             105             110

ggt cgc caa act ctc aag aga tcc gat acg ctc acg aga tcc gat atc
384
Gly Arg Gln Thr Leu Lys Arg Ser Asp Thr Leu Thr Arg Ser Asp Ile
        115             120             125

tcc gcc gca acg act cgt agt ttc aaa ttt acc ttc ctt ggc gac gtt
432
Ser Ala Ala Thr Thr Arg Ser Phe Lys Phe Thr Phe Leu Gly Asp Val
    130             135             140

gtc cca aga gac cct tcc gtc gtt acc gat gat ccc gtg cta cat ccg
480
Val Pro Arg Asp Pro Ser Val Val Thr Asp Asp Pro Val Leu His Pro
145             150             155             160

gac ggt gaa gta ctt cct ccg gga acg gtg ata gga tat ccg gtg ttt
528
Asp Gly Glu Val Leu Pro Pro Gly Thr Val Ile Gly Tyr Pro Val Phe
                165             170             175

gat tgt aat ggt gtg tac gcg tca ccg cca cag atg cag gag tgg ccg
576
Asp Cys Asn Gly Val Tyr Ala Ser Pro Pro Gln Met Gln Glu Trp Pro
            180             185             190

gcg gtg cct ggt gac gga gag gag gca gct ggg gaa att gga gga agc
624
Ala Val Pro Gly Asp Gly Glu Glu Ala Ala Gly Glu Ile Gly Gly Ser
        195             200             205

agc ggc ggt aat tga
639
Ser Gly Gly Asn
        210
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404

Met Glu Glu Asn Asn Gly Asn Asn Asn His Tyr Leu Pro Gln Pro Ser
1   5   10   15

Ser Ser Gln Leu Pro Pro Pro Pro Leu Tyr Tyr Gln Ser Met Pro Leu
            20   25   30

Pro Ser Tyr Ser Leu Pro Leu Pro Tyr Ser Pro Gln Met Arg Asn Tyr
            35   40   45

Trp Ile Ala Gln Met Gly Asn Ala Thr Asp Val Lys His His Ala Phe
    50   55   60

Pro Leu Thr Arg Ile Lys Lys Ile Met Lys Ser Asn Pro Glu Val Asn
65   70   75   80

Met Val Thr Ala Glu Ala Pro Val Leu Ile Ser Lys Ala Cys Glu Met
                85   90   95

Leu Ile Leu Asp Leu Thr Met Arg Ser Trp Leu His Thr Val Glu Gly
            100   105   110

Gly Arg Gln Thr Leu Lys Arg Ser Asp Thr Leu Thr Arg Ser Asp Ile
        115   120   125

Ser Ala Ala Thr Thr Arg Ser Phe Lys Phe Thr Phe Leu Gly Asp Val
    130   135   140

Val Pro Arg Asp Pro Ser Val Val Thr Asp Asp Pro Val Leu His Pro
145   150   155   160

Asp Gly Glu Val Leu Pro Pro Gly Thr Val Ile Gly Tyr Pro Val Phe
                165   170   175

Asp Cys Asn Gly Val Tyr Ala Ser Pro Pro Gln Met Gln Glu Trp Pro
            180   185   190

Ala Val Pro Gly Asp Gly Glu Glu Ala Ala Gly Glu Ile Gly Gly Ser
        195   200   205

Ser Gly Gly Asn
    210

<210> 405 <211> 954 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(954) <223> G1895

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atg aat .aac caa tct gtt act gac aat aca agt ctt aag ctg tca tct
48
Met Asn Asn Gln Ser Val Thr Asp Asn Thr Ser Leu Lys Leu Ser Ser
1               5                   10                  15


aat ctt aac aac gag tca aaa gaa aca tct gag aac agt gat gac caa
96
Asn Leu Asn Asn Glu Ser Lys Glu Thr Ser Glu Asn Ser Asp Asp Gln
            20                   25                  30


cac agc gag atc aca aca att aca tcg gaa gaa gag aaa aca act gaa
144
His Ser Glu Ile Thr Thr Ile Thr Ser Glu Glu Glu Lys Thr Thr Glu
        35                  40                  45


ctg aag aaa cca gac aag att ctt cca tgt ccg aga tgc aac agc gca
192
Leu Lys Lys Pro Asp Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Ala
    50                  55                  60


gac acc aaa ttc tgt tac tac aac aac tac aac gtt aac cag cca cgt
240
Asp Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg
65              70                  75                  80


cac ttc tgt aga aaa tgc cag agg tat tgg acc gct ggt gga tcc atg
288
His Phe Cys Arg Lys Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met
                85                  90                  95


agg atc gtc ccg gtt ggc tca ggc cgt cgc aag aac aag gga tgg gtt
336
Arg Ile Val Pro Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Val
            100                 105                 110


tct tca gac cag tac ctg cac atc act tcc gag gat act gac aat tac
384
Ser Ser Asp Gln Tyr Leu His Ile Thr Ser Glu Asp Thr Asp Asn Tyr
        115                 120                 125


aat agc tcc tca aca aag att cta agc ttc gag tct tcg gac tct ttg
432
Asn Ser Ser Ser Thr Lys Ile Leu Ser Phe Glu Ser Ser Asp Ser Leu
    130                 135                 140


gta act gag agg cct aag cat caa tca aac gaa gtg aag ata aac gct
480
Val Thr Glu Arg Pro Lys His Gln Ser Asn Glu Val Lys Ile Asn Ala
145                 150                 155                 160


gaa cct gtt tca caa gaa ccc aac aac ttc caa ggg tta ctt cct ccc
528
Glu Pro Val Ser Gln Glu Pro Asn Asn Phe Gln Gly Leu Leu Pro Pro
                165                 170                 175


caa gca tcc cct gtt tcg cct cct tgg cct tac caa tac cct cca aac
576
Gln Ala Ser Pro Val Ser Pro Pro Trp Pro Tyr Gln Tyr Pro Pro Asn
            180                 185                 190
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cct agt ttc tac cac atg ccc gtc tac tgg ggc tgc gcg ata ccg gtt
624
Pro Ser Phe Tyr His Met Pro Val Tyr Trp Gly Cys Ala Ile Pro Val
        195   200   205

tgg tct acc ctc gac act tct aca tgt ctt ggg aaa agg aca aga gac
672
Trp Ser Thr Leu Asp Thr Ser Thr Cys Leu Gly Lys Arg Thr Arg Asp
    210   215   220

gaa act tct cat gaa act gtt aaa gag agt aaa aat gct ttt gag aga
720
Glu Thr Ser His Glu Thr Val Lys Glu Ser Lys Asn Ala Phe Glu Arg
225   230   235   240

aca agc ttg ctt ttg gaa tct cag agc atc aaa aat gaa aca agt atg
768
Thr Ser Leu Leu Leu Glu Ser Gln Ser Ile Lys Asn Glu Thr Ser Met
            245   250   255

gct aca aat aac cat gtg tgg tat cca gta ccg atg acc cgc gag aag
816
Ala Thr Asn Asn His Val Trp Tyr Pro Val Pro Met Thr Arg Glu Lys
            260   265   270

aca caa gaa ttc agc ttt ttc agt aat gga gct gaa aca aag agc agc
864
Thr Gln Glu Phe Ser Phe Phe Ser Asn Gly Ala Glu Thr Lys Ser Ser
        275   280   285

aac aac aga ttc gtc cct gaa acg tat ctt aac ctg caa gca aac cct
912
Asn Asn Arg Phe Val Pro Glu Thr Tyr Leu Asn Leu Gln Ala Asn Pro
    290   295   300

gca gcc atg gca aga tct atg aac ttc aga gag agc ata taa
954
Ala Ala Met Ala Arg Ser Met Asn Phe Arg Glu Ser Ile
305   310   315

<210> 406 <211> 317 <212> PRT <213> Arabidopsis thaliana <400>
406

Met Asn Asn Gln Ser Val Thr Asp Asn Thr Ser Leu Lys Leu Ser Ser
1   5   10   15

Asn Leu Asn Asn Glu Ser Lys Glu Thr Ser Glu Asn Ser Asp Asp Gln
            20   25   30

His Ser Glu Ile Thr Thr Ile Thr Ser Glu Glu Glu Lys Thr Thr Glu
        35   40   45

Leu Lys Lys Pro Asp Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Ala
    50   55   60

```
Asp Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg
65                  70              75                  80


His Phe Cys Arg Lys Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met
            85              90              95


Arg Ile Val Pro Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Val
            100             105             110


Ser Ser Asp Gln Tyr Leu His Ile Thr Ser Glu Asp Thr Asp Asn Tyr
        115             120             125


Asn Ser Ser Ser Thr Lys Ile Leu Ser Phe Glu Ser Ser Asp Ser Leu
    130             135             140


Val Thr Glu Arg Pro Lys His Gln Ser Asn Glu Val Lys Ile Asn Ala
145             150             155             160


Glu Pro Val Ser Gln Glu Pro Asn Asn Phe Gln Gly Leu Leu Pro Pro
            165             170             175


Gln Ala Ser Pro Val Ser Pro Pro Trp Pro Tyr Gln Tyr Pro Pro Asn
            180             185             190


Pro Ser Phe Tyr His Met Pro Val Tyr Trp Gly Cys Ala Ile Pro Val
        195             200             205


Trp Ser Thr Leu Asp Thr Ser Thr Cys Leu Gly Lys Arg Thr Arg Asp
    210             215             220


Glu Thr Ser His Glu Thr Val Lys Glu Ser Lys Asn Ala Phe Glu Arg
225             230             235             240


Thr Ser Leu Leu Leu Glu Ser Gln Ser Ile Lys Asn Glu Thr Ser Met
            245             250             255


Ala Thr Asn Asn His Val Trp Tyr Pro Val Pro Met Thr Arg Glu Lys
            260             265             270


Thr Gln Glu Phe Ser Phe Phe Ser Asn Gly Ala Glu Thr Lys Ser Ser
            275             280             285


Asn Asn Arg Phe Val Pro Glu Thr Tyr Leu Asn Leu Gln Ala Asn Pro
    290             295             300


Ala Ala Met Ala Arg Ser Met Asn Phe Arg Glu Ser Ile
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305   310   315

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<221> CDS <222> (5)..(592) <223> G1931

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atca atg gaa ggg gtt gac aac aca aat cct atg tta acc cta gaa gaa
49
     Met Glu Gly Val Asp Asn Thr Asn Pro Met Leu Thr Leu Glu Glu
      1   5   10   15

ggc gaa aac aac aat cct ttt tct tcc tta gat gac aaa aca tta atg
97
Gly Glu Asn Asn Asn Pro Phe Ser Ser Leu Asp Asp Lys Thr Leu Met
                20   25   30

atg atg gct cct tcg tta atc ttt tcg ggc gat gta ggt cca tct tct
145
Met Met Ala Pro Ser Leu Ile Phe Ser Gly Asp Val Gly Pro Ser Ser
            35   40   45

tct tct tgt act cca gca ggt tat cat cta tct gct cag ctg gag aac
193
Ser Ser Cys Thr Pro Ala Gly Tyr His Leu Ser Ala Gln Leu Glu Asn
        50   55   60

ttt cga gga ggt gga gga gag atg gga gga tta gtg agt aat aat agc
241
Phe Arg Gly Gly Gly Gly Glu Met Gly Gly Leu Val Ser Asn Asn Ser
    65   70   75

aat aat agt gat cat aat aag aat tgc aac aaa gga aaa ggg aag aga
289
Asn Asn Ser Asp His Asn Lys Asn Cys Asn Lys Gly Lys Gly Lys Arg
80   85   90   95

act ttg gca atg cag agg ata gct ttt cat aca agg agt gat gat gat
337
Thr Leu Ala Met Gln Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp
                100   105   110

gtt ctt gat gat ggt tat cgt tgg cga aag tac ggt cag aaa tct gtc
385
Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val
            115   120   125

aag aac aat gct cat ccc agg agc tat tat aga tgt aca tac cac aca
433
Lys Asn Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr
        130   135   140

tgc aac gtg aag aaa caa gtg caa aga ctg gca aaa gat cca aac gtt
481
Cys Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val
    145   150   155

gtc gta aca acc tac gaa ggt gtt cat aat cat cct tgt gag aag ctc
529
Val Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu
160   165   170   175

768

atg gag act ctt agc cct ctc ctt agg caa ctt cag ttc ctc tca aga
577
Met Glu Thr Leu Ser Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Arg
            180   185   190

gtt tct gat ctg taa ttattgaatg ttaattagtg gtgtaataca ttaattatgc
632
Val Ser Asp Leu
            195

tttaatctct ccattgaccc tcaatc
658

<210> 408 <211> 195 <212> PRT <213> Arabidopsis thaliana <400>
408

Met Glu Gly Val Asp Asn Thr Asn Pro Met Leu Thr Leu Glu Glu Gly
1   5   10   15

Glu Asn Asn Asn Pro Phe Ser Ser Leu Asp Asp Lys Thr Leu Met Met
            20   25   30

Met Ala Pro Ser Leu Ile Phe Ser Gly Asp Val Gly Pro Ser Ser Ser
            35   40   45

Ser Cys Thr Pro Ala Gly Tyr His Leu Ser Ala Gln Leu Glu Asn Phe
        50   55   60

Arg Gly Gly Gly Gly Glu Met Gly Gly Leu Val Ser Asn Asn Ser Asn
65   70   75   80

Asn Ser Asp His Asn Lys Asn Cys Asn Lys Gly Lys Gly Lys Arg Thr
                85   90   95

Leu Ala Met Gln Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp Val
            100   105   110

Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys
        115   120   125

Asn Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr Cys
        130   135   140

Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val Val
145   150   155   160

Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu Met
            165   170   175

```
Glu Thr Leu Ser Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Arg Val
          180                 185                 190


Ser Asp Leu
        195


<210>  409 <211>  1172 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (92)..(844) <223>  G1939

 <400>  409
aatcattagc ttcttctctt ctcttctctc acagagagag taatcacaag ccaagtgaga
60

aaaagaaaac actaaaccca gatcgaaaac c atg tct att aac aac aac aac
112
                                   Met Ser Ile Asn Asn Asn Asn
                                   1               5

aac aac aac aac aat aac aac gat ggt ctt atg atc tca tca aac gga
160
Asn Asn Asn Asn Asn Asn Asn Asp Gly Leu Met Ile Ser Ser Asn Gly
        10                  15                  20

gct tta atc gaa caa caa cca tca gtc gtt gtg aag aaa cca ccg gcg
208
Ala Leu Ile Glu Gln Gln Pro Ser Val Val Val Lys Lys Pro Pro Ala
        25                  30                  35

aaa gat cga cat agc aaa gtc gat gga aga ggg aga aga atc cgt atg
256
Lys Asp Arg His Ser Lys Val Asp Gly Arg Gly Arg Arg Ile Arg Met
40                  45                  50                  55

ccg att ata tgt gct gct cgt gtt ttt cag cta acg aga gag ctt ggt
304
Pro Ile Ile Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu Gly
                60                  65                  70

cat aag tca gat ggc caa aca att gaa tgg tta ctt cgt caa gca gag
352
His Lys Ser Asp Gly Gln Thr Ile Glu Trp Leu Leu Arg Gln Ala Glu
                75                  80                  85

cct tct att ata gct gca aca gga act ggt aca act cca gcg agt ttc
400
Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Thr Pro Ala Ser Phe
                90                  95                  100

tca act gct tct gtc tct atc cgt gga gcc acc aat tct act tct tta
448
Ser Thr Ala Ser Val Ser Ile Arg Gly Ala Thr Asn Ser Thr Ser Leu
        105                 110                 115

gat cat aaa ccc act tct tta ctt ggt ggt acg tca ccg ttt ata ctt
496
Asp His Lys Pro Thr Ser Leu Leu Gly Gly Thr Ser Pro Phe Ile Leu
120                 125                 130                 135
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770

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ggg aaa cgt gtt aga gct gat gag gat agt aat aat agt cat aat cat
544
Gly Lys Arg Val Arg Ala Asp Glu Asp Ser Asn Asn Ser His Asn His
            140             145             150


agt tct gtt ggt aaa gat gag acc ttt acg aca aca cca gct ggg ttt
592
Ser Ser Val Gly Lys Asp Glu Thr Phe Thr Thr Thr Pro Ala Gly Phe
            155             160             165


tgg gct gtt ccg gcg agg ccg gat ttt gga caa gtt tgg agt ttt gct
640
Trp Ala Val Pro Ala Arg Pro Asp Phe Gly Gln Val Trp Ser Phe Ala
            170             175             180


gga gct cca caa gag atg ttt tta caa caa caa cat cat cat cag caa
688
Gly Ala Pro Gln Glu Met Phe Leu Gln Gln Gln His His His Gln Gln
        185             190             195


cca ttg ttt gtt cat cag caa cag caa caa caa gct gca atg ggt gaa
736
Pro Leu Phe Val His Gln Gln Gln Gln Gln Gln Ala Ala Met Gly Glu
200             205             210             215


gct tct gct gct aga gtt ggg aat tat. ctt ccg ggt cat ctt aat ttg
784
Ala Ser Ala Ala Arg Val Gly Asn Tyr Leu Pro Gly His Leu Asn Leu
            220             225             230


ctt gct tct tta tcc ggt gga tct ccc ggg tcg gat cga aga gag gaa
832
Leu Ala Ser Leu Ser Gly Gly Ser Pro Gly Ser Asp Arg Arg Glu Glu
            235             240             245


gat cca cgt taa tggtttaagc cctttaggt ttgagggcaa aatttggtat
884
Asp Pro Arg
        250


atatatttat tatcttctct tctctattgt tgtcattgtt tctctatgtg tgtgttttag
944


tgttgttaga gattgatttg gtttcagaat ctctgcaagt gatttgagag ttttcgttag
1004


ctttaagtaa gttaaagacg gttgtttttg attagggtta aattagggtt taagaatctg
1064


ttgttttttt ggagggagat cgatttctta tcggatccaa gattactttt aggaaaaaag
1124


ggaaaatttc agaaccacg gtggtttctt ttcctctttt tttttttg
1172



<210> 410 <211> 250 <212> PRT <213> Arabidopsis thaliana <400>
410


Met Ser Ile Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asp Gly
1           5               10              15
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Leu Met Ile Ser Ser Asn Gly Ala Leu Ile Glu Gln Gln Pro Ser Val
        20                      25                  30

Val Val Lys Lys Pro Pro Ala Lys Asp Arg His Ser Lys Val Asp Gly
        35                      40                  45

Arg Gly Arg Arg Ile Arg Met Pro Ile Ile Cys Ala Ala Arg Val Phe
    50                      55                  60

Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Gln Thr Ile Glu
65                      70                  75                  80

Trp Leu Leu Arg Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr
                85                      90                  95

Gly Thr Thr Pro Ala Ser Phe Ser Thr Ala Ser Val Ser Ile Arg Gly
            100                     105                 110

Ala Thr Asn Ser Thr Ser Leu Asp His Lys Pro Thr Ser Leu Leu Gly
        115                     120                 125

Gly Thr Ser Pro Phe Ile Leu Gly Lys Arg Val Arg Ala Asp Glu Asp
    130                     135                 140

Ser Asn Asn Ser His Asn His Ser Ser Val Gly Lys Asp Glu Thr Phe
145                     150                 155                 160

Thr Thr Thr Pro Ala Gly Phe Trp Ala Val Pro Ala Arg Pro Asp Phe
            165                     170                 175

Gly Gln Val Trp Ser Phe Ala Gly Ala Pro Gln Glu Met Phe Leu Gln
    .       180                     185                 190

Gln Gln His His His Gln Gln Pro Leu Phe Val His Gln Gln Gln Gln
        195                     200                 205

Gln Gln Ala Ala Met Gly Glu Ala Ser Ala Ala Arg Val Gly Asn Tyr
    210                     215                 220

Leu Pro Gly His Leu Asn Leu Leu Ala Ser Leu Ser Gly Gly Ser Pro
225                     230                 235                 240

Gly Ser Asp Arg Arg Glu Glu Asp Pro Arg
                245                 250
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772

<210> 411 <211> 513 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(513) <223> G1974

<400> 411
atg gtt gct gaa agt gat aat cgt gat ctg acg gtg gat acg gcg gcg
48
Met Val Ala Glu Ser Asp Asn Arg Asp Leu Thr Val Asp Thr Ala Ala
1   5   10   15

agc tgt ctg atg ttg tta tca gga att gga gaa cac gac gga aga aag
96
Ser Cys Leu Met Leu Leu Ser Gly Ile Gly Glu His Asp Gly Arg Lys
            20   25   30

aaa cgt gtt ttc cga tgc aag act tgt gag aga gac ttc gat tcg ttc
144
Lys Arg Val Phe Arg Cys Lys Thr Cys Glu Arg Asp Phe Asp Ser Phe
        35   40   45

caa gct tta gga ggc cac cgt gca agc cac tcg aaa cta acc aac agt
192
Gln Ala Leu Gly Gly His Arg Ala Ser His Ser Lys Leu Thr Asn Ser
    50   55   60

gac gat aaa tca ctt cct gga tca cca aag aag aag cct aaa act acg
240
Asp Asp Lys Ser Leu Pro Gly Ser Pro Lys Lys Lys Pro Lys Thr Thr
65   70   75   80

act acg acg acg gct cat act tgt ccg att tgt ggc ttg gag ttt ccg
288
Thr Thr Thr Thr Ala His Thr Cys Pro Ile Cys Gly Leu Glu Phe Pro
                85   90   95

atg gga caa gct ctt ggt ggt cac atg agg aaa cat agg aac gag aaa
336
Met Gly Gln Ala Leu Gly Gly His Met Arg Lys His Arg Asn Glu Lys
            100   105   110

gaa cga gaa aag gct tct aac gta ttg gtt acg cat tct ttc atg ccg
384
Glu Arg Glu Lys Ala Ser Asn Val Leu Val Thr His Ser Phe Met Pro
        115   120   125

gag acg aca acg gtg acg act ttg aag aaa tcg agt agt ggg aag aga
432
Glu Thr Thr Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg
    130   135   140

gtg gcg tgt ttg gat ttc gac tta act tcg gtg gag agc ttt gtc aac
480
Val Ala Cys Leu Asp Phe Asp Leu Thr Ser Val Glu Ser Phe Val Asn
145   150   155   160

acg gaa ttg gag ttg gga aga acg atg tac tga
513
Thr Glu Leu Glu Leu Gly Arg Thr Met Tyr
                165   170

773

<210> 412 <211> 170 <212> PRT <213> Arabidopsis thaliana <400>
412

Met Val Ala Glu Ser Asp Asn Arg Asp Leu Thr Val Asp Thr Ala Ala
1   5   10   15

Ser Cys Leu Met Leu Leu Ser Gly Ile Gly Glu His Asp Gly Arg Lys
            20   25   30

Lys Arg Val Phe Arg Cys Lys Thr Cys Glu Arg Asp Phe Asp Ser Phe
            35   40   45

Gln Ala Leu Gly Gly His Arg Ala Ser His Ser Lys Leu Thr Asn Ser
        50   55   .   60

Asp Asp Lys Ser Leu Pro Gly Ser Pro Lys Lys Lys Pro Lys Thr Thr
65   70   75   80

Thr Thr Thr Thr Ala His Thr Cys Pro Ile Cys Gly Leu Glu Phe Pro
                85   90   .   95

Met Gly Gln Ala Leu Gly Gly His Met Arg Lys His Arg Asn Glu Lys
            100   105   110

Glu Arg Glu Lys Ala Ser Asn Val Leu Val Thr His Ser Phe Met Pro
        115   120   125

Glu Thr Thr Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg
    130   135   140

Val Ala Cys Leu Asp Phe Asp Leu Thr Ser Val Glu Ser Phe Val Asn
145   150   155   .   160

Thr Glu Leu Glu Leu Gly Arg Thr Met Tyr
            165   170

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<221> CDS <222> (42)..(1487) <223> G2105

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ctctctgact tgaactcttc tcttctaccg aatcaaacca a atg gag gat cat caa
56
                                            Met Glu Asp His Gln
                                            1   5

aac cat cca cag tac ggt ata gaa caa cca tct tct caa ttc tcc tct
104
Asn His Pro Gln Tyr Gly Ile Glu Gln Pro Ser Ser Gln Phe Ser Ser
                10   15   20

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gat ctc ttc ggc ttc aac ctc gtt tca gcg ccg gac cag cac cat cgt
152
Asp Leu Phe Gly Phe Asn Leu Val Ser Ala Pro Asp Gln His His Arg
        25              30              35

ctt cat ttc acc gac cat gag ata agt tta ttg cca cgt gga ata caa
200
Leu His Phe Thr Asp His Glu Ile Ser Leu Leu Pro Arg Gly Ile Gln
        40              45              50

ggg ctt acg gtg gct gga aac aac agt aac act att aca acg atc cag
248
Gly Leu Thr Val Ala Gly Asn Asn Ser Asn Thr Ile Thr Thr Ile Gln
    55              60              65

agt ggt ggc tgt gtt ggt ggg ttt agt ggc ttt acg gac ggc gga gga
296
Ser Gly Gly Cys Val Gly Gly Phe Ser Gly Phe Thr Asp Gly Gly Gly
70              75              80              85

aca ggg agg tgg ccg agg caa gag acg ttg atg ttg ttg gag gtc aga
344
Thr Gly Arg Trp Pro Arg Gln Glu Thr Leu Met Leu Leu Glu Val Arg
            90              95              100

tct cgt ctt gat cac aag ttc aaa gaa gct aat caa aag ggt cct ctc
392
Ser Arg Leu Asp His Lys Phe Lys Glu Ala Asn Gln Lys Gly Pro Leu
        105             110             115

tgg gat gaa gtt tct agg att atg tcg gag gaa cat gga tac act agg
440
Trp Asp Glu Val Ser Arg Ile Met Ser Glu Glu His Gly Tyr Thr Arg
        120             125             130

agt ggc aag aag tgt aga gag aag ttc gag aat ctc tac aag tac tat
488
Ser Gly Lys Lys Cys Arg Glu Lys Phe Glu Asn Leu Tyr Lys Tyr Tyr
    135             140             145

aaa aaa aca aaa gaa ggc aaa tcc ggt cgg cga caa gat ggt aaa aac
536
Lys Lys Thr Lys Glu Gly Lys Ser Gly Arg Arg Gln Asp Gly Lys Asn
150             155             160             165

tat aga ttt ttc cgg cag ctt gaa gcg ata tac ggc gaa tcc aaa gac
584
Tyr Arg Phe Phe Arg Gln Leu Glu Ala Ile Tyr Gly Glu Ser Lys Asp
            170             175             180

tcg gtt tct tgc tat aac aac acg cag ttc ata atg acc aat gct ctt
632
Ser Val Ser Cys Tyr Asn Asn Thr Gln Phe Ile Met Thr Asn Ala Leu
            185             190             195

cat agt aat ttc cgc gct tct aac att cat aac atc gtc cct cat cat
680
His Ser Asn Phe Arg Ala Ser Asn Ile His Asn Ile Val Pro His His
        200             205             210
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775

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cag aat ccc ttg atg acc aat acc aat act caa agt caa agc ctt agc
728
Gln Asn Pro Leu Met Thr Asn Thr Asn Thr Gln Ser Gln Ser Leu Ser
    215                 220                 225

att tct aac aat ttc aac tcc tcc tcc gat ttg gat cta act tct tcc
776
Ile Ser Asn Asn Phe Asn Ser Ser Ser Asp Leu Asp Leu Thr Ser Ser
230                 235                 240                 245

tct gaa gga aac gaa act act aaa aga gag ggg atg cat tgg aag gaa
824
Ser Glu Gly Asn Glu Thr Thr Lys Arg Glu Gly Met His Trp Lys Glu
                250                 255                 260

aag atc aag gaa ttc att ggt gtt cat atg gag agg ttg ata gag aag
872
Lys Ile Lys Glu Phe Ile Gly Val His Met Glu Arg Leu Ile Glu Lys
            265                 270                 275

caa gat ttt tgg ctt gag aag ttg atg aag att gtg gaa gac aaa gaa
920
Gln Asp Phe Trp Leu Glu Lys Leu Met Lys Ile Val Glu Asp Lys Glu
        280                 285                 290

cat caa agg atg ctg aga gaa gag gaa tgg aga agg att gaa gcg gaa
968
His Gln Arg Met Leu Arg Glu Glu Glu Trp Arg Arg Ile Glu Ala Glu
    295                 300                 305

agg atc gat aag gaa cgt tcg ttt tgg aca aaa gag agg gag agg att
1016
Arg Ile Asp Lys Glu Arg Ser Phe Trp Thr Lys Glu Arg Glu Arg Ile
310                 315                 320                 325

gaa gct cgg gat gtt gcg gtg att aat gcc ttg cag tac ttg acg gga
1064
Glu Ala Arg Asp Val Ala Val Ile Asn Ala Leu Gln Tyr Leu Thr Gly
                330                 335                 340

agg gca ttg ata agg ccg gat tct tcg tct cct aca gag agg att aat
1112
Arg Ala Leu Ile Arg Pro Asp Ser Ser Ser Pro Thr Glu Arg Ile Asn
            345                 350                 355

ggg aat gga agc gat aaa atg atg gct gat aat gaa ttt gct gat gaa
1160
Gly Asn Gly Ser Asp Lys Met Met Ala Asp Asn Glu Phe Ala Asp Glu
        360                 365                 370

gga aat aag ggc aag atg gat aaa aaa caa atg aat aag aaa agg aag
1208
Gly Asn Lys Gly Lys Met Asp Lys Lys Gln Met Asn Lys Lys Arg Lys
    375                 380                 385

gag aaa tgg tca agc cac gga ggg aat cat cca aga acc aaa gag aat
1256
Glu Lys Trp Ser Ser His Gly Gly Asn His Pro Arg Thr Lys Glu Asn
390                 395                 400                 405
```

776

atg atg ata tac aac aat caa gaa act aag att aat gat ttt tgt cga
1304
Met Met Ile Tyr Asn Asn Gln Glu Thr Lys Ile Asn Asp Phe Cys Arg
            410   415   420

gat gat gac caa tgc cat cat gaa ggt tac tca cct tca aac tcc aag
1352
Asp Asp Asp Gln Cys His His Glu Gly Tyr Ser Pro Ser Asn Ser Lys
            425   430   435

aac gca gga act ccg agc tgc agc aat gcc atg gca gct agt aca aag
1400
Asn Ala Gly Thr Pro Ser Cys Ser Asn Ala Met Ala Ala Ser Thr Lys
            440   445   450

tgc ttt cca ttg ctt gaa gga gaa gga gat cag aac ttg tgg gag ggt
1448
Cys Phe Pro Leu Leu Glu Gly Glu Gly Asp Gln Asn Leu Trp Glu Gly
        455   460   465

tat ggt ttg aag caa agg aaa gaa aat aat cat cag taa gctacatttt
1497
Tyr Gly Leu Lys Gln Arg Lys Glu Asn Asn His Gln
470   475   480

tcattctcaa aatgaagaat aagagaactt agaaacgat
1536

<210> 414 <211> 481 <212> PRT <213> Arabidopsis thaliana <400>
414

Met Glu Asp His Gln Asn His Pro Gln Tyr Gly Ile Glu Gln Pro Ser
1   5   10   15

Ser Gln Phe Ser Ser Asp Leu Phe Gly Phe Asn Leu Val Ser Ala Pro
            20   25   30

Asp Gln His His Arg Leu His Phe Thr Asp His Glu Ile Ser Leu Leu
            35   40   45

Pro Arg Gly Ile Gln Gly Leu Thr Val Ala Gly Asn Asn Ser Asn Thr
        50   55   60

Ile Thr Thr Ile Gln Ser Gly Gly Cys Val Gly Gly Phe Ser Gly Phe
65   70   75   80

Thr Asp Gly Gly Gly Thr Gly Arg Trp Pro Arg Gln Glu Thr Leu Met
            85   90   95

Leu Leu Glu Val Arg Ser Arg Leu Asp His Lys Phe Lys Glu Ala Asn
            100   105   110

Gln Lys Gly Pro Leu Trp Asp Glu Val Ser Arg Ile Met Ser Glu Glu
                        777

                115   120   125

His Gly Tyr Thr Arg Ser Gly Lys Lys Cys Arg Glu Lys Phe Glu Asn
    130   135   140

Leu Tyr Lys Tyr Tyr Lys Lys Thr Lys Glu Gly Lys Ser Gly Arg Arg
145   150   155   160

Gln Asp Gly Lys Asn Tyr Arg Phe Phe Arg Gln Leu Glu Ala Ile Tyr
                 165   170   175

Gly Glu Ser Lys Asp Ser Val Ser Cys Tyr Asn Asn Thr Gln Phe Ile
             180   185   190

Met Thr Asn Ala Leu His Ser Asn Phe Arg Ala Ser Asn Ile His Asn
        195   200   205

Ile Val Pro His His Gln Asn Pro Leu Met Thr Asn Thr Asn Thr Gln
    210   215   220

Ser Gln Ser Leu Ser Ile Ser Asn Asn Phe Asn Ser Ser Ser Asp Leu
225   230   235   240

Asp Leu Thr Ser Ser Ser Glu Gly Asn Glu Thr Thr Lys Arg Glu Gly
             245   250   255

Met His Trp Lys Glu Lys Ile Lys Glu Phe Ile Gly Val His Met Glu
             260   265   270

Arg Leu Ile Glu Lys Gln Asp Phe Trp Leu Glu Lys Leu Met Lys Ile
        275   280   285

Val Glu Asp Lys Glu His Gln Arg Met Leu Arg Glu Glu Glu Trp Arg
    290   295   300

Arg Ile Glu Ala Glu Arg Ile Asp Lys Glu Arg Ser Phe Trp Thr Lys
305   310   315   320

Glu Arg Glu Arg Ile Glu Ala Arg Asp Val Ala Val Ile Asn Ala Leu
             325   330   335

Gln Tyr Leu Thr Gly Arg Ala Leu Ile Arg Pro Asp Ser Ser Ser Pro
             340   345   350

Thr Glu Arg Ile Asn Gly Asn Gly Ser Asp Lys Met Met Ala Asp Asn
             355   360   365

                                    778

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Glu Phe Ala Asp Glu Gly Asn Lys Gly Lys Met Asp Lys Lys Gln Met
    370             375             380

Asn Lys Lys Arg Lys Glu Lys Trp Ser Ser His Gly Gly Asn His Pro
385             390             395             400

Arg Thr Lys Glu Asn Met Met Ile Tyr Asn Asn Gln Glu Thr Lys Ile
            405             410             415

Asn Asp Phe Cys Arg Asp Asp Asp Gln Cys His His Glu Gly Tyr Ser
            420             425             430

Pro Ser Asn Ser Lys Asn Ala Gly Thr Pro Ser Cys Ser Asn Ala Met
        435             440             445

Ala Ala Ser Thr Lys Cys Phe Pro Leu Leu Glu Gly Glu Gly Asp Gln
    450             455             460

Asn Leu Trp Glu Gly Tyr Gly Leu Lys Gln Arg Lys Glu Asn Asn His
465             470             475             480

Gln
```

<210> 415 <211> 1215 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1215) <223> G2109

<400> 415

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atg gga agg gtt aag ttg aag att aaa aga ctt gag agc aca agc aac
48
Met Gly Arg Val Lys Leu Lys Ile Lys Arg Leu Glu Ser Thr Ser Asn
1               5               10              15

agg caa gtt aca tac acg aag aga aaa aat ggg att ttg aag aaa gcc
96
Arg Gln Val Thr Tyr Thr Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala
            20              25              30

aaa gag tta tcg att ttg tgt gat att gat att gtc ctt ctt atg ttt
144
Lys Glu Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe
        35              40              45

tcc cct acc gga aga gct act gct ttc cat gga gaa cac agg tat aat
192
Ser Pro Thr Gly Arg Ala Thr Ala Phe His Gly Glu His Arg Tyr Asn
    50              55              60

tat caa aat cat tct tat gca ttg aag aaa act ttt aag aaa ctg gat
240
Tyr Gln Asn His Ser Tyr Ala Leu Lys Lys Thr Phe Lys Lys Leu Asp
```

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      65                    70                    75                    80

cat gat gta aat ata cat gac ttt tta gga gca agg aat caa act att
288
His Asp Val Asn Ile His Asp Phe Leu Gly Ala Arg Asn Gln Thr Ile
                85                    90                    95

gag gta tgg atc gac cat ctt cgg ttc atg aat ttt ctt gga tac ttt
336
Glu Val Trp Ile Asp His Leu Arg Phe Met Asn Phe Leu Gly Tyr Phe
                100                   105                   110

tta atc tct ttg agt caa att gct aaa gtc tgt gtt aac att acc aca
384
Leu Ile Ser Leu Ser Gln Ile Ala Lys Val Cys Val Asn Ile Thr Thr
            115                   120                   125

cga cag ggt cta agt aac caa gta gcc att tac caa gct cag cta atg
432
Arg Gln Gly Leu Ser Asn Gln Val Ala Ile Tyr Gln Ala Gln Leu Met
        130                   135                   140

gag tgt cat agg agg ttg agt tgt tgg acg aac atc gat aga ata gaa
480                                         -
Glu Cys His Arg Arg Leu Ser Cys Trp Thr Asn Ile Asp Arg Ile Glu
145                   150                   155                   160

aac act gag cac ctc gat tta ttg gaa gaa tca ttg agg aaa tcc att
528
Asn Thr Glu His Leu Asp Leu Leu Glu Glu Ser Leu Arg Lys Ser Ile
                165                   170                   175

gaa aga atc cag att cac aag gaa cat tac aga aag aac caa ctc ttg
576
Glu Arg Ile Gln Ile His Lys Glu His Tyr Arg Lys Asn Gln Leu Leu
                180                   185                   190

cca ata gaa tgt gca aca aca cag ttt cac agc ggg ata cag ttg cct
624
Pro Ile Glu Cys Ala Thr Thr Gln Phe His Ser Gly Ile Gln Leu Pro
            195                   200                   205

atg gcg atg gga ggt aat agt agt atg caa gaa gct cac tcc atg tct
672
Met Ala Met Gly Gly Asn Ser Ser Met Gln Glu Ala His Ser Met Ser
        210                   215                   220

tgg ctt cct gat aat gat cac cag caa aca atc tta cct ggt gat tcc
720
Trp Leu Pro Asp Asn Asp His Gln Gln Thr Ile Leu Pro Gly Asp Ser
225                   230                   235                   240

agt ttt ctt ccc cat aga gag atg gat ggt tcg att ccc gtt tac tca
768
Ser Phe Leu Pro His Arg Glu Met Asp Gly Ser Ile Pro Val Tyr Ser
                245                   250                   255

agc tgc ttc ttt gag tct acg aaa cca gaa gat cag ata tgc agc aac
816
Ser Cys Phe Phe Glu Ser Thr Lys Pro Glu Asp Gln Ile Cys Ser Asn
                260                   265                   270
```

780

ccg gga caa cag ttt gag cag tta gaa caa caa gga aac ggt tgt ttg   .
864
Pro Gly Gln Gln Phe Glu Gln Leu Glu Gln Gln Gly Asn Gly Cys Leu
        275   280   285

ggg tta caa caa ctt gga gag gaa tat tca tat cct aca ccg ttt ggt
912
Gly Leu Gln Gln Leu Gly Glu Glu Tyr Ser Tyr Pro Thr Pro Phe Gly
    290   295   300

act act ttg gga atg gaa gaa gat caa gag aaa aag ata aaa tct gaa
960
Thr Thr Leu Gly Met Glu Glu Asp Gln Glu Lys Lys Ile Lys Ser Glu
305   310   315   320

atg gaa ttg aac aac ttg caa caa cag caa cag caa caa caa caa caa
1008
Met Glu Leu Asn Asn Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
            325   330   335

caa caa caa gat cct tca atg tat gat ccc atg gct aat aat aat ggt
1056
Gln Gln Gln Asp Pro Ser Met Tyr Asp Pro Met Ala Asn Asn Asn Gly
            340   345   350

ggc tgc ttt cag att cct cat gat cag tcc atg ttt gtc aat gat cat
1104
Gly Cys Phe Gln Ile Pro His Asp Gln Ser Met Phe Val Asn Asp His
            355   360   365

cat cat cat cat cac cac cat cat caa aat tgg gtt cca gat tca atg
1152
His His His His His His His His Gln Asn Trp Val Pro Asp Ser Met
        370   375   380

ttt ggt cag act tct tac aac cag gtt tgt gtg ttc aca cct cca ttg
1200
Phe Gly Gln Thr Ser Tyr Asn Gln Val Cys Val Phe Thr Pro Pro Leu
385   390   395   400

gaa cta tct agg tag ·
1215
Glu Leu Ser Arg

<210> 416 <211> 404 <212> PRT <213> Arabidopsis thaliana <400>
416

Met Gly Arg Val Lys Leu Lys Ile Lys Arg Leu Glu Ser Thr Ser Asn
1   5   10   15

Arg Gln Val Thr Tyr Thr Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala
            20   ·   25   30

Lys Glu Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe
        35   40   45

781

Ser Pro Thr Gly Arg Ala Thr Ala Phe His Gly Glu His Arg Tyr Asn
    50   55   60

Tyr Gln Asn His Ser Tyr Ala Leu Lys Lys Thr Phe Lys Lys Leu Asp
65   70   75   80

His Asp Val Asn Ile His Asp Phe Leu Gly Ala Arg Asn Gln Thr Ile
                85   90   95

Glu Val Trp Ile Asp His Leu Arg Phe Met Asn Phe Leu Gly Tyr Phe
            100   105   110

Leu Ile Ser Leu Ser Gln Ile Ala Lys Val Cys Val Asn Ile Thr Thr
            115   120   125

Arg Gln Gly Leu Ser Asn Gln Val Ala Ile Tyr Gln Ala Gln Leu Met
    130   135   140

Glu Cys His Arg Arg Leu Ser Cys Trp Thr Asn Ile Asp Arg Ile Glu
145   150   155 .   160

Asn Thr Glu His Leu Asp Leu Leu Glu Glu Ser Leu Arg Lys Ser Ile
            165   170   175

Glu Arg Ile Gln Ile His Lys Glu His Tyr Arg Lys Asn Gln Leu Leu
            180   185   190

Pro Ile Glu Cys Ala Thr Thr Gln Phe His Ser Gly Ile Gln Leu Pro
    195   200   205

Met Ala Met Gly Gly Asn Ser Ser Met Gln Glu Ala His Ser Met Ser
    210   215   220

Trp Leu Pro Asp Asn Asp His Gln Gln Thr Ile Leu Pro Gly Asp Ser
225   230   235   240

Ser Phe Leu Pro His Arg Glu Met Asp Gly Ser Ile Pro Val Tyr Ser
            245   250   255

Ser Cys Phe Phe Glu Ser Thr Lys Pro Glu Asp Gln Ile Cys Ser Asn
            260   265   270

Pro Gly Gln Gln Phe Glu Gln Leu Glu Gln Gln Gly Asn Gly Cys Leu
    275   280   285

782

```
Gly Leu Gln Gln Leu Gly Glu Glu Tyr Ser Tyr Pro Thr Pro Phe Gly
    290                 295             300

Thr Thr Leu Gly Met Glu Glu Asp Gln Glu Lys Lys Ile Lys Ser Glu
305                 310                 315                 320

Met Glu Leu Asn Asn Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
                325                 330                 335

Gln Gln Gln Asp Pro Ser Met Tyr Asp Pro Met Ala Asn Asn Asn Gly
            340                 345             350

Gly Cys Phe Gln Ile Pro His Asp Gln Ser Met Phe Val Asn Asp His
        355                 360                 365

His His His His His His His His Gln Asn Trp Val Pro Asp Ser Met
    370                 375                 380

Phe Gly Gln Thr Ser Tyr Asn Gln Val Cys Val Phe Thr Pro Pro Leu
385                 390                 395                 400

Glu Leu Ser Arg
```

<210> 417 <211> 1019 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (41)..(988) <223> G2130

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cctctcttca tttttaact ccctctctct ctctctctct atg gag aga cga acg
55
                                          Met Glu Arg Arg Thr
                                          1               5

aga cga gtg aag ttc aca gag aat cgt acg gtc aca aac gta gca gct
103
Arg Arg Val Lys Phe Thr Glu Asn Arg Thr Val Thr Asn Val Ala Ala
            10              15              ·20

aca cca tct aac ggg tct ccg aga ctg gtc cgt atc act gtt act gat
151
Thr Pro Ser Asn Gly Ser Pro Arg Leu Val Arg Ile Thr Val Thr Asp
            25              30              35

cct ttc gct act gac tcg tct agc gac gac gac gac aac aac aac gtc
199
Pro Phe Ala Thr Asp Ser Ser Ser Asp Asp Asp Asp Asn Asn Asn Val
            40              45              50

acg gtg gtt cca aga gtg aaa cga tac gtg aag gag att aga ttc tgc
247
Thr Val Val Pro Arg Val Lys Arg Tyr Val Lys Glu Ile Arg Phe Cys
    55 ·             60              65
```

```
caa ggt gaa tct tct tcc tcc acc gcg gcg agg aaa ggt aag cac aag
295
Gln Gly Glu Ser Ser Ser Ser Thr Ala Ala Arg Lys Gly Lys His Lys
70              75          80              85

gag gag gaa agc gta gtg gtt gaa gat gac gtg tcg acg tcg gtg aag
343
Glu Glu Glu Ser Val Val Val Glu Asp Asp Val Ser Thr Ser Val Lys
              90          95              100

cct aaa aag tac aga ggc gtg aga cag aga cct tgg gga aaa ttc gcg
391
Pro Lys Lys Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
            105             110             115

gcg gag att aga gat ccg tcg agc cgt act cgg att tgg ctt ggg act
439
Ala Glu Ile Arg Asp Pro Ser Ser Arg Thr Arg Ile Trp Leu Gly Thr
            120             125             130

ttt gtc acg gcg gag gaa gct gct ata gcg tac gat aga gcc gcg att
487
Phe Val Thr Ala Glu Glu Ala Ala Ile Ala Tyr Asp Arg Ala Ala Ile
        135             140             145

cat ctc aaa gga cct aaa gcg ctc acg aat ttc cta act ccg ccg acg
535
His Leu Lys Gly Pro Lys Ala Leu Thr Asn Phe Leu Thr Pro Pro Thr
150             155             160             165

cca acg ccg gtt atc gat ctc caa acg gtt tcc gcc tgc gat tac ggt
583
Pro Thr Pro Val Ile Asp Leu Gln Thr Val Ser Ala Cys Asp Tyr Gly
            170             175             180

aga gat tct cgg cag agc ctt cat tca ccg acc tct gtt cta aga ttc
631
Arg Asp Ser Arg Gln Ser Leu His Ser Pro Thr Ser Val Leu Arg Phe
            185             190             195

aac gtc aac gag gaa aca gag cat gag att gaa gcg atc gag cta tct
679
Asn Val Asn Glu Glu Thr Glu His Glu Ile Glu Ala Ile Glu Leu Ser
        200             205             210

ccg gag aga aag tcg acg gtt ata aaa gaa gaa gaa gaa tcg tcg gcg
727
Pro Glu Arg Lys Ser Thr Val Ile Lys Glu Glu Glu Glu Ser Ser Ala
        215             220             225

ggt ttg gtg ttc ccg gat ccg tat ctg tta ccg gat tta tct ctc gcc
775
Gly Leu Val Phe Pro Asp Pro Tyr Leu Leu Pro Asp Leu Ser Leu Ala
230             235             240             245

ggc gaa tgt ttt tgg gat acc gaa att gcc cct gac ctt ttg ttt ctc
823
Gly Glu Cys Phe Trp Asp Thr Glu Ile Ala Pro Asp Leu Leu Phe Leu
            250             255             260
```

784

```
gat gaa gaa acc aaa atc caa tca acg ttg tta cca aac aca gag gtt
871
Asp Glu Glu Thr Lys Ile Gln Ser Thr Leu Leu Pro Asn Thr Glu Val
        265             270             275

tcg aaa caa gga gaa aac gaa act gaa gat ttc gag ttt ggt ttg att
919
Ser Lys Gln Gly Glu Asn Glu Thr Glu Asp Phe Glu Phe Gly Leu Ile
        280             285             290

gat gat ttc gag tct tct cca tgg gat gtg gat cat ttc ttc gac cat
967
Asp Asp Phe Glu Ser Ser Pro Trp Asp Val Asp His Phe Phe Asp His
    295             300             305

cat cat cac tct ttc gat taa aaatctcttc tttttggggg aaatttttgt g
1019
His His His Ser Phe Asp
310             315
```

<210> 418 <211> 315 <212> PRT <213> Arabidopsis thaliana <400> 418

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Met Glu Arg Arg Thr Arg Arg Val Lys Phe Thr Glu Asn Arg Thr Val
1               5               10              15


Thr Asn Val Ala Ala Thr Pro Ser Asn Gly Ser Pro Arg Leu Val Arg
            20              25              30


Ile Thr Val Thr Asp Pro Phe Ala Thr Asp Ser Ser Ser Asp Asp Asp
            35              40              45


Asp Asn Asn Asn Val Thr Val Val Pro Arg Val Lys Arg Tyr Val Lys
    50              55              60


Glu Ile Arg Phe Cys Gln Gly Glu Ser Ser Ser Ser Thr Ala Ala Arg
65              70              75              80


Lys Gly Lys His Lys Glu Glu Glu Ser Val Val Val Glu Asp Asp Val
            85              90              95


Ser Thr Ser Val Lys Pro Lys Lys Tyr Arg Gly Val Arg Gln Arg Pro
            100             105             110


Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Ser Ser Arg Thr Arg
            115             120             125


Ile Trp Leu Gly Thr Phe Val Thr Ala Glu Glu Ala Ala Ile Ala Tyr
        130             135             140


Asp Arg Ala Ala Ile His Leu Lys Gly Pro Lys Ala Leu Thr Asn Phe
```

```
         145                    150                    155                    160


         Leu Thr Pro Pro Thr Pro Thr Pro Val Ile Asp Leu Gln Thr Val Ser
                     165                 170                 175


         Ala Cys Asp Tyr Gly Arg Asp Ser Arg Gln Ser Leu His Ser Pro Thr
                     180                 185                 190


         Ser Val Leu Arg Phe Asn Val Asn Glu Glu Thr Glu His Glu Ile Glu
                     195                 200                 205


         Ala Ile Glu Leu Ser Pro Glu Arg Lys Ser Thr Val Ile Lys Glu Glu
             210                 215                 220


         Glu Glu Ser Ser Ala Gly Leu Val Phe Pro Asp Pro Tyr Leu Leu Pro
         225                 230                 235                 240


         Asp Leu Ser Leu Ala Gly Glu Cys Phe Trp Asp Thr Glu Ile Ala Pro
                     245                 250                 255


         Asp Leu Leu Phe Leu Asp Glu Glu Thr Lys Ile Gln Ser Thr Leu Leu
                     260                 265                 270


         Pro Asn Thr Glu Val Ser Lys Gln Gly Glu Asn Glu Thr Glu Asp Phe
                     275                 280                 285


         Glu Phe Gly Leu Ile Asp Asp Phe Glu Ser Ser Pro Trp Asp Val Asp
             290                 295                 300


         His Phe Phe Asp His His His Ser Phe Asp
         305                 310                 315
```

<210> 419 <211> 1803 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (151)..(1569) <223> G2159

 <400> 419
gaagcagaga agaggaaaaa agctgtgact ttcatacatt actctccctc tccatctctc
60

tcgttgtcac atatcagtat atcacaaaac aaattgcagc cattcacatc tttctcttcc
120

atctctcaac attctctttc tctctgtaaa atg gag aaa cca gtg ttt gca cca
174
                                  Met Glu Lys Pro Val Phe Ala Pro
                                   1   5

tgg cgt tcc gac caa gtt ttc cgg cca ccg gag aca cca tta gag ccg
222
Trp Arg Ser Asp Gln Val Phe Arg Pro Pro Glu Thr Pro Leu Glu Pro

                10   15   20

atg gag ttt ctc tct cgc tcc tgg agc gta tca gct cac gaa gtc tcc
270
Met Glu Phe Leu Ser Arg Ser Trp Ser Val Ser Ala His Glu Val Ser
25   30   35   40

aaa gct ctc act cct tct cag caa ctc ctc tca aaa gcc tca atc gaa
318
Lys Ala Leu Thr Pro Ser Gln Gln Leu Leu Ser Lys Ala Ser Ile Glu
                    45   50   55

aac acc acc gtc att ctc gaa gaa ccc atc gcc gcc ggc gag acc gaa
366
Asn Thr Thr Val Ile Leu Glu Glu Pro Ile Ala Ala Gly Glu Thr Glu
                    60   65   70

acg gag gac aac agc ttc gtc tcc gga aac cct ttc tcc ttc gct tgc
414
Thr Glu Asp Asn Ser Phe Val Ser Gly Asn Pro Phe Ser Phe Ala Cys
                    75   80   85

tca gaa act tct cag atg gtc atg gat cgt atc tta tct cag tct cag
462
Ser Glu Thr Ser Gln Met Val Met Asp Arg Ile Leu Ser Gln Ser Gln
        90   95   100

gaa gtg tcg cca cga aca tct ggt cgg ctt tct cat agc agc ggt cct
510
Glu Val Ser Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser Gly Pro
105   110   115   120

ctc aat ggt tct tta acc gac agt cct ccg att tcg ccg cat caa gtc
558
Leu Asn Gly Ser Leu Thr Asp Ser Pro Pro Ile Ser Pro His Gln Val
                    125   130   135

gac gac att aag caa ttt tgc cga tca aac aac aat ttc aac tct caa
606
Asp Asp Ile Lys Gln Phe Cys Arg Ser Asn Asn Asn Phe Asn Ser Gln
                    140   145   150

tac cgt tca acg gga aca act ccg gga cct atc act gca aca act aca
654
Tyr Arg Ser Thr Gly Thr Thr Pro Gly Pro Ile Thr Ala Thr Thr Thr
            155   160   165

cag tcc aag aca gtt gga cgg tgg ttg aaa gac agg agg gag aaa aag
702
Gln Ser Lys Thr Val Gly Arg Trp Leu Lys Asp Arg Arg Glu Lys Lys
        170   175   180

aag gaa gag atg aga gca cac aat gct cag ata cat gct gct gta tca
750
Lys Glu Glu Met Arg Ala His Asn Ala Gln Ile His Ala Ala Val Ser
185   190   ·   195   ·   200

gta gct ggt gtg gca gcc gcg gtg gct gct atc gcg gct gca act gct
798
Val Ala Gly Val Ala Ala Ala Val Ala Ala Ile Ala Ala Ala Thr Ala
                    205   210   215

```
gct tcg tcg agt gct gga aaa gat gag aat atg gct aag acg gat atg
846
Ala Ser Ser Ser Ala Gly Lys Asp Glu Asn Met Ala Lys Thr Asp Met
            220             225             230

gct gtg gct tct gct gca aca ctt gtg gct gct caa tgt gtg gaa gct
894
Ala Val Ala Ser Ala Ala Thr Leu Val Ala Ala Gln Cys Val Glu Ala
            235             240             245

gct gaa gtt atg gga gct gag agg gat cat tta gct tcc gtt gtt agt
942
Ala Glu Val Met Gly Ala Glu Arg Asp His Leu Ala Ser Val Val Ser
        250             255             260

tct gct gtt aat gtt cga tct gcg gga gat atc atg aca tta acc gct
990
Ser Ala Val Asn Val Arg Ser Ala Gly Asp Ile Met Thr Leu Thr Ala
265             270             275             280

gga gca gcc aca gcg tta aga gga gtg gct aca ttg aag gct aga gct
1038
Gly Ala Ala Thr Ala Leu Arg Gly Val Ala Thr Leu Lys Ala Arg Ala
            285             290             295

atg aag gag gtg tgg cac att gca tca gtt att cca atg gat aaa gga
1086
Met Lys Glu Val Trp His Ile Ala Ser Val Ile Pro Met Asp Lys Gly
            300             305             310

atc aat ctc gga ggt tgc agc aat gtt aat ggt aac ggg agc tat gtc
1134
Ile Asn Leu Gly Gly Cys Ser Asn Val Asn Gly Asn Gly Ser Tyr Val
            315             320             325

agc tca agc agc agt cat agt ggc gaa ttt cta gtt gag gat aat ttc
1182
Ser Ser Ser Ser Ser His Ser Gly Glu Phe Leu Val Glu Asp Asn Phe
        330             335             340

ttg gga cat tgc aat aga gaa tgg ctt gct cga ggt ggc caa ctt ctt
1230
Leu Gly His Cys Asn Arg Glu Trp Leu Ala Arg Gly Gly Gln Leu Leu
345             350             355             360

aaa cgc acc cgc aaa ggt gat ctt cat tgg aaa ata gtt tca gtt tac
1278
Lys Arg Thr Arg Lys Gly Asp Leu His Trp Lys Ile Val Ser Val Tyr
            365             370             375

ata aac agg cta aat caa gtt ata ttg aag atg aag agc agg cat gta
1326
Ile Asn Arg Leu Asn Gln Val Ile Leu Lys Met Lys Ser Arg His Val
            380             385             390

gga ggg acc ttc acg aag aag aac aaa aat gtt gtg att gat gtg atc
1374
Gly Gly Thr Phe Thr Lys Lys Asn Lys Asn Val Val Ile Asp Val Ile
            395             400             405
```

```
aaa aac gtt caa gct tgg cca ggc cgc cat ttg ctg gaa gga gga gag
1422
Lys Asn Val Gln Ala Trp Pro Gly Arg His Leu Leu Glu Gly Gly Glu
    410                 415                 420

gat ttg aga tac ttt ggg tta aag acg gtt ccg cga ggg att gta gaa
1470
Asp Leu Arg Tyr Phe Gly Leu Lys Thr Val Pro Arg Gly Ile Val Glu
425                 430                 435                 440

ttt cag tgc aag agc cag aga gag tat gaa atg tgg aca caa ggt gtc
1518
Phe Gln Cys Lys Ser Gln Arg Glu Tyr Glu Met Trp Thr Gln Gly Val
                445                 450                 455

tca agg ctt att gct gtt gct gcc gag agg aat aac aga tat agg ata
1566
Ser Arg Leu Ile Ala Val Ala Ala Glu Arg Asn Asn Arg Tyr Arg Ile
            460                 465                 470

tga agggagtagt agttttaaga gttcagagct acttttgag gggtgatatc
1619

taacttatgg ggccaaatta taacttggag aaagttaagg gtgttttctt tagagtaatg
1679

tcttttgta aggtatatag gattaaatgt ggcctctata agggtagcta gtgaaacaaa
1739

tcttggtgtt tgtatatata tttttttgg ggaaaaagtt taatatcaaa tttttaattt
1799

aaaa
1803


<210>  420 <211>  472 <212>  PRT <213>  Arabidopsis thaliana  <400>
420

Met Glu Lys Pro Val Phe Ala Pro Trp Arg Ser Asp Gln Val Phe Arg
1               5               10              15


Pro Pro Glu Thr Pro Leu Glu Pro Met Glu Phe Leu Ser Arg Ser Trp
            20              25              30


Ser Val Ser Ala His Glu Val Ser Lys Ala Leu Thr Pro Ser Gln Gln
        35              40              45


Leu Leu Ser Lys Ala Ser Ile Glu Asn Thr Thr Val Ile Leu Glu Glu
    50              55              60


Pro Ile Ala Ala Gly Glu Thr Glu Thr Glu Asp Asn Ser Phe Val Ser
65              70              75              80


Gly Asn Pro Phe Ser Phe Ala Cys Ser Glu Thr Ser Gln Met Val Met
                85              90              95
```

```
Asp Arg Ile Leu Ser Gln Ser Gln Glu Val Ser Pro Arg Thr Ser Gly
            100                 105             110

Arg Leu Ser His Ser Ser Gly Pro Leu Asn Gly Ser Leu Thr Asp Ser
        115             120             125

Pro Pro Ile Ser Pro His Gln Val Asp Asp Ile Lys Gln Phe Cys Arg
    130             135             140

Ser Asn Asn Asn Phe Asn Ser Gln Tyr Arg Ser Thr Gly Thr Thr Pro
145             150             155             160

Gly Pro Ile Thr Ala Thr Thr Thr Gln Ser Lys Thr Val Gly Arg Trp
            165             170             175

Leu Lys Asp Arg Arg Glu Lys Lys Lys Glu Glu Met Arg Ala His Asn
        180             185             190

Ala Gln Ile His Ala Ala Val Ser Val Ala Gly Val Ala Ala Ala Val
        195             200             205

Ala Ala Ile Ala Ala Ala Thr Ala Ala Ser Ser Ser Ala Gly Lys Asp
    210             215             220

Glu Asn Met Ala Lys Thr Asp Met Ala Val Ala Ser Ala Ala Thr Leu
225             230             235             240

Val Ala Ala Gln Cys Val Glu Ala Ala Glu Val Met Gly Ala Glu Arg
            245             250             255

Asp His Leu Ala Ser Val Val Ser Ser Ala Val Asn Val Arg Ser Ala
            260             265             270

Gly Asp Ile Met Thr Leu Thr Ala Gly Ala Ala Thr Ala Leu Arg Gly
            275             280             285

Val Ala Thr Leu Lys Ala Arg Ala Met Lys Glu Val Trp His Ile Ala
    290             295             300

Ser Val Ile Pro Met Asp Lys Gly Ile Asn Leu Gly Gly Cys Ser Asn
305             310             315             320

Val Asn Gly Asn Gly Ser Tyr Val Ser Ser Ser Ser Ser His Ser Gly
            325             330             335
```

790

```
Glu Phe Leu Val Glu Asp Asn Phe Leu Gly His Cys Asn Arg Glu Trp
         340              345              350
```

```
Leu Ala Arg Gly Gly Gln Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu
         355              360              365
```

```
His Trp Lys Ile Val Ser Val Tyr Ile Asn Arg Leu Asn Gln Val Ile
    370              375              380
```

```
Leu Lys Met Lys Ser Arg His Val Gly Gly Thr Phe Thr Lys Lys Asn
385              390              395              400
```

```
Lys Asn Val Val Ile Asp Val Ile Lys Asn Val Gln Ala Trp Pro Gly
             405              410              415
```

```
Arg His Leu Leu Glu Gly Gly Glu Asp Leu Arg Tyr Phe Gly Leu Lys
         420              425              430
```

```
Thr Val Pro Arg Gly Ile Val Glu Phe Gln Cys Lys Ser Gln Arg Glu
         435              440              445
```

```
Tyr Glu Met Trp Thr Gln Gly Val Ser Arg Leu Ile Ala Val Ala Ala
    450              455              460
```

```
Glu Arg Asn Asn Arg Tyr Arg Ile
465              470
```

<210> 421 <211> 1128 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1128) <223> G2331

<400> 421
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atg gat cta tca aac cgt cgc aat cct ctc cgg gat ctg agc ttt cct
48
Met Asp Leu Ser Asn Arg Arg Asn Pro Leu Arg Asp Leu Ser Phe Pro
1               5               10              15
```

```
cct cct ccg ccg cca cct att ttc cac cgt gcg agc tct acg ggg acg
96
Pro Pro Pro Pro Pro Pro Ile Phe His Arg Ala Ser Ser Thr Gly Thr
             20              25              30
```

```
agt ttt ccg atc tta gcc gtc gcg gtg atc gga atc tta gcc aca gca
144
Ser Phe Pro Ile Leu Ala Val Ala Val Ile Gly Ile Leu Ala Thr Ala
         35              40              45
```

```
ttt tta ctt gta agc tat tat gtt ttt gtt atc aaa tgt tgt ctc aac
192
Phe Leu Leu Val Ser Tyr Tyr Val Phe Val Ile Lys Cys Cys Leu Asn
    50              55              60
```

791

```
tgg cac cga atc gac att ctt ggt cga ttc tcg tta tct cga agg cga
240
Trp His Arg Ile Asp Ile Leu Gly Arg Phe Ser Leu Ser Arg Arg Arg
65                 70          75                    80

cgc aac gac caa gat cct tta atg gtt tac tct cca gag ctt aga agc
288
Arg Asn Asp Gln Asp Pro Leu Met Val Tyr Ser Pro Glu Leu Arg Ser
              85              90                    95

cgc ggt ctt gat gaa tcc gtc att aga gca atc cca atc ttt aag ttc
336
Arg Gly Leu Asp Glu Ser Val Ile Arg Ala Ile Pro Ile Phe Lys Phe
          100              105             110

aag aag aga tac gac caa aac gac ggc gtt ttt aca gga gaa gga gaa
384
Lys Lys Arg Tyr Asp Gln Asn Asp Gly Val Phe Thr Gly Glu Gly Glu
          115              120             125

gaa gaa gaa gag aag aga tct caa gaa tgc tct gtt tgt ttg agt gag
432
Glu Glu Glu Glu Lys Arg Ser Gln Glu Cys Ser Val Cys Leu Ser Glu
    130              135         --      140

ttt caa gat gag gag aag ctg agg att atc cca aat tgt tct cat ttg
480
Phe Gln Asp Glu Glu Lys Leu Arg Ile Ile Pro Asn Cys Ser His Leu
145              150              155                 160

ttt cat atc gac tgt atc gat gtg tgg ctt cag aac aac gcc aat tgt
528
Phe His Ile Asp Cys Ile Asp Val Trp Leu Gln Asn Asn Ala Asn Cys
              165              170             175

cct ttg tgt aga act agg gtt tct tgt gac aca agt ttt cct ccg gat
576
Pro Leu Cys Arg Thr Arg Val Ser Cys Asp Thr Ser Phe Pro Pro Asp
          180              185             190

cgg gtt tct gcg ccg agc act tct ccc gag aat ctg gtc atg tta aga
624
Arg Val Ser Ala Pro Ser Thr Ser Pro Glu Asn Leu Val Met Leu Arg
          195              200             205

ggt gag aac gag tat gtg gtc att gag ctg ggc agt agc atc ggt agt
672
Gly Glu Asn Glu Tyr Val Val Ile Glu Leu Gly Ser Ser Ile Gly Ser
    210              215              220

gac aga gat agt cca aga cac gga agg tta ctt acg gga caa gaa agg
720
Asp Arg Asp Ser Pro Arg His Gly Arg Leu Leu Thr Gly Gln Glu Arg
225              230              235                 240

tca aat tca ggt tat cta ctg aac gaa aac acc caa aat tcg atc agt
768
Ser Asn Ser Gly Tyr Leu Leu Asn Glu Asn Thr Gln Asn Ser Ile Ser
              245              250             255
```

cca tct ccg aag aag ctt gac cgc gga ggg ctt cca aga aaa ttc cga
816
Pro Ser Pro Lys Lys Leu Asp Arg Gly Gly Leu Pro Arg Lys Phe Arg
            260   265   270

aag ctt cac aag atg acg agt atg gga gac gaa tgc atc gac ata aga
864
Lys Leu His Lys Met Thr Ser Met Gly Asp Glu Cys Ile Asp Ile Arg
            275   280   285

aga ggt aaa gac gaa cag ttc ggt agt att cag ccc att aga aga tca
912
Arg Gly Lys Asp Glu Gln Phe Gly Ser Ile Gln Pro Ile Arg Arg Ser
            290   295   300

atc tca atg gat tca tcg gcg gat aga cag ctt tac ttg gcg gtt caa
960
Ile Ser Met Asp Ser Ser Ala Asp Arg Gln Leu Tyr Leu Ala Val Gln
305   310   315   320

gag gcg att cgg aaa aac cgc gaa gtt ctg gtg gtt gga gac gga gga
1008
Glu Ala Ile Arg Lys Asn Arg Glu Val Leu Val Val Gly Asp Gly Gly
            325   330   335

gga tgt agc agt agt agt ggc aat gtt agt aat tcc aaa gtg aag aga
1056
Gly Cys Ser Ser Ser Ser Gly Asn Val Ser Asn Ser Lys Val Lys Arg
            340   345   350

tct ttc ttc tct ttt ggg agc agt aga cgt tct aga agt tcc tct aaa
1104
Ser Phe Phe Ser Phe Gly Ser Ser Arg Arg Ser Arg Ser Ser Ser Lys
            355   360   365

ttg cca ctt tat ttt gaa ccc taa
1128
Leu Pro Leu Tyr Phe Glu Pro
        370   375

<210> 422 <211> 375 <212> PRT <213> Arabidopsis thaliana <400>
422

Met Asp Leu Ser Asn Arg Arg Asn Pro Leu Arg Asp Leu Ser Phe Pro
1   5   10   15

Pro Pro Pro Pro Pro Pro Ile Phe His Arg Ala Ser Ser Thr Gly Thr
            20   25   30

Ser Phe Pro Ile Leu Ala Val Ala Val Ile Gly Ile Leu Ala Thr Ala
        35   40   45

Phe Leu Leu Val Ser Tyr Tyr Val Phe Val Ile Lys Cys Cys Leu Asn
    50   55   60

Trp His Arg Ile Asp Ile Leu Gly Arg Phe Ser Leu Ser Arg Arg Arg

793

65   70   75   80

Arg Asn Asp Gln Asp Pro Leu Met Val Tyr Ser Pro Glu Leu Arg Ser
            85   90   95

Arg Gly Leu Asp Glu Ser Val Ile Arg Ala Ile Pro Ile Phe Lys Phe
            100   105   110

Lys Lys Arg Tyr Asp Gln Asn Asp Gly Val Phe Thr Gly Glu Gly Glu
            115   120   125

Glu Glu Glu Glu Lys Arg Ser Gln Glu Cys Ser Val Cys Leu Ser Glu
    130   135   140

Phe Gln Asp Glu Glu Lys Leu Arg Ile Ile Pro Asn Cys Ser His Leu
145   150   155   160

Phe His Ile Asp Cys Ile Asp Val Trp Leu Gln Asn Asn Ala Asn Cys
            165   170   175

Pro Leu Cys Arg Thr Arg Val Ser Cys Asp Thr Ser Phe Pro Pro Asp
            180   185   190

Arg Val Ser Ala Pro Ser Thr Ser Pro Glu Asn Leu Val Met Leu Arg
            195   200   205

Gly Glu Asn Glu Tyr Val Val Ile Glu Leu Gly Ser Ser Ile Gly Ser
    210   215   220

Asp Arg Asp Ser Pro Arg His Gly Arg Leu Leu Thr Gly Gln Glu Arg
225   230   235   240

Ser Asn Ser Gly Tyr Leu Leu Asn Glu Asn Thr Gln Asn Ser Ile Ser
            245   250   255

Pro Ser Pro Lys Lys Leu Asp Arg Gly Gly Leu Pro Arg Lys Phe Arg
            260   265   270

Lys Leu His Lys Met Thr Ser Met Gly Asp Glu Cys Ile Asp Ile Arg
            275   280   285

Arg Gly Lys Asp Glu Gln Phe Gly Ser Ile Gln Pro Ile Arg Arg Ser
            290   295   300

Ile Ser Met Asp Ser Ser Ala Asp Arg Gln Leu Tyr Leu Ala Val Gln
305   310   315   320

794

Glu Ala Ile Arg Lys Asn Arg Glu Val Leu Val Val Gly Asp Gly Gly
                325   330   335

Gly Cys Ser Ser Ser Ser Gly Asn Val Ser Asn Ser Lys Val Lys Arg
                340   345   350

Ser Phe Phe Ser Phe Gly Ser Ser Arg Arg Ser Arg Ser Ser Ser Lys
                355   360   365

Leu Pro Leu Tyr Phe Glu Pro
        370   375

<210> 423 <211> 1398 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1398) <223> G2242

<400> 423
atg aaa tgg gtt ttc cca gaa atc aaa aca act cag aat ttc ctc tct   48
Met Lys Trp Val Phe Pro Glu Ile Lys Thr Thr Gln Asn Phe Leu Ser
1   5   10   15

cct tca tca ctt cca caa gaa cca ccg tta tct ctc cgc tcc agc gca   96
Pro Ser Ser Leu Pro Gln Glu Pro Pro Leu Ser Leu Arg Ser Ser Ala
                20   25   30

aac ttc gat cta aac agc aaa atc agt cca agt att ctc ctc ata atc   144
Asn Phe Asp Leu Asn Ser Lys Ile Ser Pro Ser Ile Leu Leu Ile Ile
            35   40   45

ata atc ctc tca atc atc ttc ttc atc tcc ggt ctc ctt cat ctc tta   192
Ile Ile Leu Ser Ile Ile Phe Phe Ile Ser Gly Leu Leu His Leu Leu
        50   55   60

gtc aga ttc ctc ctc aca cca tcg agc aga gac aga gaa gat tac ttc   240
Val Arg Phe Leu Leu Thr Pro Ser Ser Arg Asp Arg Glu Asp Tyr Phe
65   70   75   80

gac aac gtc act gct ctt caa ggc cag ctt caa cag ctt ttt cat ctc   288
Asp Asn Val Thr Ala Leu Gln Gly Gln Leu Gln Gln Leu Phe His Leu
                85   90   95

cat gat tct gga gtt gac caa tcc ttc atc gac acg tta cct gtt ttc   336
His Asp Ser Gly Val Asp Gln Ser Phe Ile Asp Thr Leu Pro Val Phe
                100   105   110

cat tac aaa tcc ata atc ggt ctc aag aac tat cct ttt gat tgt gca   384
His Tyr Lys Ser Ile Ile Gly Leu Lys Asn Tyr Pro Phe Asp Cys Ala
            115   120   125

795

```
gtt tgt ctt tgt gag ttc gaa aca gag gat aag ctc agg ctc tta cct
432
Val Cys Leu Cys Glu Phe Glu Thr Glu Asp Lys Leu Arg Leu Leu Pro
    130             135             140

aaa tgc agc cac gcc ttt cac atg gat tgt atc gat act tgg ctt cta
480
Lys Cys Ser His Ala Phe His Met Asp Cys Ile Asp Thr Trp Leu Leu
145             150             155             160

tct cac tct act tgt cct ttg tgt aga tcc agt ctc ctc tct gat ctc
528
Ser His Ser Thr Cys Pro Leu Cys Arg Ser Ser Leu Leu Ser Asp Leu
                165             170             175

tct tcg cac caa gat cct cgt tct tct ttc ctc ctt gtg ctc gag tct
576
Ser Ser His Gln Asp Pro Arg Ser Ser Phe Leu Leu Val Leu Glu Ser
            180             185             190

gcg agt gat cat agc tcg aga gag att gga gga gat aga gac agt gca
624
Ala Ser Asp His Ser Ser Arg Glu Ile Gly Gly Asp Arg Asp Ser Ala
            195             200             205

gct tgt gtg gct gca aat gat gat att gat gtg tct agt gct cat ctt
672
Ala Cys Val Ala Ala Asn Asp Asp Ile Asp Val Ser Ser Ala His Leu
    210             215             220

ggt ttg gtc gga aac aat gat ctt gga tca acc agg ata gat tcg ggt
720
Gly Leu Val Gly Asn Asn Asp Leu Gly Ser Thr Arg Ile Asp Ser Gly
225             230             235             240

cac gga gat cag tac ctg gat ggt gaa ttg ggt ggt tcg gtt gga aag
768
His Gly Asp Gln Tyr Leu Asp Gly Glu Leu Gly Gly Ser Val Gly Lys
            245             250             255

gtt gtt cct ttt tca gtt aag cta ggg aag ttt agg aat ata gat att
816
Val Val Pro Phe Ser Val Lys Leu Gly Lys Phe Arg Asn Ile Asp Ile
            260             265             270

ggt gaa gga act agt agc aac aac aac att ggt aat agt agt agt tta
864
Gly Glu Gly Thr Ser Ser Asn Asn Asn Ile Gly Asn Ser Ser Ser Leu
            275             280             285

gat gag agg agg tgt ttc tca atg gga tca tat gag tat ata atg gat
912
Asp Glu Arg Arg Cys Phe Ser Met Gly Ser Tyr Glu Tyr Ile Met Asp
        290             295             300

gaa gaa acg act ctt aag gtt cat gtt tca acc aag aaa caa tca agc
960
Glu Glu Thr Thr Leu Lys Val His Val Ser Thr Lys Lys Gln Ser Ser
305             310             315             320
```

796

aag aac cgt ggc ttg ccc ggt cat agg aca gcg atg tcc gaa tgc ggg
1008
Lys Asn Arg Gly Leu Pro Gly His Arg Thr Ala Met Ser Glu Cys Gly
            325   330   335

ttt gat cca aca ggg aga ttg aaa ttc agt ggg agt gga tcg atg agg
1056
Phe Asp Pro Thr Gly Arg Leu Lys Phe Ser Gly Ser Gly Ser Met Arg
            340   345   350

ata gtg gaa gaa gcg gcc gag aag aat gta gtg gaa aga gag agc ttt
1104
Ile Val Glu Glu Ala Ala Glu Lys Asn Val Val Glu Arg Glu Ser Phe
            355   360   365

tcg gta tcg aaa ata tgg cta agg ggg aag aag gag aag cat agt aaa
1152
Ser Val Ser Lys Ile Trp Leu Arg Gly Lys Lys Glu Lys His Ser Lys
    370   375   380

gtt caa gga aaa gag gat agt tca ttg gtt tct tcg tct tcg gga aga
1200
Val Gln Gly Lys Glu Asp Ser Ser Leu Val Ser Ser Ser Ser Gly Arg
385   390   395   400

gca ttc tct ttc agg tta tcg aac cag cgg aac cat ccc gat gcg atg
1248
Ala Phe Ser Phe Arg Leu Ser Asn Gln Arg Asn His Pro Asp Ala Met
            405   410   415

atc gaa agt ggt tgc gaa gaa gat aat caa aag tgc gaa aac tcg gag
1296
Ile Glu Ser Gly Cys Glu Glu Asp Asn Gln Lys Cys Glu Asn Ser Glu
            420   425   430

tct ttg gag act aaa aca cca tct ttt gct agg agg act atg ctt tgg
1344
Ser Leu Glu Thr Lys Thr Pro Ser Phe Ala Arg Arg Thr Met Leu Trp
            435   440   445

ctt gca ggg aga caa aac aag gtt gtt cat tct tct tct tca act aat
1392
Leu Ala Gly Arg Gln Asn Lys Val Val His Ser Ser Ser Ser Thr Asn
    450   455   460

gtc tag
1398
Val
465

<210> 424 <211> 465 <212> PRT <213> Arabidopsis thaliana <400>
424

Met Lys Trp Val Phe Pro Glu Ile Lys Thr Thr Gln Asn Phe Leu Ser
1   5   10   15

Pro Ser Ser Leu Pro Gln Glu Pro Pro Leu Ser Leu Arg Ser Ser Ala
            20   25   30

```
Asn Phe Asp Leu Asn Ser Lys Ile Ser Pro Ser Ile Leu Leu Ile Ile
        35              40              45


Ile Ile Leu Ser Ile Ile Phe Phe Ile Ser Gly Leu Leu His Leu Leu
        50              55              60


Val Arg Phe Leu Leu Thr Pro Ser Ser Arg Asp Arg Glu Asp Tyr Phe
65               70              75              80


Asp Asn Val Thr Ala Leu Gln Gly Gln Leu Gln Gln Leu Phe His Leu
            85              90              95


His Asp Ser Gly Val Asp Gln Ser Phe Ile Asp Thr Leu Pro Val Phe
            100             105             110


His Tyr Lys Ser Ile Ile Gly Leu Lys Asn Tyr Pro Phe Asp Cys Ala
        115             120             125


Val Cys Leu Cys Glu Phe Glu Thr Glu Asp Lys Leu Arg Leu Leu Pro
    130             135             140


Lys Cys Ser His Ala Phe His Met Asp Cys Ile Asp Thr Trp Leu Leu
145             150             155             160


Ser His Ser Thr Cys Pro Leu Cys Arg Ser Ser Leu Leu Ser Asp Leu
            165             170             175


Ser Ser His Gln Asp Pro Arg Ser Ser Phe Leu Leu Val Leu Glu Ser
            180             185             190


Ala Ser Asp His Ser Ser Arg Glu Ile Gly Gly Asp Arg Asp Ser Ala
        195             200             205


Ala Cys Val Ala Ala Asn Asp Asp Ile Asp Val Ser Ser Ala His Leu
    210             215             220


Gly Leu Val Gly Asn Asn Asp Leu Gly Ser Thr Arg Ile Asp Ser Gly
225             230             235             240


His Gly Asp Gln Tyr Leu Asp Gly Glu Leu Gly Gly Ser Val Gly Lys
            245             250             255


Val Val Pro Phe Ser Val Lys Leu Gly Lys Phe Arg Asn Ile Asp Ile
            260             265             270
```

```
Gly Glu Gly Thr Ser Ser Asn Asn Asn Ile Gly Asn Ser Ser Ser Leu
        275               280               285
```

```
Asp Glu Arg Arg Cys Phe Ser Met Gly Ser Tyr Glu Tyr Ile Met Asp
        290               295               300
```

```
Glu Glu Thr Thr Leu Lys Val His Val Ser Thr Lys Lys Gln Ser Ser
305               310               315               320
```

```
Lys Asn Arg Gly Leu Pro Gly His Arg Thr Ala Met Ser Glu Cys Gly
                325               330               335
```

```
Phe Asp Pro Thr Gly Arg Leu Lys Phe Ser Gly Ser Gly Ser Met Arg
                340               345               350
```

```
Ile Val Glu Glu Ala Ala Glu Lys Asn Val Val Glu Arg Glu Ser Phe
        355               360               365
```

```
Ser Val Ser Lys Ile Trp Leu Arg Gly Lys Lys Glu Lys His Ser Lys
    370               375               380
```

```
Val Gln Gly Lys Glu Asp Ser Ser Leu Val Ser Ser Ser Ser Gly Arg
385               390               395               400
```

```
Ala Phe Ser Phe Arg Leu Ser Asn Gln Arg Asn His Pro Asp Ala Met
                405               410               415
```

```
Ile Glu Ser Gly Cys Glu Glu Asp Asn Gln Lys Cys Glu Asn Ser Glu
                420               425               430
```

```
Ser Leu Glu Thr Lys Thr Pro Ser Phe Ala Arg Arg Thr Met Leu Trp
        435               440               445
```

```
Leu Ala Gly Arg Gln Asn Lys Val Val His Ser Ser Ser Ser Thr Asn
        450               455               460
```

```
Val
465
```

```
<210> 425 <211> 850 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (81)..(626) <223> G2347
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<400> 425
agcccatcct tcaacattgc ttcctaacca gaaatccacc atcatcttcc cacgaataca
60

acttaaagct ttaccagaaa atg gag ggt cag aga aca caa cgc cgg ggt tac
113
```

```
                        Met Glu Gly Gln Arg Thr Gln Arg Arg Gly Tyr
                         1               5                    10

ttg aaa gac aag gct aca gtc tcc aac ctt gtt gaa gaa gaa atg gag
161
Leu Lys Asp Lys Ala Thr Val Ser Asn Leu Val Glu Glu Glu Met Glu
             15                20                25

aat ggc atg gat gga gaa gag gag gat gga gga gac gaa gac aaa agg
209
Asn Gly Met Asp Gly Glu Glu Glu Asp Gly Gly Asp Glu Asp Lys Arg
         30                35                40

aag aag gtg atg gaa aga gtt aga ggt cct agc act gac cgt gtt cca
257
Lys Lys Val Met Glu Arg Val Arg Gly Pro Ser Thr Asp Arg Val Pro
     45                50                55

tcg cga ctg tgc cag gtc gat agg tgc act gtt aat ttg act gag gcc
305
Ser Arg Leu Cys Gln Val Asp Arg Cys Thr Val Asn Leu Thr Glu Ala
60                65                70                75

aag cag tat tac cgc aga cac aga gta tgt gaa gta cat gca aag gca
353
Lys Gln Tyr Tyr Arg Arg His Arg Val Cys Glu Val His Ala Lys Ala
                 80                85        .        90

tct gct gcg act gtt gca ggg gtc agg caa cgc ttt tgt caa caa tgc
401
Ser Ala Ala Thr Val Ala Gly Val Arg Gln Arg Phe Cys Gln Gln Cys
                 95                100               105

agc agg ttt cat gag cta cca gag ttt gat gaa gct aaa aga agc tgc
449
Ser Arg Phe His Glu Leu Pro Glu Phe Asp Glu Ala Lys Arg Ser Cys
         110               115               120

agg agg cgc tta gct gga cac aat gag agg agg agg aag atc tct ggt
497
Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ile Ser Gly
     125               130               135

gac agt ttt gga gaa ggg tca ggc cgg aga ggg ttt agc ggt caa ctg
545
Asp Ser Phe Gly Glu Gly Ser Gly Arg Arg Gly Phe Ser Gly Gln Leu
140               145               150               155

atc cag act caa gaa aga aac agg gta gac agg aaa ctt cct atg acc
593
Ile Gln Thr Gln Glu Arg Asn Arg Val Asp Arg Lys Leu Pro Met Thr
                 160               165               170

aac tca tca ttc aag cga cca cag atc aga taa accctcccgc tctctctctt
646
Asn Ser Ser Phe Lys Arg Pro Gln Ile Arg
                 175               180

ctgtcatcta catatgctct atctacactc ttattagaca aataatggca tctaacaatg
706
```

800

tcaagaaaag ttggtcatgg tattaaatcc tacacggata tataactata aacctctagt
766

cccctctatg ctgtcctgta atgaatatct atccggaaat gtattcgcat agtcttgcgt
826

ctaataatgt ttattgattt tgta
850

<210> 426 <211> 181 <212> PRT <213> Arabidopsis thaliana <400>
426

Met Glu Gly Gln Arg Thr Gln Arg Arg Gly Tyr Leu Lys Asp Lys Ala
1   5   10   15

Thr Val Ser Asn Leu Val Glu Glu Glu Met Glu Asn Gly Met Asp Gly
            20   25   30

Glu Glu Glu Asp Gly Gly Asp Glu Asp Lys Arg Lys Lys Val Met Glu
        35   40   45

Arg Val Arg Gly Pro Ser Thr Asp Arg Val Pro Ser Arg Leu Cys Gln
    50   55   60

Val Asp Arg Cys Thr Val Asn Leu Thr Glu Ala Lys Gln Tyr Tyr Arg
65   70   75   80

Arg His Arg Val Cys Glu Val His Ala Lys Ala Ser Ala Ala Thr Val
                85   90   95

Ala Gly Val Arg Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Glu
            100   105   110

Leu Pro Glu Phe Asp Glu Ala Lys Arg Ser Cys Arg Arg Arg Leu Ala
            115   120   125

Gly His Asn Glu Arg Arg Arg Lys Ile Ser Gly Asp Ser Phe Gly Glu
    130   135   140

Gly Ser Gly Arg Arg Gly Phe Ser Gly Gln Leu Ile Gln Thr Gln Glu
145   150   155   160

Arg Asn Arg Val Asp Arg Lys Leu Pro Met Thr Asn Ser Ser Phe Lys
                165   170   175

Arg Pro Gln Ile Arg
            180

<210> 427 <211> 762 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(630) <223> G2421

<400> 427
atg gag ggt tcg tcc aaa ggg ttg agg aaa ggt gca tgg act gct gaa
48
Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu
1   5   10   15

gaa gat agt ctc ttg agg cag tgt att ggt aag tat gga gaa ggc aaa
96
Glu Asp Ser Leu Leu Arg Gln Cys Ile Gly Lys Tyr Gly Glu Gly Lys
            20   25   30

tgg cat caa gtt cct tta aga gct ggg cta aat cgg tgc agg aaa agt
144
Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
        35   40   45

tgt aga cta aga tgg tta aac tat ttg aag cca agt atc aag aga gga
192
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
    50   55   60

aaa ttt agt tct gat gaa gtt gat ctt ctt ctt cgt ctt cat aag ctt
240
Lys Phe Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
65   70   75   80

cta gga aat agg tgg tcc ttg att gct ggt cga tta cct ggt cgg acc
288
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
                85   90   95

gct aat gat gtc aag aac tac tgg aac acc cat ctg agt aag aag cat
336
Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
            100   105   110

gaa ccg tgt tgt aaa act aag ata aaa agg ata aat att ata acc cct
384
Glu Pro Cys Cys Lys Thr Lys Ile Lys Arg Ile Asn Ile Ile Thr Pro
        115   120   125

cct aat aca ccg gcc caa aaa gtt tgt gaa aat agt atc aca tgt aac
432
Pro Asn Thr Pro Ala Gln Lys Val Cys Glu Asn Ser Ile Thr Cys Asn
    130   135   140

aaa gat gat gag aaa gat gat ttt gtg gat aat ttt atg gtt gga gat
480
Lys Asp Asp Glu Lys Asp Asp Phe Val Asp Asn Phe Met Val Gly Asp
145   150   155   160

aat ata tgg ttg gag cgt ttg cta gac gag ggc caa gag gta gat gtg
528
Asn Ile Trp Leu Glu Arg Leu Leu Asp Glu Gly Gln Glu Val Asp Val
                165   170   175

ctg gtt aca gaa gcg gcg gca aca gaa aag gag ggc act ttg gcg ttt
576

802

```
Leu Val Thr Glu Ala Ala Ala Thr Glu Lys Glu Gly Thr Leu Ala Phe
          180                 185                 190

gac gtt gag caa ctt tgg aat ttg ttc gat gga gag act gtg atc ttt
624
Asp Val Glu Gln Leu Trp Asn Leu Phe Asp Gly Glu Thr Val Ile Phe
          195                 200                 205

gat tag tgtttataaa cgtttgtgtt ctcttgtttg tgaggtttct ctatttaatt
680
Asp


tagtatctat tttctaaatt aactaatatc ttatagtatt ttaggcaaac cttatgtttc
740

cgtttctgtg cggccgctct ag
762


<210>  428 <211>  209 <212>  PRT <213>  Arabidopsis thaliana  <400>
428

Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu
1               5                  10                  15


Glu Asp Ser Leu Leu Arg Gln Cys Ile Gly Lys Tyr Gly Glu Gly Lys
          20                  25                  30


Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
          35                  40                  45


Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
     50                  55                  60


Lys Phe Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
65                  70                  75                  80


Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
               85                  90                  95


Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
          100                 105                 110


Glu Pro Cys Cys Lys Thr Lys Ile Lys Arg Ile Asn Ile Ile Thr Pro
          115                 120                 125


Pro Asn Thr Pro Ala Gln Lys Val Cys Glu Asn Ser Ile Thr Cys Asn
          130                 135                 140


Lys Asp Asp Glu Lys Asp Asp Phe Val Asp Asn Phe Met Val Gly Asp
145                 150                 155                 160
```

```
Asn Ile Trp Leu Glu Arg Leu Leu Asp Glu Gly Gln Glu Val Asp Val
              165                 170                 175


Leu Val Thr Glu Ala Ala Ala Thr Glu Lys Glu Gly Thr Leu Ala Phe
              180                 185                 190


Asp Val Glu Gln Leu Trp Asn Leu Phe Asp Gly Glu Thr Val Ile Phe
              195                 200                 205


Asp
```

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<210>   429 <211>   741 <212>   DNA <213>   Arabidopsis thaliana  <220>
<221>   CDS <222>   (1)..(741) <223>   G2422


<400>   429
atg ggc gaa tca ccc aaa ggg ttg aga aaa ggt aca tgg act act gaa
48
Met Gly Glu Ser Pro Lys Gly Leu Arg Lys Gly Thr Trp Thr Thr Glu
1               5                   10                  15


gaa gat att ctc ttg agg caa tgc att gat aag tat gga gaa ggc aaa
96
Glu Asp Ile Leu Leu Arg Gln Cys Ile Asp Lys Tyr Gly Glu Gly Lys
                20                  25                  30


tgg cat cga gtt cct tta aga act ggt ctc aat cgg tgc cga aag agt
144
Trp His Arg Val Pro Leu Arg Thr Gly Leu Asn Arg Cys Arg Lys Ser
            35                  40                  45


tgt aga ctt aga tgg ttg aat tat ttg aag cca agt att aag aga gga
192
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
        50                  55                  60


aaa ctc tgc tcc gat gaa gtt gat ctt gtt ctt cgc ctt cat aaa ctt
240
Lys Leu Cys Ser Asp Glu Val Asp Leu Val Leu Arg Leu His Lys Leu
65                  70                  75                  80


cta gga aat agg tgg tcc ttg atc gct ggt aga ttg cct ggt cgg act
288
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
                85                  90                  95


gct aat gat gtc aag aat tac tgg aac act cat ttg agt aag aag cac
336
Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
            100                 105                 110


gat gaa cga tgc tgt aag acg aag atg ata aac aaa aac att act tct
384
Asp Glu Arg Cys Cys Lys Thr Lys Met Ile Asn Lys Asn Ile Thr Ser
        115                 120                 125
```

804

cat cct act tca tcg gcc caa aaa atc gat gtt tta aag cct cgg cct
432
His Pro Thr Ser Ser Ala Gln Lys Ile Asp Val Leu Lys Pro Arg Pro
    130   135   140

cga tcc ttc tcc gat aaa aat agt tgc aac gat gtc aat atc ttg cca
480
Arg Ser Phe Ser Asp Lys Asn Ser Cys Asn Asp Val Asn Ile Leu Pro
145   150   155   160

aaa gtt gac gtt gtt cct tta cat ctt gga ctc aac aac aat tat gtt
528
Lys Val Asp Val Val Pro Leu His Leu Gly Leu Asn Asn Asn Tyr Val
            165   170   175

tgt gaa agt agt att aca tgt aac aaa gat gag caa aaa gat aag ctt
576
Cys Glu Ser Ser Ile Thr Cys Asn Lys Asp Glu Gln Lys Asp Lys Leu
        180   185   190

att aat att aat cta ttg gat gga gat aat atg tgg tgg gaa agt tta
624
Ile Asn Ile Asn Leu Leu Asp Gly Asp Asn Met Trp Trp Glu Ser Leu
        195   200   205

ctg gag gca gat gtg ttg ggt cca gaa gct acg gaa aca gca aag ggt
672
Leu Glu Ala Asp Val Leu Gly Pro Glu Ala Thr Glu Thr Ala Lys Gly
    210   215   220

gtg acc tta ccg ctt gac ttt gag caa att tgg gct cgg ttt gat gaa
720
Val Thr Leu Pro Leu Asp Phe Glu Gln Ile Trp Ala Arg Phe Asp Glu
225   230   235   240

gag act tta gaa ctg aat tag
741
Glu Thr Leu Glu Leu Asn
                245

<210> 430 <211> 246 <212> PRT <213> Arabidopsis thaliana <400>
430

Met Gly Glu Ser Pro Lys Gly Leu Arg Lys Gly Thr Trp Thr Thr Glu
1   5   10   15

Glu Asp Ile Leu Leu Arg Gln Cys Ile Asp Lys Tyr Gly Glu Gly Lys
            20   25   30

Trp His Arg Val Pro Leu Arg Thr Gly Leu Asn Arg Cys Arg Lys Ser
        35   40   45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
    50   55   60

```
Lys Leu Cys Ser Asp Glu Val Asp Leu Val Leu Arg Leu His Lys Leu
65              70              75              80


Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
                85              90              95


Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
            100             105             110


Asp Glu Arg Cys Cys Lys Thr Lys Met Ile Asn Lys Asn Ile Thr Ser
        115             120             125


His Pro Thr Ser Ser Ala Gln Lys Ile Asp Val Leu Lys Pro Arg Pro
    130             135             140


Arg Ser Phe Ser Asp Lys Asn Ser Cys Asn Asp Val Asn Ile Leu Pro
145             150             155             160


Lys Val Asp Val Val Pro Leu His Leu Gly Leu Asn Asn Asn Tyr Val
            165             170             175


Cys Glu Ser Ser Ile Thr Cys Asn Lys Asp Glu Gln Lys Asp Lys Leu
            180             185             190


Ile Asn Ile Asn Leu Leu Asp Gly Asp Asn Met Trp Trp Glu Ser Leu
        195             200             205


Leu Glu Ala Asp Val Leu Gly Pro Glu Ala Thr Glu Thr Ala Lys Gly
    210             215             220


Val Thr Leu Pro Leu Asp Phe Glu Gln Ile Trp Ala Arg Phe Asp Glu
225             230             235             240


Glu Thr Leu Glu Leu Asn
                245
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<210>  431 <211>  972 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (1)..(972) <223>  G2423

 <400>  431
atg gat gaa aaa gga aga agc ttg aag aac aac aac atg gaa gac gag
48
Met Asp Glu Lys Gly Arg Ser Leu Lys Asn Asn Asn Met Glu Asp Glu
1               5               10              15


atg gac cta aag aga ggt ccg tgg act gct gaa gaa gat ttt aag ctc
96
Met Asp Leu Lys Arg Gly Pro Trp Thr Ala Glu Glu Asp Phe Lys Leu
                20              25              30
```

atg aat tac att gct act aat gga gaa ggt cgc tgg aac tct ctt tct
144
Met Asn Tyr Ile Ala Thr Asn Gly Glu Gly Arg Trp Asn Ser Leu Ser
        35   40   45

cgt tgc gcc ggc ctc caa cgc acc ggt aaa agc tgt aga cta agg tgg
192
Arg Cys Ala Gly Leu Gln Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp
    50   55   60

tta aac tat ctc cgc cct gac gtc cgc cgt gga aac att aca ctt gaa
240
Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu Glu
65   70   75   80

gaa caa ctc ttg atc ctc gaa ctt cat tcc cgt tgg gga aat aga tgg
288
Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn Arg Trp
            85   90   95

tca aaa atc gca caa tat tta ccg gga aga acg gac aac gag atc aag
336
Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
            100   105   110

aac tac tgg agg acg cgg gtg caa aag cat gcg aaa cag ttg aaa tgt
384
Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Lys Cys
        115   120   125

gat gtg aat agc caa caa ttc aaa gac aca atg aag tac ttg tgg atg
432
Asp Val Asn Ser Gln Gln Phe Lys Asp Thr Met Lys Tyr Leu Trp Met
    130   135   140

cct cga cta gtc gag agg att cag tca gcc tcg gcc tca tcc gca gca
480
Pro Arg Leu Val Glu Arg Ile Gln Ser Ala Ser Ala Ser Ser Ala Ala
145   150   155   160

gca gcc acc acc aca acc acc acc acc aca gga tca gcc ggc acg tca
528
Ala Ala Thr Thr Thr Thr Thr Thr Thr Thr Gly Ser Ala Gly Thr Ser
            165   170   175

tct tgc atc aca acc tct aac aat caa ttc atg aat tac gac tac aac
576
Ser Cys Ile Thr Thr Ser Asn Asn Gln Phe Met Asn Tyr Asp Tyr Asn
            180   185   190

aac aac aac atg gga caa cag ttt ggt gta atg agc aac aat gat tat
624
Asn Asn Asn Met Gly Gln Gln Phe Gly Val Met Ser Asn Asn Asp Tyr
        195   200   205

atc acg cct gaa aat tcc agc gtg gca gtg tct ccg gcg tca gac tta
672
Ile Thr Pro Glu Asn Ser Ser Val Ala Val Ser Pro Ala Ser Asp Leu
    210   215   220

807

```
acg gag tac tac agc gct cca aac cct aac ccg gaa tac tat tcg ggt
720
Thr Glu Tyr Tyr Ser Ala Pro Asn Pro Asn Pro Glu Tyr Tyr Ser Gly
225                 230                 235                 240

caa atg ggg aat agt tat tat cca gat cag aat tta gtg agt tca caa
768
Gln Met Gly Asn Ser Tyr Tyr Pro Asp Gln Asn Leu Val Ser Ser Gln
                245                 250                 255

tta tta ccg gat aat tat ttc gac tat agt gga tta tta gac gaa gat
816
Leu Leu Pro Asp Asn Tyr Phe Asp Tyr Ser Gly Leu Leu Asp Glu Asp
                260                 265                 270

cta acg gct atg caa gag cag agt aac ctc agc tgg ttt gaa aac att
864
Leu Thr Ala Met Gln Glu Gln Ser Asn Leu Ser Trp Phe Glu Asn Ile
            275                 280                 285

aat ggt gct gct tct tct tca gac agt tta tgg aac att gga gaa act
912
Asn Gly Ala Ala Ser Ser Ser Asp Ser Leu Trp Asn Ile Gly Glu Thr
        290                 295                 300

gat gaa gaa ttc tgg ttc tta cag cag caa caa cag ttc aac aat aat
960
Asp Glu Glu Phe Trp Phe Leu Gln Gln Gln Gln Gln Phe Asn Asn Asn
305                 310                 315                 320

ggt agc ttc tga
972
Gly Ser Phe
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<210>  432 <211>  323 <212>  PRT <213>  Arabidopsis thaliana  <400>
432

Met Asp Glu Lys Gly Arg Ser Leu Lys Asn Asn Asn Met Glu Asp Glu
1               5               10                  15

Met Asp Leu Lys Arg Gly Pro Trp Thr Ala Glu Glu Asp Phe Lys Leu
            20                  25                  30

Met Asn Tyr Ile Ala Thr Asn Gly Glu Gly Arg Trp Asn Ser Leu Ser
            35                  40                  45

Arg Cys Ala Gly Leu Gln Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp
        50                  55                  60

Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu Glu
65                  70                  75                  80

Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn Arg Trp
                85                  90                  95
```

Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
        100   105   110

Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Lys Cys
        115   120   125

Asp Val Asn Ser Gln Gln Phe Lys Asp Thr Met Lys Tyr Leu Trp Met
    130   135   140

Pro Arg Leu Val Glu Arg Ile Gln Ser Ala Ser Ala Ser Ser Ala Ala
145   150   155   160

Ala Ala Thr Thr Thr Thr Thr Thr Thr Thr Gly Ser Ala Gly Thr Ser
            165   170   175

Ser Cys Ile Thr Thr Ser Asn Asn Gln Phe Met Asn Tyr Asp Tyr Asn
            180   185   190

Asn Asn Asn Met Gly Gln Gln Phe Gly Val Met Ser Asn Asn Asp Tyr
        195   200   205

Ile Thr Pro Glu Asn Ser Ser Val Ala Val Ser Pro Ala Ser Asp Leu
    210   215   220

Thr Glu Tyr Tyr Ser Ala Pro Asn Pro Asn Pro Glu Tyr Tyr Ser Gly
225   230   235   240

Gln Met Gly Asn Ser Tyr Tyr Pro Asp Gln Asn Leu Val Ser Ser Gln
            245   250   255

Leu Leu Pro Asp Asn Tyr Phe Asp Tyr Ser Gly Leu Leu Asp Glu Asp
            260   265   270

Leu Thr Ala Met Gln Glu Gln Ser Asn Leu Ser Trp Phe Glu Asn Ile
        275   280   285

Asn Gly Ala Ala Ser Ser Ser Asp Ser Leu Trp Asn Ile Gly Glu Thr
    290   295   300

Asp Glu Glu Phe Trp Phe Leu Gln Gln Gln Gln Gln Phe Asn Asn Asn
305   310   315   320

Gly Ser Phe

<210> 433 <211> 849 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(849) <223> G2467

<400> 433
atg gac ccg tcg tca agc tcc aga gca cgg tca atg cca ccg ccg gtg
48
Met Asp Pro Ser Ser Ser Ser Arg Ala Arg Ser Met Pro Pro Pro Val
1   5   10   15

cct atg gag gga ttg cag gaa gca ggg cct tct cct ttt cta aca aag
96
Pro Met Glu Gly Leu Gln Glu Ala Gly Pro Ser Pro Phe Leu Thr Lys
                20   25   30

acg ttc gag atg gtt ggt gat cca aac aca aac cac att gtg tct tgg
144
Thr Phe Glu Met Val Gly Asp Pro Asn Thr Asn His Ile Val Ser Trp
            35   40   45

aac agg gga ggc atc agt ttt gtc gtg tgg gat cca cat tcc ttc tcg
192
Asn Arg Gly Gly Ile Ser Phe Val Val Trp Asp Pro His Ser Phe Ser
        50   55   -   60

gcc act att ctg cct cta tac ttc aag cac aac aac ttc tcc agc ttt
240
Ala Thr Ile Leu Pro Leu Tyr Phe Lys His Asn Asn Phe Ser Ser Phe
65   70   75   80

gtc aga caa ctt aac act tat gga ttc aga aag atc gag gca gag aga
288
Val Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala Glu Arg
                85   90   95

tgg gag ttt atg aat gaa ggt ttc ttg atg ggt cag agg gac ctt ctc
336
Trp Glu Phe Met Asn Glu Gly Phe Leu Met Gly Gln Arg Asp Leu Leu
            100   105   110

aaa agc atc aag cga cga acc tcc tct tct tcc cct cct tcg ctt aac
384
Lys Ser Ile Lys Arg Arg Thr Ser Ser Ser Ser Pro Pro Ser Leu Asn
        115   120   125

tac tct cag tct cag ccc gag gct cat gac cca ggc gtc gag ctt ccg
432
Tyr Ser Gln Ser Gln Pro Glu Ala His Asp Pro Gly Val Glu Leu Pro
        130   135   140

cag ctc cga gaa gag agg cat gtc cta atg atg gag atc tcg acg ctc
480
Gln Leu Arg Glu Glu Arg His Val Leu Met Met Glu Ile Ser Thr Leu
145   150   155   160

aga cag gag gag caa aga gcg aga ggc tac gtc caa gcc atg gag cag
528
Arg Gln Glu Glu Gln Arg Ala Arg Gly Tyr Val Gln Ala Met Glu Gln
                165   170   175

810

agg att aat gga gca gag aag aaa cag agg cat atg atg tcc ttc ttg
576
Arg Ile Asn Gly Ala Glu Lys Lys Gln Arg His Met Met Ser Phe Leu
          180   185   190

agg cgt gcg gtg gag aat cct tcc ctt ctg cag cag att ttc gag cag
624
Arg Arg Ala Val Glu Asn Pro Ser Leu Leu Gln Gln Ile Phe Glu Gln
          195   200   205

aag aga gac cga gag gag gcc gcg atg att gat cag gct ggc ttg atc
672
Lys Arg Asp Arg Glu Glu Ala Ala Met Ile Asp Gln Ala Gly Leu Ile
          210   215   220

aaa atg gaa gag gtg gag cac ctg tcg gag ctg gag gct ctg gcg ctt
720
Lys Met Glu Glu Val Glu His Leu Ser Glu Leu Glu Ala Leu Ala Leu
225   230   235   240

gag atg caa gga tat gga cgg caa cgg act gat ggt gtg gag agg gag
768
Glu Met Gln Gly Tyr Gly Arg Gln Arg Thr Asp Gly Val Glu Arg Glu
              245   250   255

ctt gac gac ggg ttt tgg gaa gag tta ctc atg aac aat gaa aac tcc
816
Leu Asp Asp Gly Phe Trp Glu Glu Leu Leu Met Asn Asn Glu Asn Ser
          260   265   270

gac gaa gaa gag gcg aat gtg aag caa gat tag
849
Asp Glu Glu Glu Ala Asn Val Lys Gln Asp
          275   280

<210> 434 <211> 282 <212> PRT <213> Arabidopsis thaliana <400>
434

Met Asp Pro Ser Ser Ser Ser Arg Ala Arg Ser Met Pro Pro Pro Val
1   5   10   15

Pro Met Glu Gly Leu Gln Glu Ala Gly Pro Ser Pro Phe Leu Thr Lys
              20   25   30

Thr Phe Glu Met Val Gly Asp Pro Asn Thr Asn His Ile Val Ser Trp
          35   40   45

Asn Arg Gly Gly Ile Ser Phe Val Val Trp Asp Pro His Ser Phe Ser
    50   55   60

Ala Thr Ile Leu Pro Leu Tyr Phe Lys His Asn Asn Phe Ser Ser Phe
65   70   75   80

Val Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala Glu Arg
                  85   90   95

```
Trp Glu Phe Met Asn Glu Gly Phe Leu Met Gly Gln Arg Asp Leu Leu
            100                 105                 110

Lys Ser Ile Lys Arg Arg Thr Ser Ser Ser Ser Pro Pro Ser Leu Asn
            115                 120                 125

Tyr Ser Gln Ser Gln Pro Glu Ala His Asp Pro Gly Val Glu Leu Pro
    130                 135                 140

Gln Leu Arg Glu Glu Arg His Val Leu Met Met Glu Ile Ser Thr Leu
145                 150                 155                 160

Arg Gln Glu Glu Gln Arg Ala Arg Gly Tyr Val Gln Ala Met Glu Gln
                165                 170                 175

Arg Ile Asn Gly Ala Glu Lys Lys Gln Arg His Met Met Ser Phe Leu
            180                 185                 190

Arg Arg Ala Val Glu Asn Pro Ser Leu Leu Gln Gln Ile Phe Glu Gln
            195                 200                 205

Lys Arg Asp Arg Glu Glu Ala Ala Met Ile Asp Gln Ala Gly Leu Ile
    210                 215                 220

Lys Met Glu Glu Val Glu His Leu Ser Glu Leu Glu Ala Leu Ala Leu
225                 230                 235                 240

Glu Met Gln Gly Tyr Gly Arg Gln Arg Thr Asp Gly Val Glu Arg Glu
                245                 250                 255

Leu Asp Asp Gly Phe Trp Glu Glu Leu Leu Met Asn Asn Glu Asn Ser
            260                 265                 270

Asp Glu Glu Glu Ala Asn Val Lys Gln Asp
    275                 280
```

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<210>  435 <211>  690 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (112)..(690) <223>  G2514

 <400>  435
aaaacttctt catcttcttt aattagtttg ccacctcgca cgtgtgacaa atccttcttc
60

gccacgtgtg aaaacccttc tccggcttgc tactaatata cgactaatag t atg aat
117
                                                          Met Asn
                                                            1
```

agt tca atg gct tct gcc ggc tta ggt agc cgg aga aag gat ccg gtg
165
Ser Ser Met Ala Ser Ala Gly Leu Gly Ser Arg Arg Lys Asp Pro Val
        5   10   15

tac aga gga atc cgg tgc cga agt ggg aaa tgg gtc tcc gag att cgt
213
Tyr Arg Gly Ile Arg Cys Arg Ser Gly Lys Trp Val Ser Glu Ile Arg
    20   25   30

gag ccg agg aaa acc acg aga atc tgg ctt gga act tac ccc atg gca
261
Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Met Ala
35   40   45   50

gag atg gca gca gcc gcc tat gat gtg gct gct atg gct ctt aaa gga
309
Glu Met Ala Ala Ala Ala Tyr Asp Val Ala Ala Met Ala Leu Lys Gly
                55   60   65

aga gaa gct gtc ttg aac ttc cct gga tcc gtc ggg tca tac ccg gtt
357
Arg Glu Ala Val Leu Asn Phe Pro Gly Ser Val Gly Ser Tyr Pro Val
            70   75   80

cct gaa tca aca tcc gca gca gat ata cga gcc gct gcg gca gcc gca
405
Pro Glu Ser Thr Ser Ala Ala Asp Ile Arg Ala Ala Ala Ala Ala Ala
            85   90   95

gca gca atg aag gga tgt gag gaa ggg gag gag gag aaa aag gca aag
453
Ala Ala Met Lys Gly Cys Glu Glu Gly Glu Glu Glu Lys Lys Ala Lys
        100   105   110

gag aag aag agt agt agt tcg aag tcg aga gcg cgt gag tgc cac gta
501
Glu Lys Lys Ser Ser Ser Ser Lys Ser Arg Ala Arg Glu Cys His Val
115   120   125   130

gat aat gat gtt gga tct tcg tcg tgg tgt ggg aca gag ttc atg gac
549
Asp Asn Asp Val Gly Ser Ser Ser Trp Cys Gly Thr Glu Phe Met Asp
                135   140   145

gaa gaa gaa gtc ttg aat atg cct aat ctg ctg gct aat atg gca gaa
597
Glu Glu Glu Val Leu Asn Met Pro Asn Leu Leu Ala Asn Met Ala Glu
            150   155   160

ggg atg atg gtt gcg ccg ccg tcg tgg atg ggt tct cgg ccg tcg gat
645
Gly Met Met Val Ala Pro Pro Ser Trp Met Gly Ser Arg Pro Ser Asp
        165   170   175

gac tct ccg gag aat tca aat gat gag gac ttg tgg ggc tat tga
690
Asp Ser Pro Glu Asn Ser Asn Asp Glu Asp Leu Trp Gly Tyr
        180   185   190

813

<210> 436 <211> 192 <212> PRT <213> Arabidopsis thaliana <400>
436

Met Asn Ser Ser Met Ala Ser Ala Gly Leu Gly Ser Arg Arg Lys Asp
1   5   10   15

Pro Val Tyr Arg Gly Ile Arg Cys Arg Ser Gly Lys Trp Val Ser Glu
            20   25   30

Ile Arg Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro
        35   40   45

Met Ala Glu Met Ala Ala Ala Ala Tyr Asp Val Ala Ala Met Ala Leu
.   50   55   60

Lys Gly Arg Glu Ala Val Leu Asn Phe Pro Gly Ser Val Gly Ser Tyr
65   70   75   80

Pro Val Pro Glu Ser Thr Ser Ala Ala Asp Ile Arg Ala Ala Ala Ala
            85   90   95

Ala Ala Ala Ala Met Lys Gly Cys Glu Glu Gly Glu Glu Glu Lys Lys
            100   105   110

Ala Lys Glu Lys Lys Ser Ser Ser Ser Lys Ser Arg Ala Arg Glu Cys
        115   120   125

His Val Asp Asn Asp Val Gly Ser Ser Ser Trp Cys Gly Thr Glu Phe
    130   135   140

Met Asp Glu Glu Glu Val Leu Asn Met Pro Asn Leu Leu Ala Asn Met
145   150   155   160

Ala Glu Gly Met Met Val Ala Pro Pro Ser Trp Met Gly Ser Arg Pro
                165   170   175

Ser Asp Asp Ser Pro Glu Asn Ser Asn Asp Glu Asp Leu Trp Gly Tyr
            180   185   190

<210> 437 <211> 994 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(711) <223> G2547

<400> 437
atg gac caa gaa caa aca cca cat agc cca acc cgc cat agt cgc tca
48
Met Asp Gln Glu Gln Thr Pro His Ser Pro Thr Arg His Ser Arg Ser
1   5   10   15

```
ccc cca tcc tcc gcc tcc ggt tcc acc tca gca gaa ccg gtt cgg tcc
96
Pro Pro Ser Ser Ala Ser Gly Ser Thr Ser Ala Glu Pro Val Arg Ser
            20              25              30


cga tgg tca cct aaa ccg gaa caa ata ctc ata ctt gag tcg atc ttc
144
Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu Glu Ser Ile Phe
            35              40              45


cac agt ggt atg gtt aac cct ccc aaa gaa gag acg gta agg ata aga
192
His Ser Gly Met Val Asn Pro Pro Lys Glu Glu Thr Val Arg Ile Arg
    50              55              60


aag atg ctc gag aaa ttt ggc gcg gtg gga gat gca aat gtc ttc tat
240
Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala Asn Val Phe Tyr
65              70              75              80


tgg ttt caa aac cgg cgg tca agg tcc cgt cgg aga cag cga cag cta
288
Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg Gln Arg Gln Leu
                85              90              95


cag gct gca gct gca gca gcg gac gca acc acc aac act tct agc tct
336
Gln Ala Ala Ala Ala Ala Ala Asp Ala Thr Thr Asn Thr Ser Ser Ser
            100             105             110


tct tct tct tat ggt ggt gga tgt gat aat caa agc aat agt ggc atg
384
Ser Ser Ser Tyr Gly Gly Gly Cys Asp Asn Gln Ser Asn Ser Gly Met
            115             120             125


gag aat ctc tta aca atg tct ggc caa atg agt tac cat gaa gct act
432
Glu Asn Leu Leu Thr Met Ser Gly Gln Met Ser Tyr His Glu Ala Thr
    130             135             140


cat cat cat tat caa aat cat agc tca aat gtc aca tcg att ttg tgc
480
His His His Tyr Gln Asn His Ser Ser Asn Val Thr Ser Ile Leu Cys
145             150             155             160


cca tct gat caa aac tcc aat ttt caa tac caa caa ggg gct ata acg
528
Pro Ser Asp Gln Asn Ser Asn Phe Gln Tyr Gln Gln Gly Ala Ile Thr
                165             170             175


gtg ttt ata aac gga gtt ccg aca gaa gtg acg aga gga gga ata gac
576
Val Phe Ile Asn Gly Val Pro Thr Glu Val Thr Arg Gly Gly Ile Asp
            180             185             190


atg aaa gca acg ttt gga gaa gat ttg gtt ttg gtg cat tcc tca ggt
624
Met Lys Ala Thr Phe Gly Glu Asp Leu Val Leu Val His Ser Ser Gly
        195             200             205
```

gtt cct ctt cct act gat gag ttt ggt ttt ttg atg cat agc tta caa
672
Val Pro Leu Pro Thr Asp Glu Phe Gly Phe Leu Met His Ser Leu Gln
    210   215   220

cat ggt gaa gct tat ttc ctg gtt cca aga cag aca tga actggctttta
721
His Gly Glu Ala Tyr Phe Leu Val Pro Arg Gln Thr
225   230   235

ctcgtatgtg tggtgatgca acagatgtct tgtttttcta ccttggactt tattgcaacg
781

gtccttccat tttttctttt cttttcgagt ctatcgtata atcaaagttt cttctattgg
841

tttttttta aaaatttta ttttgcaatt tattttataa agatgaagtc aaaagctctt
901

gtacgacgaa gatatctagg ttgtatcaat ttagttattt agatgtaaaa tacgtatgta
961

taattgattt gcaataaaat ctctgtctag gga
994   —

<210> 438 <211> 236 <212> PRT <213> Arabidopsis thaliana <400>
438

Met Asp Gln Glu Gln Thr Pro His Ser Pro Thr Arg His Ser Arg Ser
1   5   10   15

Pro Pro Ser Ser Ala Ser Gly Ser Thr Ser Ala Glu Pro Val Arg Ser
            20   25   30

Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu Glu Ser Ile Phe
        35   40   45

His Ser Gly Met Val Asn Pro Pro Lys Glu Glu Thr Val Arg Ile Arg
    50   55   60

Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala Asn Val Phe Tyr
65   70   75   80

Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg Gln Arg Gln Leu
            85   90   95

Gln Ala Ala Ala Ala Ala Ala Asp Ala Thr Thr Asn Thr Ser Ser Ser
            100   105   110

Ser Ser Ser Tyr Gly Gly Gly Cys Asp Asn Gln Ser Asn Ser Gly Met
        115   120   125

816

```
Glu Asn Leu Leu Thr Met Ser Gly Gln Met Ser Tyr His Glu Ala Thr
    130             135             140

His His His Tyr Gln Asn His Ser Ser Asn Val Thr Ser Ile Leu Cys
145             150             155             160

Pro Ser Asp Gln Asn Ser Asn Phe Gln Tyr Gln Gln Gly Ala Ile Thr
            165             170             175

Val Phe Ile Asn Gly Val Pro Thr Glu Val Thr Arg Gly Gly Ile Asp
            180             185             190

Met Lys Ala Thr Phe Gly Glu Asp Leu Val Leu Val His Ser Ser Gly
        195             200             205

Val Pro Leu Pro Thr Asp Glu Phe Gly Phe Leu Met His Ser Leu Gln
    210             215             220

His Gly Glu Ala Tyr Phe Leu Val Pro Arg Gln Thr
225             230             235
```

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<210>  439 <211>  1020 <212>  DNA <213>  Arabidopsis thaliana  <220>
<221>  CDS <222>  (1)..(1020) <223>  G2657
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 <400>  439
atg gat cca gtt caa tct cat gga tca caa agc tct ctt cct cct cct
48
Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro
1               5               10              15

ttc cat gct aga gat ttc caa tta cat ctt caa caa caa caa caa cat
96
Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Gln His
            20              25              30

caa caa caa cat caa caa caa caa caa caa cag ttc ttt ctc cac cat
144
Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Phe Phe Leu His His
        35              40              45

cat cag caa cca caa aga aac ctt gat caa gat cac gag cag caa gga
192
His Gln Gln Pro Gln Arg Asn Leu Asp Gln Asp His Glu Gln Gln Gly
    50              55              60

ggg tca ata ttg aat aga tct atc aag atg gat cgc gaa gag aca agc
240
Gly Ser Ile Leu Asn Arg Ser Ile Lys Met Asp Arg Glu Glu Thr Ser
65              70              75              80

gat aac atg gac aac atc gct aat acc aac agc ggt agc gaa ggt aaa
288
Asp Asn Met Asp Asn Ile Ala Asn Thr Asn Ser Gly Ser Glu Gly Lys
            85              90              95
```

817

```
gag atg agt tta cac gga gga gaa gga gga agc ggt ggt gga gga agt
336
Glu Met Ser Leu His Gly Gly Glu Gly Gly Ser Gly Gly Gly Gly Ser
        100               105               110

gga gaa cag atg aca aga agg cca aga gga aga cca gca gga tcc aag
384
Gly Glu Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys
        115               120               125

aac aaa cct aaa gct cca ata atc ata aca aga gac agc gca aac gcg
432
Asn Lys Pro Lys Ala Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala
    130               135               140

ctt cga act cac gtc atg gag ata gga gac gga tgt gac ata gtt gac
480
Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp Ile Val Asp
145               150               155               160

tgt atg gct acg ttc gct aga cgc cgc caa aga ggc gtt tgc gtt atg
528
Cys Met Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Met
            165               170               175

agc ggt aca gga agc gtt act aac gtc act ata cgt cag cct gga tcg
576
Ser Gly Thr Gly Ser Val Thr Asn Val Thr Ile Arg Gln Pro Gly Ser
            180               185               190

cca cct ggc tcg gtg gtt agc ctt cac ggc cgg ttt gaa atc ctc tct
624
Pro Pro Gly Ser Val Val Ser Leu His Gly Arg Phe Glu Ile Leu Ser
        195               200               205

ctt tcg gga tct ttc ttg cct ccg cct gcg ccg cct gca gcc acc gga
672
Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala Thr Gly
    210               215               220

cta agc gtt tac cta gcc gga gga caa ggg cag gtc gtt gga ggt agt
720
Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser
225               230               235               240

gtg gtg gga cct ttg ttg tgt tcg ggt cct gtg gtg gtt atg gcg gct
768
Val Val Gly Pro Leu Leu Cys Ser Gly Pro Val Val Val Met Ala Ala
            245               250               255

tct ttt agc aat gcg gcg tac gaa agg ctg cct ttg gaa gaa gat gag
816
Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu
            260               265               270

atg cag acg cca gtt caa gga ggc ggt gga gga gga gga ggt ggt ggt
864
Met Gln Thr Pro Val Gln Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
        275               280               285
```

818

gga atg gga tct ccc ccg atg atg gga`cag caa caa gct atg gca gct
912
Gly Met Gly Ser Pro Pro Met Met Gly Gln Gln Gln Ala Met Ala Ala
    290   295   300

atg gcg gcg gct caa gga cta cca ccg aat ctt ctt ggt tcg gtt cag
960
Met Ala Ala Ala Gln Gly Leu Pro Pro Asn Leu Leu Gly Ser Val Gln
305   310   315   320

ttg cca ccg cca caa cag aat gat cag cag tat tgg tct acg ggt cgg
1008
Leu Pro Pro Pro Gln Gln Asn Asp Gln Gln Tyr Trp Ser Thr Gly Arg
                325   330   335

cca ccg tat tga
1020
Pro Pro Tyr

<210> 440 <211> 339 <212> PRT <213> Arabidopsis thaliana <400>
440

Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro
1   5   10   15

Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Gln His
        20   25   30

Gln Gln Gln His·Gln Gln Gln Gln Gln Gln Gln Phe Phe Leu His His
    35   40   45

His Gln Gln Pro Gln Arg Asn Leu Asp Gln Asp His Glu Gln Gln Gly
    50   55   60

Gly Ser Ile Leu Asn Arg Ser Ile Lys Met Asp Arg Glu Glu Thr Ser
65   70   75   80

Asp Asn Met Asp Asn Ile Ala Asn Thr Asn Ser Gly Ser Glu Gly Lys
                85   90   95

Glu Met Ser Leu His Gly Gly Glu Gly Gly Ser Gly Gly Gly Gly Ser
            100   105   110

Gly Glu Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys
            115   120   125

Asn Lys Pro Lys Ala Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala
    130   135   140

Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp Ile Val Asp

819

145   150   155   160

Cys Met Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Met
                165   170   175

Ser Gly Thr Gly Ser Val Thr Asn Val Thr Ile Arg Gln Pro Gly Ser
                180   185   190

Pro Pro Gly Ser Val Val Ser Leu His Gly Arg Phe Glu Ile Leu Ser
                195   200   205

Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala Thr Gly
    210   215   220

Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser
225   230   235   240

Val Val Gly Pro Leu Leu Cys Ser Gly Pro Val Val Val Met Ala Ala
                245   250   255

Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu
                260   265   270

Met Gln Thr Pro Val Gln Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
        275   280   285

Gly Met Gly Ser Pro Pro Met Met Gly Gln Gln Gln Ala Met Ala Ala
        290   295   300

Met Ala Ala Ala Gln Gly Leu Pro Pro Asn Leu Leu Gly Ser Val Gln
305   310   315   320

Leu Pro Pro Pro Gln Gln Asn Asp Gln Gln Tyr Trp Ser Thr Gly Arg
                325   330   335

Pro Pro Tyr

<210> 441 <211> 880 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (188)..(880) <223> G2659

 <400> 441
agtatatatc tatgtacata cgacgacaaa aaaaaatatg tatgtacata catctcctct
60

cactctaagc ttattttcgt ataaattata gtatagtcat attctttttag gacagaaccc
120

accgaaagaa agctccaaac ccaacaaaaa gggaggcggc ggagaagcaa acaacagcaa
180

caaaaaa atg cag cca gag gtt tca gat caa ata ttt tat gcc ttc ctc
229
        Met Gln Pro Glu Val Ser Asp Gln Ile Phe Tyr Ala Phe Leu
        1   5   10

acc gga gga tta tgt gcc tcg tct act tcc acc acc gtg acg tcg tcg
277
Thr Gly Gly Leu Cys Ala Ser Ser Thr Ser Thr Thr Val Thr Ser Ser
15   20   25   30

tct gac cct ttt gcc acg gtt tat gaa gac aaa gct ctt gct tct ctg
325
Ser Asp Pro Phe Ala Thr Val Tyr Glu Asp Lys Ala Leu Ala Ser Leu
                35   40   45

agg aac cat aaa gag gct gag cga aag aga aga gca aga atc aat tcc
373
Arg Asn His Lys Glu Ala Glu Arg Lys Arg Arg Ala Arg Ile Asn Ser
            50   55   60

cat ctc aac aag ctc cgc aag tta ctc tct tgt aac tcc aag aca gac
421
His Leu Asn Lys Leu Arg Lys Leu Leu Ser Cys Asn Ser Lys Thr Asp
            65   70   75

aaa tcc aca cta cta gca aaa gtg gtt caa cga gtc aaa gaa cta aaa
469
Lys Ser Thr Leu Leu Ala Lys Val Val Gln Arg Val Lys Glu Leu Lys
        80   85   90

caa caa acc cta gaa atc acc gac gaa aca ata ccg tcg gag act gac
517
Gln Gln Thr Leu Glu Ile Thr Asp Glu Thr Ile Pro Ser Glu Thr Asp
95   100   105   110

gaa atc agt gta ctc aac att gag gac tgt tcc aga ggc gac gat cga
565
Glu Ile Ser Val Leu Asn Ile Glu Asp Cys Ser Arg Gly Asp Asp Arg
                115   120   125

cgg ata atc ttt aag gta tcg ttt tgc tgc gag gac cgg cca gag ctc
613
Arg Ile Ile Phe Lys Val Ser Phe Cys Cys Glu Asp Arg Pro Glu Leu
            130   135   140

ttg aaa gat ctc atg gag aca ctc aaa tct ctt cag atg gaa act ctc
661
Leu Lys Asp Leu Met Glu Thr Leu Lys Ser Leu Gln Met Glu Thr Leu
            145   150   155

ttt gcc gac atg aca aca gtc ggt ggt cga aca aga aac gtt ctc gtt
709
Phe Ala Asp Met Thr Thr Val Gly Gly Arg Thr Arg Asn Val Leu Val
        160   165   170

gtg gcc gct gac aaa gag cat cac ggc gtc cag tcg gtg aat ttt cta
757
Val Ala Ala Asp Lys Glu His His Gly Val Gln Ser Val Asn Phe Leu

821

175   180   185   190

```
cag aac gca ctc aag tct tta ctc gaa cgg tca agc aag tcg gtg atg
805
Gln Asn Ala Leu Lys Ser Leu Leu Glu Arg Ser Ser Lys Ser Val Met
              195                200                205

gtg gga cat ggt ggt ggt ggt ggg gaa gaa agg tta aaa cga cgt cgt
853
Val Gly His Gly Gly Gly Gly Gly Glu Glu Arg Leu Lys Arg Arg Arg
              210                215                220

gcg ctg gat cac atc ata atg gtc tga
880
Ala Leu Asp His Ile Ile Met Val
          225                230
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<210> 442 <211> 230 <212> PRT <213> Arabidopsis thaliana <400>
442

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Met Gln Pro Glu Val Ser Asp Gln Ile Phe Tyr Ala Phe Leu Thr Gly
1               5                10                15

Gly Leu Cys Ala Ser Ser Thr Ser Thr Thr Val Thr Ser Ser Ser Asp
              20                25                30

Pro Phe Ala Thr Val Tyr Glu Asp Lys Ala Leu Ala Ser Leu Arg Asn
          35                40                45

His Lys Glu Ala Glu Arg Lys Arg Arg Ala Arg Ile Asn Ser His Leu
      50                55                60

Asn Lys Leu Arg Lys Leu Leu Ser Cys Asn Ser Lys Thr Asp Lys Ser
65                70                75                80

Thr Leu Leu Ala Lys Val Val Gln Arg Val Lys Glu Leu Lys Gln Gln
              85                90                95

Thr Leu Glu Ile Thr Asp Glu Thr Ile Pro Ser Glu Thr Asp Glu Ile
          100                105                110

Ser Val Leu Asn Ile Glu Asp Cys Ser Arg Gly Asp Asp Arg Arg Ile
          115                120                125

Ile Phe Lys Val Ser Phe Cys Cys Glu Asp Arg Pro Glu Leu Leu Lys
          130                135                140

Asp Leu Met Glu Thr Leu Lys Ser Leu Gln Met Glu Thr Leu Phe Ala
145                150                155                160
```

Asp Met Thr Thr Val Gly Gly Arg Thr Arg Asn Val Leu Val Val Ala
　　　　　　　　165　　　　　　　170　　　　　　　175

Ala Asp Lys Glu His His Gly Val Gln Ser Val Asn Phe Leu Gln Asn
　　　　　180　　　　　　　185　　　　　　　190

Ala Leu Lys Ser Leu Leu Glu Arg Ser Ser Lys Ser Val Met Val Gly
　　　　195　　　　　　　200　　　　　　　205

His Gly Gly Gly Gly Gly Glu Glu Arg Leu Lys Arg Arg Arg Ala Leu
　　　210　　　　　　　215　　　　　　　220

Asp His Ile Ile Met Val
225　　　　　　　230

<210> 443 <211> 866 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (46)..(837) <223> G2701

　<400> 443
gtgtttgtag ttgaaactta ttcttccctt tttttgtttt taggt atg gag act ctg
57
　　　　　　　　　　　　　　　　　　　　　　　　　　　　Met Glu Thr Leu
　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　1

cat cca ttc tct cac cta cct atc tct gac cac cgg ttc gtt gtt caa
105
His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg Phe Val Val Gln
5　　　　　　　　　10　　　　　　　　15　　　　　　　　20

gag atg gtg agc tta cac agc tcg agt agc ggt agc tgg act aaa gaa
153
Glu Met Val Ser Leu His Ser Ser Ser Ser Gly Ser Trp Thr Lys Glu
　　　　　　　　25　　　　　　　　30　　　　　　　　35

gag aac aag atg ttc gaa cga gct ctt gcg ata tac gct gaa gac tcg
201
Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr Ala Glu Asp Ser
　　　　　40　　　　　　　　45　　　　　　　　50

cct gat cgc tgg ttt aaa gtt gct tcc atg atc cct gga aag act gtt
249
Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro Gly Lys Thr Val
　　　　　55　　　　　　　　60　　　　　　　　65

ttt gat gtt atg aag caa tat agt aag ctt gaa gaa gac gtt ttc gat
297
Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu Asp Val Phe Asp
　　　　70　　　　　　　　75　　　　　　　　80

att gaa gca gga cgt gtt ccc att cct ggt tat cct gca gct tct tct
345
Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro Ala Ala Ser Ser
85　　　　　　　　90　　　　　　　　95　　　　　　　　100

ccc ttg ggg ttt gac acg gac atg tgt cgt aaa cgg cct agt gga gct
393

```
Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg Pro Ser Gly Ala
                105                 110             115

aga gga tct gat caa gat cga aag aaa gga gtc cct tgg aca gag gaa
441
Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro Trp Thr Glu Glu
                120                 125             130

gaa cac agg aga ttc ttg tta ggc ctt ctc aag tac ggt aaa gga gat
489
Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr Gly Lys Gly Asp
            135                 140             145

tgg aga aac ata tcg aga aac ttc gtg gtg tca aag acg cca acg caa
537
Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys Thr Pro Thr Gln
        150                 155             160

gtg gcg agc cac gcc caa aag tat tac cag aga cag ctc tcc gga gcc
585
Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln Leu Ser Gly Ala
165                 170                 175             180

aag gac aaa cgc agg cca agt atc cat gac atc aca acc ggc aat ctt
633
Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr Thr Gly Asn Leu
                185                 190             195

ctc aat gcc aat ctc aac cgt tcc ttt tcc gat cat aga gat att ctc
681
Leu Asn Ala Asn Leu Asn Arg Ser Phe Ser Asp His Arg Asp Ile Leu
            200                 205             210

cct gat tta ggg ttt atc gat aag gat gat acg gag gag gga gta ata
729
Pro Asp Leu Gly Phe Ile Asp Lys Asp Asp Thr Glu Glu Gly Val Ile
            215                 220             225

ttt atg ggt cag aat ctc tct tca gaa aat ctg ttt tct cca tca cca
777
Phe Met Gly Gln Asn Leu Ser Ser Glu Asn Leu Phe Ser Pro Ser Pro
        230                 235             240

act tca ttc gaa gct gcc att aac ttc gcc gga gaa aat gtc ttc agt
825
Thr Ser Phe Glu Ala Ala Ile Asn Phe Ala Gly Glu Asn Val Phe Ser
245                 250                 255             260

gcc gga gct taa ggcaacatag aatccccaaa ctcagcggc
866
Ala Gly Ala
```

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<210> 444 <211> 263 <212> PRT <213> Arabidopsis thaliana <400>
444
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Met Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg
1               5                   10              15
```

Phe Val Val Gln Glu Met Val Ser Leu His Ser Ser Ser Ser Gly Ser
            20   25   30

Trp Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr
            35   40   45

Ala Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro
    50   55   60

Gly Lys Thr Val Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu
65   70   75   80

Asp Val Phe Asp Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro
            85   90   95

Ala Ala Ser Ser Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg
            100   105   110

Pro Ser Gly Ala Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro
        115   120   125

Trp Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr
    130   135   140

Gly Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys
145   150   155   160

Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln
            165   170   175

Leu Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr
        180   185   190

Thr Gly Asn Leu Leu Asn Ala Asn Leu Asn Arg Ser Phe Ser Asp His
        195   200   205

Arg Asp Ile Leu Pro Asp Leu Gly Phe Ile Asp Lys Asp Asp Thr Glu
    210   215   220

Glu Gly Val Ile Phe Met Gly Gln Asn Leu Ser Ser Glu Asn Leu Phe
225   230   235   240

Ser Pro Ser Pro Thr Ser Phe Glu Ala Ala Ile Asn Phe Ala Gly Glu
            245   250   255

Asn Val Phe Ser Ala Gly Ala

825

260

<210> 445 <211> 972 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(972) <223> G2741

<400> 445
atg gga gag gaa gta caa atg agc gat tac gat gtt tcc ggc gac gga
48
Met Gly Glu Glu Val Gln Met Ser Asp Tyr Asp Val Ser Gly Asp Gly
1   5   10   15

gat agg gtt tct gaa tgg gag atg gga tta cca agc gac gaa gat cta
96
Asp Arg Val Ser Glu Trp Glu Met Gly Leu Pro Ser Asp Glu Asp Leu
            20   25   30

gca tct ctt tct tac tct ctg att cca ccg aat ttg gcg atg gcg ttt
144
Ala Ser Leu Ser Tyr Ser Leu Ile Pro Pro Asn Leu Ala Met Ala Phe
        35   40   45

agt atc aca ccg gag aga agc cgt acg att cag gat gtg aat cgt gca
192
Ser Ile Thr Pro Glu Arg Ser Arg Thr Ile Gln Asp Val Asn Arg Ala
    50   55   60

tcg gag acg acg ctc tcg tcg cta cgt ggt gga tct tca ggt cca aat
240
Ser Glu Thr Thr Leu Ser Ser Leu Arg Gly Gly Ser Ser Gly Pro Asn
65   70   75   80

acc tcg tcg tcg aat aat aac gtg gag gag gaa gat cga gtt gga tct
288
Thr Ser Ser Ser Asn Asn Asn Val Glu Glu Glu Asp Arg Val Gly Ser
                85   90   95

agc agt cct gga tcg gat tcg aag aag caa aag aca tca aac ggt gat
336
Ser Ser Pro Gly Ser Asp Ser Lys Lys Gln Lys Thr Ser Asn Gly Asp
            100   105   110

gga gat gac ggt ggc ggt gtg gat ccg gat tcg gcg atg gcg gcg gaa
384
Gly Asp Asp Gly Gly Gly Val Asp Pro Asp Ser Ala Met Ala Ala Glu
        115   120   125

gaa gga gat tca gga act gaa gat cta tct ggg aaa aca ctt aaa cga
432
Glu Gly Asp Ser Gly Thr Glu Asp Leu Ser Gly Lys Thr Leu Lys Arg
    130   135   140

ccg cgt tta gtg tgg aca ccg cag cta cac aag aga ttc gtt gac gtt
480
Pro Arg Leu Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val
145   150   155   160

gta gct cac tta ggg atc aaa aac gct gtt ccg aag acg att atg cag
528
Val Ala His Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln
                165   170   175

826

```
ctg atg aac gtt gaa gga tta act cgt gag aac gtt gcg tct cat ctt
576
Leu Met Asn Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu
            180                 185                 190

caa aag tat agg ctt tac ctc aaa agg atg cag gga ttg act aat gaa
624
Gln Lys Tyr Arg Leu Tyr Leu Lys Arg Met Gln Gly Leu Thr Asn Glu
            195                 200                 205

ggt ccc tct gct tcg gat aag ctc ttc tct tca aca cct gtt cct cca
672
Gly Pro Ser Ala Ser Asp Lys Leu Phe Ser Ser Thr Pro Val Pro Pro
        210                 215                 220

cag agc ttc caa gat atc ggt ggc ggt ggc ggt agc agc ggt aat gtt
720
Gln Ser Phe Gln Asp Ile Gly Gly Gly Gly Gly Ser Ser Gly Asn Val
225                 230                 235                 240

gga gtg ccg att ccg ggg gcg tat gga acg caa cag atg atg cag atg
768
Gly Val Pro Ile Pro Gly Ala Tyr Gly Thr Gln Gln Met Met Gln Met
                245                 250                 255

cca gtt tat gca cat cat atg ggt atg caa gga tat cat cat caa aat
816
Pro Val Tyr Ala His His Met Gly Met Gln Gly Tyr His His Gln Asn
            260                 265                 270

cat aat cat gat cct tat cat cag aat cat cgt cat cat cat gga gct
864
His Asn His Asp Pro Tyr His Gln Asn His Arg His His His Gly Ala
            275                 280                 285

ggt gga aat ggt gcg ttt gag tca aat cct tat atg atg cag cag aat
912
Gly Gly Asn Gly Ala Phe Glu Ser Asn Pro Tyr Met Met Gln Gln Asn
        290                 295                 300

aag ttt gga tcc atg gct tct tat cct tct gtt gga ggt gga agc gca
960
Lys Phe Gly Ser Met Ala Ser Tyr Pro Ser Val Gly Gly Gly Ser Ala
305                 310                 315                 320

aat gag aat taa
972
Asn Glu Asn
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<210> 446 <211> 323 <212> PRT <213> Arabidopsis thaliana <400>
446

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Met Gly Glu Glu Val Gln Met Ser Asp Tyr Asp Val Ser Gly Asp Gly
1               5                   10                  15


Asp Arg Val Ser Glu Trp Glu Met Gly Leu Pro Ser Asp Glu Asp Leu
            20                  25                  30
```

Ala Ser Leu Ser Tyr Ser Leu Ile Pro Pro Asn Leu Ala Met Ala Phe
        35   40   45

Ser Ile Thr Pro Glu Arg Ser Arg Thr Ile Gln Asp Val Asn Arg Ala
    50   55   60

Ser Glu Thr Thr Leu Ser Ser Leu Arg Gly Gly Ser Ser Gly Pro Asn
65   70   75   80

Thr Ser Ser Ser Asn Asn Asn Val Glu Glu Glu Asp Arg Val Gly Ser
                85   90   95

Ser Ser Pro Gly Ser Asp Ser Lys Lys Gln Lys Thr Ser Asn Gly Asp
            100   105   110

Gly Asp Asp Gly Gly Gly Val Asp Pro Asp Ser Ala Met Ala Ala Glu
        115   120   -   125

Glu Gly Asp Ser Gly Thr Glu Asp Leu Ser Gly Lys Thr Leu Lys Arg
    130   135   140

Pro Arg Leu Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val
145   150   155   160

Val Ala His Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln
            165   170   175

Leu Met Asn Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu
            180   185   190

Gln Lys Tyr Arg Leu Tyr Leu Lys Arg Met Gln Gly Leu Thr Asn Glu
        195   200   205

Gly Pro Ser Ala Ser Asp Lys Leu Phe Ser Ser Thr Pro Val Pro Pro
    210   215   220

Gln Ser Phe Gln Asp Ile Gly Gly Gly Gly Gly Ser Ser Gly Asn Val
225   230   235   240

Gly Val Pro Ile Pro Gly Ala Tyr Gly Thr Gln Gln Met Met Gln Met
            245   250   255

Pro Val Tyr Ala His His Met Gly Met Gln Gly Tyr His His Gln Asn
            260   265   270

```
His Asn His Asp Pro Tyr His Gln Asn His Arg His His His Gly Ala
        275                 280                 285

Gly Gly Asn Gly Ala Phe Glu Ser Asn Pro Tyr Met Met Gln Gln Asn
        290                 295                 300

Lys Phe Gly Ser Met Ala Ser Tyr Pro Ser Val Gly Gly Gly Ser Ala
305                 310                 315                 320

Asn Glu Asn
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<210> 447 <211> 1362 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1362) <223> G2781

<400> 447

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atg gat caa aaa agt aaa acg att gga gaa caa tgg tgg agg tca aat
48
Met Asp Gln Lys Ser Lys Thr Ile Gly Glu Gln Trp Trp Arg Ser Asn
1               5                   10                  15

cca acg ttt aaa ccg cct gaa acg cca tta gat tct atg gag ttt ttg
96
Pro Thr Phe Lys Pro Pro Glu Thr Pro Leu Asp Ser Met Glu Phe Leu
                20                  25                  30

tca cgt act tgg agt gct tcc gct act gaa gtt tca aga gct gtc gtc
144
Ser Arg Thr Trp Ser Ala Ser Ala Thr Glu Val Ser Arg Ala Val Val
            35                  40                  45

gcg tct cca ccg act tct caa ccg ccg caa atg cgt ttc tcg gag atc
192
Ala Ser Pro Pro Thr Ser Gln Pro Pro Gln Met Arg Phe Ser Glu Ile
        50                  55                  60

caa aac ggt tct tct gac gtc act ttg gtg ccg gaa gat gaa gaa aac
240
Gln Asn Gly Ser Ser Asp Val Thr Leu Val Pro Glu Asp Glu Glu Asn
65                  70                  75                  80

ggc atc gtt ctt gga aat act ttt tct ttt gct tct tca gaa act tct
288
Gly Ile Val Leu Gly Asn Thr Phe Ser Phe Ala Ser Ser Glu Thr Ser
                85                  90                  95

tta atg gtc atg gaa cgt atc atg gct cag tca ccg gag att tca tcg
336
Leu Met Val Met Glu Arg Ile Met Ala Gln Ser Pro Glu Ile Ser Ser
                100                 105                 110

cca cga aca tca ggg aga ctt tct cat agc tca ttc acc gac agt cct
384
Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser Phe Thr Asp Ser Pro
            115                 120                 125
```

ccg atc tct ccc tcc gac atc gac gac ttt aag caa ttc tac cgt gtg
432
Pro Ile Ser Pro Ser Asp Ile Asp Asp Phe Lys Gln Phe Tyr Arg Val
    130   135   140

agc cct tcc ttt aac ggc cac ata cgt ggt tca tca gcc att ccc ggc
480
Ser Pro Ser Phe Asn Gly His Ile Arg Gly Ser Ser Ala Ile Pro Gly
145   150   155   160

acc gcc gga ggg tct aaa act gtt ggt cgt tgg cta aag gac cgg cga
528
Thr Ala Gly Gly Ser Lys Thr Val Gly Arg Trp Leu Lys Asp Arg Arg
            165   170   175

gag aag aag aga gaa gag acg cgt gca caa aat gca cag ctt cac gcg
576
Glu Lys Lys Arg Glu Glu Thr Arg Ala Gln Asn Ala Gln Leu His Ala
        180   185   190

gct gta tct gta gct gga gtg gct gcc gcg gtg gct gct atc gct gca
624
Ala Val Ser Val Ala Gly Val Ala Ala Ala Val Ala Ala Ile Ala Ala
        195   200   205

gcc act gcc tct cag tcg agt tct gga act gac gag caa gtg gcc aaa
672
Ala Thr Ala Ser Gln Ser Ser Ser Gly Thr Asp Glu Gln Val Ala Lys
    210   215   220

aat gac tcc gcg gtg gct tct gcc gcg act ttg gtg gcg gcg aag tgt
720
Asn Asp Ser Ala Val Ala Ser Ala Ala Thr Leu Val Ala Ala Lys Cys
225   230   235   240

gtg gaa gct gca gag att atg gga gct gat cgt gag cac ttg gcc tcc
768
Val Glu Ala Ala Glu Ile Met Gly Ala Asp Arg Glu His Leu Ala Ser
            245   250   255

gtt gtt agt tct gcg gtt aac gtt cgt tct gcc gga gat atc atg act
816
Val Val Ser Ser Ala Val Asn Val Arg Ser Ala Gly Asp Ile Met Thr
            260   265   270

ttg acc gcc gct gct gcc aca gct ttg aga gga gct gca caa tta aag
864
Leu Thr Ala Ala Ala Ala Thr Ala Leu Arg Gly Ala Ala Gln Leu Lys
        275   280   285

gca aga gca ttg aag gag gta tgg aac att gcg gct gtg att cct gta
912
Ala Arg Ala Leu Lys Glu Val Trp Asn Ile Ala Ala Val Ile Pro Val
    290   295   300

gat aag ggt aca cca aaa ggc ggt ggt ggt ggt tat aga ggt ggc gag
960
Asp Lys Gly Thr Pro Lys Gly Gly Gly Gly Gly Tyr Arg Gly Gly Glu
305   310   315   320

830

tta gcc cct gta gat aat ttt ctt ggg att tgc agt aaa gaa ttg cta
1008
Leu Ala Pro Val Asp Asn Phe Leu Gly Ile Cys Ser Lys Glu Leu Leu
                325   330   335

gct aaa ggt tgc gaa ttg ctt aaa cgc acc cgc aaa ggt gat ctt cat
1056
Ala Lys Gly Cys Glu Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu His
            340   345   350

tgg aaa gtt gtt tcg atc tac att aat aga aca aag cag gta ata ttg
1104
Trp Lys Val Val Ser Ile Tyr Ile Asn Arg Thr Lys Gln Val Ile Leu
            355   360   365

aag act aag agc aaa cat gtt gct ggg acc atc aca aag aag aaa aag
1152
Lys Thr Lys Ser Lys His Val Ala Gly Thr Ile Thr Lys Lys Lys Lys
    370   375   380

aat gtg gtg gtg gga ttg gtt aag gga tta ccg gcg tgg cct ggc cgg
1200
Asn Val Val Val Gly Leu Val Lys Gly Leu Pro Ala Trp Pro Gly Arg
385   390   395   400

gaa atg ctc gag ggt gga gag aat ttg agg tat ttc ggg ctg aag acg
1248
Glu Met Leu Glu Gly Gly Glu Asn Leu Arg Tyr Phe Gly Leu Lys Thr
                405   410   415

gtg gag aaa aga gtg att gaa ttc gag tgc aaa agc caa agg gaa tat
1296
Val Glu Lys Arg Val Ile Glu Phe Glu Cys Lys Ser Gln Arg Glu Tyr
            420   425   430

gat ctt tgg aca caa ggt gtt tcc atg ctt ctt tcc att gct tct gat
1344
Asp Leu Trp Thr Gln Gly Val Ser Met Leu Leu Ser Ile Ala Ser Asp
            435   440   445

agg aaa cat aaa tgt tga
1362
Arg Lys His Lys Cys
        450

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448

Met Asp Gln Lys Ser Lys Thr Ile Gly Glu Gln Trp Trp Arg Ser Asn
1   5   10   15

Pro Thr Phe Lys Pro Pro Glu Thr Pro Leu Asp Ser Met Glu Phe Leu
            20   25   30

Ser Arg Thr Trp Ser Ala Ser Ala Thr Glu Val Ser Arg Ala Val Val
            35   40   45

```
Ala Ser Pro Pro Thr Ser Gln Pro Pro Gln Met Arg Phe Ser Glu Ile
    50              55              60

Gln Asn Gly Ser Ser Asp Val Thr Leu Val Pro Glu Asp Glu Glu Asn
65              70              75              80

Gly Ile Val Leu Gly Asn Thr Phe Ser Phe Ala Ser Ser Glu Thr Ser
            85              90              95

Leu Met Val Met Glu Arg Ile Met Ala Gln Ser Pro Glu Ile Ser Ser
            100             105             110

Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser Phe Thr Asp Ser Pro
        115             120             125

Pro Ile Ser Pro Ser Asp Ile Asp Asp Phe Lys Gln Phe Tyr Arg Val
    130             135             140

Ser Pro Ser Phe Asn Gly His Ile Arg Gly Ser Ser Ala Ile Pro Gly
145             150             155             160

Thr Ala Gly Gly Ser Lys Thr Val Gly Arg Trp Leu Lys Asp Arg Arg
            165             170             175

Glu Lys Lys Arg Glu Glu Thr Arg Ala Gln Asn Ala Gln Leu His Ala
            180             185             190

Ala Val Ser Val Ala Gly Val Ala Ala Ala Val Ala Ala Ile Ala Ala
        195             200             205

Ala Thr Ala Ser Gln Ser Ser Ser Gly Thr Asp Glu Gln Val Ala Lys
    210             215             220

Asn Asp Ser Ala Val Ala Ser Ala Ala Thr Leu Val Ala Ala Lys Cys
225             230             235             240

Val Glu Ala Ala Glu Ile Met Gly Ala Asp Arg Glu His Leu Ala Ser
            245             250             255

Val Val Ser Ser Ala Val Asn Val Arg Ser Ala Gly Asp Ile Met Thr
            260             265             270

Leu Thr Ala Ala Ala Ala Thr Ala Leu Arg Gly Ala Ala Gln Leu Lys
        275             280             285

Ala Arg Ala Leu Lys Glu Val Trp Asn Ile Ala Ala Val Ile Pro Val
```

```
          290                      295                      300
```

```
Asp Lys Gly Thr Pro Lys Gly Gly Gly Gly Gly Tyr Arg Gly Gly Glu
305                      310                315                320
```

```
Leu Ala Pro Val Asp Asn Phe Leu Gly Ile Cys Ser Lys Glu Leu Leu
                 325                330                335
```

```
Ala Lys Gly Cys Glu Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu His
                 340                345                350
```

```
Trp Lys Val Val Ser Ile Tyr Ile Asn Arg Thr Lys Gln Val Ile Leu
                 355                360                365
```

```
Lys Thr Lys Ser Lys His Val Ala Gly Thr Ile Thr Lys Lys Lys Lys
         370                375                380
```

```
Asn Val Val Val Gly Leu Val Lys Gly Leu Pro Ala Trp Pro Gly Arg
385                      390                395                400
```

```
Glu Met Leu Glu Gly Gly Glu Asn Leu Arg Tyr Phe Gly Leu Lys Thr
                 405                410                415
```

```
Val Glu Lys Arg Val Ile Glu Phe Glu Cys Lys Ser Gln Arg Glu Tyr
                 420                425                430
```

```
Asp Leu Trp Thr Gln Gly Val Ser Met Leu Leu Ser Ile Ala Ser Asp
         435                440                445
```

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Arg Lys His Lys Cys
         450
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<221>  CDS <222>  (1)..(495) <223>  G2839
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atg gtt gcg aga agt gag gaa gtt gag ata gtg gaa gat acg gcg gcg
48
Met Val Ala Arg Ser Glu Glu Val Glu Ile Val Glu Asp Thr Ala Ala
1               5                    10                 15
```

```
aaa tgt ttg atg ttg tta tca aga gtt gga gaa tgc ggc gga gga gga
96
Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly Gly
             20                 25                 30
```

```
gag aaa cga gtt ttc cga tgc aag act tgt ctt aaa gag ttt tcg tcg
144
Glu Lys Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser
         35                 40                 45
```

ttt caa gct ttg gga ggt cat cgt gca agc cac aag aaa ctc att aac
192
Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Leu Ile Asn
    50   55   60

agt agc gat cca tca ctt ctt gga tcc ttg tct aac aag aaa act aaa
240
Ser Ser Asp Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys
65   70   75   80

acg gcg acg tct cat cct tgt ccg ata tgt ggc gtg gag ttt ccg atg
288
Thr Ala Thr Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met
                85   90   95

ggg caa gct ctt ggt ggt cac atg agg aga cat agg agt gag aaa gcc
336
Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala
            100   105   110

tca cca ggc acg ttg gtt aca cgt tct ttt tta ccg gag acg acg acg
384
Ser Pro Gly Thr Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr
        115   120   125

gtg acg act ttg aaa aaa tcg agt agt ggg aag aga gtg gct tgt ttg
432
Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu
    130   135   140

gac tta gat tcg atg gag agt tta gtc aat tgg aag ttg gag ttg gga
480
Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu Leu Gly
145   150   155   160

aga acg att tct tga
495
Arg Thr Ile Ser

<210> 450 <211> 164 <212> PRT <213> Arabidopsis thaliana <400>
450

Met Val Ala Arg Ser Glu Glu Val Glu Ile Val Glu Asp Thr Ala Ala
1   5   10   15

Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly Gly
            20   25   30

Glu Lys Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser
        35   40   45

Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Leu Ile Asn
    50   55   60

834

```
Ser Ser Asp Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys
65              70              75              80


Thr Ala Thr Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met
            85              90              95


Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala
            100             105             110


Ser Pro Gly Thr Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr
        115             120             125


Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu
    130             135             140


Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu Leu Gly
145             150             155             160


Arg Thr Ile Ser
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<221> CDS <222> (184)..(2493) <223> G3010

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60

tccctcttac tcaaggttct tctttgtcat cttgttgccg aatccacaaa gaggagaata
120

aagattcgac ctttattaga tattaacgac tctggatttt tgggttttg gagttggatc
180

```
cac atg ggt tct tat ccg gat gga ttc cct gga tcc atg gac gag ttg
228
    Met Gly Ser Tyr Pro Asp Gly Phe Pro Gly Ser Met Asp Glu Leu
    1               5               10              15


gat ttc aat aag gac ttt gat ttg cct ccc tcc tca aac caa acc tta
276
Asp Phe Asn Lys Asp Phe Asp Leu Pro Pro Ser Ser Asn Gln Thr Leu
                20              25              30


ggt tta gct aat ggg ttc tat tta gat gac tta gat ttc tca tcc ttg
324
Gly Leu Ala Asn Gly Phe Tyr Leu Asp Asp Leu Asp Phe Ser Ser Leu
            35              40              45


gat cct cca gag gca tat ccc tcc cag aac aac aac aac aac aac atc
372
Asp Pro Pro Glu Ala Tyr Pro Ser Gln Asn Asn Asn Asn Asn Asn Ile
        50              55              60
```

aac aac aaa gct gta gca gga gat ctg tta tca tct tca tct gat gac
420
Asn Asn Lys Ala Val Ala Gly Asp Leu Leu Ser Ser Ser Ser Asp Asp
    65   70   75

gct gat ttc tct gat tct gtt ttg aag tat ata agc caa gtt ctt atg
468
Ala Asp Phe Ser Asp Ser Val Leu Lys Tyr Ile Ser Gln Val Leu Met
80   85   90   95

gaa gag gat atg gaa gag aag cct tgt atg ttt cat gac gct ttg gct
516
Glu Glu Asp Met Glu Glu Lys Pro Cys Met Phe His Asp Ala Leu Ala
            100   105   110

ctt caa gct gct gag aaa tct ctc tat gag gct ctt ggt gag aaa tac
564
Leu Gln Ala Ala Glu Lys Ser Leu Tyr Glu Ala Leu Gly Glu Lys Tyr
        115   120   125

cct tct tcg tct tct gct tct tct gtg gat cat cct gag aga ttg gct
612
Pro Ser Ser Ser Ser Ala Ser Ser Val Asp His Pro Glu Arg Leu Ala
        130   135   140

agt gat agc cct gac ggt tct tgt tca ggt ggt gct ttt agt gat tac
660
Ser Asp Ser Pro Asp Gly Ser Cys Ser Gly Gly Ala Phe Ser Asp Tyr
    145   150   155

gct agc acc act acc act act tcc tct gat tct cac tgg agt gtt gat
708
Ala Ser Thr Thr Thr Thr Thr Ser Ser Asp Ser His Trp Ser Val Asp
160   165   170   175

ggt ttg gag aat aga cct tct tgg tta cat aca cct atg ccg agt aat
756
Gly Leu Glu Asn Arg Pro Ser Trp Leu His Thr Pro Met Pro Ser Asn
            180   185   190

ttt gtt ttc cag tct act tct agg tcc aac agt gtc acc ggt ggt ggt
804
Phe Val Phe Gln Ser Thr Ser Arg Ser Asn Ser Val Thr Gly Gly Gly
        195   200   205

ggt ggt ggt aat agt gcg gtt tac ggt tca ggt ttt ggc gat gat ttg
852
Gly Gly Gly Asn Ser Ala Val Tyr Gly Ser Gly Phe Gly Asp Asp Leu
        210   215   220

gtt tcg aat atg ttt aaa gat gat gaa ttg gct atg cag ttc aag aaa
900
Val Ser Asn Met Phe Lys Asp Asp Glu Leu Ala Met Gln Phe Lys Lys
    225   230   235

ggg gtt gag gaa gct agt aag ttc ctt cct aag tct tct cag ctc ttt
948
Gly Val Glu Glu Ala Ser Lys Phe Leu Pro Lys Ser Ser Gln Leu Phe
240   245   250   255

att gat gtg gat agt tac atc cct atg aat tct ggt tcc aag gaa aat
996
Ile Asp Val Asp Ser Tyr Ile Pro Met Asn Ser Gly Ser Lys Glu Asn
            260   265   270

ggt tct gag gtt ttt gtt aag acg gag aag aaa gat gag aca gag cat
1044
Gly Ser Glu Val Phe Val Lys Thr Glu Lys Lys Asp Glu Thr Glu His
            275   280   285

cat cat cat cat agc tat gct cct cct ccc aac aga tta act ggt aag
1092
His His His His Ser Tyr Ala Pro Pro Pro Asn Arg Leu Thr Gly Lys
            290   295   300

aaa agc cat tgg cgc gac gaa gat gaa gat ttc gtt gaa gaa aga agt
1140
Lys Ser His Trp Arg Asp Glu Asp Glu Asp Phe Val Glu Glu Arg Ser
    305   310   315

aac aag caa tca gct gtt tat gtt gag gaa agc gag ctt tct gaa atg
1188
Asn Lys Gln Ser Ala Val Tyr Val Glu Glu Ser Glu Leu Ser Glu Met
320   325   330   335

ttt gat aag atc ttg gta tgt ggc cct ggg aaa cct gta tgc att ctt
1236
Phe Asp Lys Ile Leu Val Cys Gly Pro Gly Lys Pro Val Cys Ile Leu
            340   345   350

aac cag aac ttt cct aca gaa tcc gct aaa gtc gtg acc gca cag tca
1284
Asn Gln Asn Phe Pro Thr Glu Ser Ala Lys Val Val Thr Ala Gln Ser
            355   360   365

aat gga gca aag att cgt ggg aag aaa tca act tct act agt cat agt
1332
Asn Gly Ala Lys Ile Arg Gly Lys Lys Ser Thr Ser Thr Ser His Ser
            370   375   380

aac gat tct aag aaa gaa act gct gat ttg agg act ctt ttg gtg tta
1380
Asn Asp Ser Lys Lys Glu Thr Ala Asp Leu Arg Thr Leu Leu Val Leu
    385   390   395

tgt gca caa gct gta tca gtg gat gat cgt aga acc gcc aac gaa atg
1428
Cys Ala Gln Ala Val Ser Val Asp Asp Arg Arg Thr Ala Asn Glu Met
400   405   410   415

cta agg cag ata cga gag cat tct tcg cct cta ggc aat ggt tca gag
1476
Leu Arg Gln Ile Arg Glu His Ser Ser Pro Leu Gly Asn Gly Ser Glu
            420   425   430

cgg ttg gct cat tat ttt gca aat agt ctt gaa gca cgc tta gct ggg
1524
Arg Leu Ala His Tyr Phe Ala Asn Ser Leu Glu Ala Arg Leu Ala Gly
            435   440   445

acc ggt aca cag atc tac acc gct tta tct tcg aag aaa acg tct gca
1572
Thr Gly Thr Gln Ile Tyr Thr Ala Leu Ser Ser Lys Lys Thr Ser Ala
        450   455   460

gca gac atg ttg aag gct tac cag aca tac atg tcg gtc tgc cct ttc
1620
Ala Asp Met Leu Lys Ala Tyr Gln Thr Tyr Met Ser Val Cys Pro Phe
    465   470   475

aag aaa gct gct atc ata ttt gct aac cac agc atg atg cgt ttc act
1668
Lys Lys Ala Ala Ile Ile Phe Ala Asn His Ser Met Met Arg Phe Thr
480   485   490   495

gca aac gcc aac acg atc cac ata ata gat ttc gga ata tct tac ggt
1716
Ala Asn Ala Asn Thr Ile His Ile Ile Asp Phe Gly Ile Ser Tyr Gly
            500   505   510

ttt cag tgg cct gct ctg att cat cgc ctc tcg ctc agc aga cct ggt
1764
Phe Gln Trp Pro Ala Leu Ile His Arg Leu Ser Leu Ser Arg Pro Gly
            515   520   525

ggt tcg cct aag ctt cga att acc ggt ata gag ctt cct cag cgc ggt
1812
Gly Ser Pro Lys Leu Arg Ile Thr Gly Ile Glu Leu Pro Gln Arg Gly
        530   535   540

ttt aga cca gcg gaa gag ttc agg aga cag gtc atc gct tgg ctc gat
1860
Phe Arg Pro Ala Glu Glu Phe Arg Arg Gln Val Ile Ala Trp Leu Asp
    545   550   555

act gtc agc gac aca atg ttc cgt ttg agt aca acg caa ttg ctc aga
1908
Thr Val Ser Asp Thr Met Phe Arg Leu Ser Thr Thr Gln Leu Leu Arg
560   565   570   575

aat ggg gaa acg atc caa gtc gaa gac tta aag ctt cga caa gga gag
1956
Asn Gly Glu Thr Ile Gln Val Glu Asp Leu Lys Leu Arg Gln Gly Glu
            580   585   590

tat gtg gtt gtg aac tct ttg ttc cgt ttc agg aac ctt cta gat gag
2004
Tyr Val Val Val Asn Ser Leu Phe Arg Phe Arg Asn Leu Leu Asp Glu
            595   600   605

acc gtt ctg gta aac agc ccg aga gat gca gtt ttg aag ctg ata aga
2052
Thr Val Leu Val Asn Ser Pro Arg Asp Ala Val Leu Lys Leu Ile Arg
        610   615   620

aaa ata aac ccg aat gtc ttc att cca gcg atc tta agc ggg aat tac
2100
Lys Ile Asn Pro Asn Val Phe Ile Pro Ala Ile Leu Ser Gly Asn Tyr
    625   630   635

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aac gcg cca ttc ttt gtc acg agg ttc aga gaa gcg ttg ttt cat tac
2148
Asn Ala Pro Phe Phe Val Thr Arg Phe Arg Glu Ala Leu Phe His Tyr
640             645         650             655

tcg gct gtg ttt gat atg tgt gac tcg aag cta gct agg gaa gac gag
2196
Ser Ala Val Phe Asp Met Cys Asp Ser Lys Leu Ala Arg Glu Asp Glu
            660         665             670

atg agg ctg atg tat gag aaa gag ttt tat ggg aga gag att gtg aat
2244
Met Arg Leu Met Tyr Glu Lys Glu Phe Tyr Gly Arg Glu Ile Val Asn
            675         680             685

gtt gtg gct tgt gaa gga aca gag aga gtg gag aga cca gag aca tat
2292
Val Val Ala Cys Glu Gly Thr Glu Arg Val Glu Arg Pro Glu Thr Tyr
        690         695             700

aag cag tgg cag gcg aga ctg atc cga gcc gga ttt aga cag ctt ccg
2340
Lys Gln Trp Gln Ala Arg Leu Ile Arg Ala Gly Phe Arg Gln Leu Pro
    705             710             715

ctt gag aag gaa ctg atg cag aat ctg aag ttg aaa atc gaa aac ggg
2388
Leu Glu Lys Glu Leu Met Gln Asn Leu Lys Leu Lys Ile Glu Asn Gly
720             725             730             735

tac gat aaa aac ttc gat gtt gat caa aac ggt aac tgg tta ctt caa
2436
Tyr Asp Lys Asn Phe Asp Val Asp Gln Asn Gly Asn Trp Leu Leu Gln
            740             745             750

ggg tgg aaa ggt aga atc gtg tat gct tca tct cta tgg gtt cct tcg
2484
Gly Trp Lys Gly Arg Ile Val Tyr Ala Ser Ser Leu Trp Val Pro Ser
            755             760             765

tct tca tag atgttgtttc ttacgttcta agcgactggg atttatgtag
2533
Ser Ser

ggcttttctg ttgatagtct ctcgccaaca cgagtggatt aagttcagag ttagggttct
2593

tgaacactag aatgttgtta tattatgctt gtgacatagc gtgtgtaaga gtgtagccta
2653

agagatatag tactcattgc atgatctttt gctatatgtt
2693


<210> 452 <211> 769 <212> PRT <213> Arabidopsis thaliana <400>
452

Met Gly Ser Tyr Pro Asp Gly Phe Pro Gly Ser Met Asp Glu Leu Asp
1               5               10              15
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839

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Phe Asn Lys Asp Phe Asp Leu Pro Pro Ser Ser Asn Gln Thr Leu Gly
        20              25                  30


Leu Ala Asn Gly Phe Tyr Leu Asp Asp Leu Asp Phe Ser Ser Leu Asp
        35              40                  45


Pro Pro Glu Ala Tyr Pro Ser Gln Asn Asn Asn Asn Asn Asn Ile Asn
    50              55                  60


Asn Lys Ala Val Ala Gly Asp Leu Leu Ser Ser Ser Ser Asp Asp Ala
65              70                  75                  80


Asp Phe Ser Asp Ser Val Leu Lys Tyr Ile Ser Gln Val Leu Met Glu
                85                  90                  95


Glu Asp Met Glu Glu Lys Pro Cys Met Phe His Asp Ala Leu Ala Leu
            100                 105                 110


Gln Ala Ala Glu Lys Ser Leu Tyr Glu Ala Leu Gly Glu Lys Tyr Pro
        115                 120                 125


Ser Ser Ser Ser Ala Ser Ser Val Asp His Pro Glu Arg Leu Ala Ser
    130                 135                 140


Asp Ser Pro Asp Gly Ser Cys Ser Gly Gly Ala Phe Ser Asp Tyr Ala
145                 150                 155                 160


Ser Thr Thr Thr Thr Thr Ser Ser Asp Ser His Trp Ser Val Asp Gly
                165                 170                 175


Leu Glu Asn Arg Pro Ser Trp Leu His Thr Pro Met Pro Ser Asn Phe
            180                 185                 190


Val Phe Gln Ser Thr Ser Arg Ser Asn Ser Val Thr Gly Gly Gly Gly
        195                 200                 205


Gly Gly Asn Ser Ala Val Tyr Gly Ser Gly Phe Gly Asp Asp Leu Val
    210                 215                 220


Ser Asn Met Phe Lys Asp Asp Glu Leu Ala Met Gln Phe Lys Lys Gly
225                 230                 235                 240


Val Glu Glu Ala Ser Lys Phe Leu Pro Lys Ser Ser Gln Leu Phe Ile
                245                 250                 255
```

840

Asp Val Asp Ser Tyr Ile Pro Met Asn Ser Gly Ser Lys Glu Asn Gly
            260   265   270

Ser Glu Val Phe Val Lys Thr Glu Lys Lys Asp Glu Thr Glu His His
            275   280   285

His His His Ser Tyr Ala Pro Pro Pro Asn Arg Leu Thr Gly Lys Lys
        290   295   300

Ser His Trp Arg Asp Glu Asp Glu Asp Phe Val Glu Glu Arg Ser Asn
305   310   315   320

Lys Gln Ser Ala Val Tyr Val Glu Glu Ser Glu Leu Ser Glu Met Phe
                325   330   335

Asp Lys Ile Leu Val Cys Gly Pro Gly Lys Pro Val Cys Ile Leu Asn
            340   . 345   350

Gln Asn Phe Pro Thr Glu Ser Ala Lys Val Val Thr Ala Gln Ser Asn
        355   360   365

Gly Ala Lys Ile Arg Gly Lys Lys Ser Thr Ser Thr Ser His Ser Asn
    370   375   380

Asp Ser Lys Lys Glu Thr Ala Asp Leu Arg Thr Leu Leu Val Leu Cys
385   390   395   400

Ala Gln Ala Val Ser Val Asp Asp Arg Arg Thr Ala Asn Glu Met Leu
                405   410   415

Arg Gln Ile Arg Glu His Ser Ser Pro Leu Gly Asn Gly Ser Glu Arg
            420   425   .   430

Leu Ala His Tyr Phe Ala Asn Ser Leu Glu Ala Arg Leu Ala Gly Thr
        435   440   445

Gly Thr Gln Ile Tyr Thr Ala Leu Ser Ser Lys Lys Thr Ser Ala Ala
    450   455   460

Asp Met Leu Lys Ala Tyr Gln Thr Tyr Met Ser Val Cys Pro Phe Lys
465   470   475   480

Lys Ala Ala Ile Ile Phe Ala Asn His Ser Met Met Arg Phe Thr Ala
            485   490   495

Asn Ala Asn Thr Ile His Ile Ile Asp Phe Gly Ile Ser Tyr Gly Phe

841

```
            500                     505                     510
```

Gln Trp Pro Ala Leu Ile His Arg Leu Ser Leu Ser Arg Pro Gly Gly
    515   520   525

Ser Pro Lys Leu Arg Ile Thr Gly Ile Glu Leu Pro Gln Arg Gly Phe
    530   535   540

Arg Pro Ala Glu Glu Phe Arg Arg Gln Val Ile Ala Trp Leu Asp Thr
545   550   555   560

Val Ser Asp Thr Met Phe Arg Leu Ser Thr Thr Gln Leu Leu Arg Asn
                565   570   575

Gly Glu Thr Ile Gln Val Glu Asp Leu Lys Leu Arg Gln Gly Glu Tyr
                580   585   590

Val Val Val Asn Ser Leu Phe Arg Phe Arg Asn Leu Leu Asp Glu Thr
                595   600   605

Val Leu Val Asn Ser Pro Arg Asp Ala Val Leu Lys Leu Ile Arg Lys
    610   615   620

Ile Asn Pro Asn Val Phe Ile Pro Ala Ile Leu Ser Gly Asn Tyr Asn
625   630   635   640

Ala Pro Phe Phe Val Thr Arg Phe Arg Glu Ala Leu Phe His Tyr Ser
                645   650   655

Ala Val Phe Asp Met Cys Asp Ser Lys Leu Ala Arg Glu Asp Glu Met
                660   665   670

Arg Leu Met Tyr Glu Lys Glu Phe Tyr Gly Arg Glu Ile Val Asn Val
                675   680   685

Val Ala Cys Glu Gly Thr Glu Arg Val Glu Arg Pro Glu Thr Tyr Lys
    690   695   700

Gln Trp Gln Ala Arg Leu Ile Arg Ala Gly Phe Arg Gln Leu Pro Leu
705   710   715   720

Glu Lys Glu Leu Met Gln Asn Leu Lys Leu Lys Ile Glu Asn Gly Tyr
                725   730   735

Asp Lys Asn Phe Asp Val Asp Gln Asn Gly Asn Trp Leu Leu Gln Gly
                740   745   750

Trp Lys Gly Arg Ile Val Tyr Ala Ser Ser Leu Trp Val Pro Ser Ser
        755   760   765

Ser

<210> 453 <211> 1320 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1320) <223> G1880

<400> 453
atg ttg tcc aac aag aac aca aac aca tgt tgt gtg gtt tct tct tct
48
Met Leu Ser Asn Lys Asn Thr Asn Thr Cys Cys Val Val Ser Ser Ser
1   5   10   15

tct tct gat cct ttc ctc tcc tct tca gaa aat ggg gtc acc acc aca
96
Ser Ser Asp Pro Phe Leu Ser Ser Ser Glu Asn Gly Val Thr Thr Thr
            20   25   30

aac aca tcc act cag aag agg aaa aga aga cct gca ggt acc cca gat
144
Asn Thr Ser Thr Gln Lys Arg Lys Arg Arg Pro Ala Gly Thr Pro Asp
        35   40   45

cca gat gca gaa gtt gtg tct tta tca cca aga act ctt ctt gaa tca
192
Pro Asp Ala Glu Val Val Ser Leu Ser Pro Arg Thr Leu Leu Glu Ser
    50   55   60

gac aga tac ata tgt gag atc tgt aac caa ggg ttt caa aga gac cag
240
Asp Arg Tyr Ile Cys Glu Ile Cys Asn Gln Gly Phe Gln Arg Asp Gln
65   70   75   80

aat ctc cag atg cat aga aga cgt cac aaa gtt cca tgg aag ctt ctt
288
Asn Leu Gln Met His Arg Arg Arg His Lys Val Pro Trp Lys Leu Leu
                85   90   95

aaa aga gac aac aac ata gag gtg aag aaa cga gtc tat gtt tgc cct
336
Lys Arg Asp Asn Asn Ile Glu Val Lys Lys Arg Val Tyr Val Cys Pro
                100   105   110

gaa ccc act tgc ctt cac cat aat cct tgt cat gct ctg gga gat ctt
384
Glu Pro Thr Cys Leu His His Asn Pro Cys His Ala Leu Gly Asp Leu
            115   120   125

gtc ggc atc aaa aaa cat ttc aga aga aaa cat agt aac cat aag caa
432
Val Gly Ile Lys Lys His Phe Arg Arg Lys His Ser Asn His Lys Gln
        130   135   140

tgg gtt tgt gag aga tgc tct aaa ggt tat gct gtt caa tct gat tac
480

843

```
Trp Val Cys Glu Arg Cys Ser Lys Gly Tyr Ala Val Gln Ser Asp Tyr
145                 150             155                 160
```

```
aaa gct cat ctc aaa act tgt ggt act aga gga cat tct tgt gac tgt
528
Lys Ala His Leu Lys Thr Cys Gly Thr Arg Gly His Ser Cys Asp Cys
                165             170                 175
```

```
ggt cgt gtc ttc tcc agg gtg gag agt ttt att gaa cat caa gat aat
576
Gly Arg Val Phe Ser Arg Val Glu Ser Phe Ile Glu His Gln Asp Asn
                180             185             190
```

```
tgt tcc gca cgg aga gtt cac cgt gaa ccg cct cga cca cca caa acc
624
Cys Ser Ala Arg Arg Val His Arg Glu Pro Pro Arg Pro Pro Gln Thr
            195             200             205
```

```
gcg gta aca gtc ccg gca tgc tct tct aga acc gcc tca acc gtc agc
672
Ala Val Thr Val Pro Ala Cys Ser Ser Arg Thr Ala Ser Thr Val Ser
        210             215             220
```

```
act ccg tct agt gaa acc aat tac ggc ggt aca gtt gcg gtt acg act
720
Thr Pro Ser Ser Glu Thr Asn Tyr Gly Gly Thr Val Ala Val Thr Thr
225             230             235                 240
```

```
cct caa cct cta gaa ggc cgt cca att cat cag aga atc tca tct tca
768
Pro Gln Pro Leu Glu Gly Arg Pro Ile His Gln Arg Ile Ser Ser Ser
            245             250                 255
```

```
att ctc acc aac tca tca aac aat ctc aac ctc gaa ctc caa ctt ctt
816
Ile Leu Thr Asn Ser Ser Asn Asn Leu Asn Leu Glu Leu Gln Leu Leu
            260             265             270
```

```
cca tta tcg tcg aat caa aac cct aat caa gaa aac caa caa caa aaa
864
Pro Leu Ser Ser Asn Gln Asn Pro Asn Gln Glu Asn Gln Gln Gln Lys
            275             280             285
```

```
gtt aaa gaa cca tct cat cat cat aat cat aat cat gat acc aca aac
912
Val Lys Glu Pro Ser His His His Asn His Asn His Asp Thr Thr Asn
        290             295             300
```

```
tta aac ctc tcc att gca cca tca tca tca tat caa cat tac aac aac
960
Leu Asn Leu Ser Ile Ala Pro Ser Ser Ser Tyr Gln His Tyr Asn Asn
305             310             315                 320
```

```
ttt gat cgt ata aaa gag att atg gcg agc gag caa att atg aag ata
1008
Phe Asp Arg Ile Lys Glu Ile Met Ala Ser Glu Gln Ile Met Lys Ile
                325             330                 335
```

```
gcg atg aag gag aaa gct tac gct gag gaa gct aaa aga gaa gcc aag
1056
Ala Met Lys Glu Lys Ala Tyr Ala Glu Glu Ala Lys Arg Glu Ala Lys
```

                    340   345   350

agg caa cga gag ata gcg gaa aac gag ttt gca aat gcc aaa aag att
1104
Arg Gln Arg Glu Ile Ala Glu Asn Glu Phe Ala Asn Ala Lys Lys Ile
        355   360   .   365

agg caa aaa gca caa gct gaa ctc gag aga gct aag ttt tta aag gaa
1152
Arg Gln Lys Ala Gln Ala Glu Leu Glu Arg Ala Lys Phe Leu Lys Glu
    370   375   .   380

caa tct atg aag aag ata agt tca acg atc atg cag gtc act tgt caa
1200
Gln Ser Met Lys Lys Ile Ser Ser Thr Ile Met Gln Val Thr Cys Gln
385   390   395   400

aca tgt aaa gga cag ttt caa gca gtt gcg gtt ccg gcg gct acg gct
1248
Thr Cys Lys Gly Gln Phe Gln Ala Val Ala Val Pro Ala Ala Thr Ala
                  ·405   410   415

gat gag acg tct ctt gtc gtg agt tac atg tcg tca gcg aat act gac
1296
Asp Glu Thr Ser Leu Val Val Ser Tyr Met Ser Ser Ala Asn Thr Asp
        420   425   430

gga gag ttg gaa aat ggt ttt taa
1320
Gly Glu Leu Glu Asn Gly Phe
        435

<210> 454 <211> 439 <212> PRT <213> Arabidopsis thaliana <400>
454

Met Leu Ser Asn Lys Asn Thr Asn Thr Cys Cys Val Val Ser Ser Ser
1   5   10   15

Ser Ser Asp Pro Phe Leu Ser Ser Ser Glu Asn Gly Val Thr Thr Thr
            20   25   30

Asn Thr Ser Thr Gln Lys Arg Lys Arg Arg Pro Ala Gly Thr Pro Asp
        35   40   45

Pro Asp Ala Glu Val Val Ser Leu Ser Pro Arg Thr Leu Leu Glu Ser
    50   55   60

Asp Arg Tyr Ile Cys Glu Ile Cys Asn Gln Gly Phe Gln Arg Asp Gln
65   70   75   80

Asn Leu Gln Met His Arg Arg Arg His Lys Val Pro Trp Lys Leu Leu
            85   90   95

Lys Arg Asp Asn Asn Ile Glu Val Lys Lys Arg Val Tyr Val Cys Pro

```
            100                      105                      110


Glu Pro Thr Cys Leu His His Asn Pro Cys His Ala Leu Gly Asp Leu
        115                  120              125


Val Gly Ile Lys Lys His Phe Arg Arg Lys His Ser Asn His Lys Gln
    130                  135              140


Trp Val Cys Glu Arg Cys Ser Lys Gly Tyr Ala Val Gln Ser Asp Tyr
145                  150              155                  160


Lys Ala His Leu Lys Thr Cys Gly Thr Arg Gly His Ser Cys Asp Cys
                165                  170                  175


Gly Arg Val Phe Ser Arg Val Glu Ser Phe Ile Glu His Gln Asp Asn
            180                  185                  190


Cys Ser Ala Arg Arg Val His Arg Glu Pro Pro Arg Pro Pro Gln Thr
            195                  200                  205


Ala Val Thr Val Pro Ala Cys Ser Ser Arg Thr Ala Ser Thr Val Ser
    210                  215                  220


Thr Pro Ser Ser Glu Thr Asn Tyr Gly Gly Thr Val Ala Val Thr Thr
225                  230                  235                  240


Pro Gln Pro Leu Glu Gly Arg Pro Ile His Gln Arg Ile Ser Ser Ser
            245                  250                  255


Ile Leu Thr Asn Ser Ser Asn Asn Leu Asn Leu Glu Leu Gln Leu Leu
            260                  265                  270


Pro Leu Ser Ser Asn Gln Asn Pro Asn Gln Glu Asn Gln Gln Gln Lys
            275                  280                  285


Val Lys Glu Pro Ser His His His Asn His Asn His Asp Thr Thr Asn
    290                  295                  300


Leu Asn Leu Ser Ile Ala Pro Ser Ser Ser Tyr Gln His Tyr Asn Asn
305                  310                  315                  320


Phe Asp Arg Ile Lys Glu Ile Met Ala Ser Glu Gln Ile Met Lys Ile
            325                  330                  335


Ala Met Lys Glu Lys Ala Tyr Ala Glu Glu Ala Lys Arg Glu Ala Lys
            340                  345                  350
```

846

Arg Gln Arg Glu Ile Ala Glu Asn Glu Phe Ala Asn Ala Lys Lys Ile
        355   360   365

Arg Gln Lys Ala Gln Ala Glu Leu Glu Arg Ala Lys Phe Leu Lys Glu
        370   375   380

Gln Ser Met Lys Lys Ile Ser Ser Thr Ile Met Gln Val Thr Cys Gln
385   390   395   400

Thr Cys Lys Gly Gln Phe Gln Ala Val Ala Val Pro Ala Ala Thr Ala
                405   410   415

Asp Glu Thr Ser Leu Val Val Ser Tyr Met Ser Ser Ala Asn Thr Asp
                420   425   430

Gly Glu Leu Glu Asn Gly Phe
        435

<210> 455 <211> 1009 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (177)..(866) <223> G1841

<400> 455
cattccgaaa agtacttgtt tattggtgtt attcatcgct gctcaaggtg gcaaaccaag
60

gagaacaaga agagtccagg gccaatgagc ctgagggtat caaatcagtg attgatgaca
120

tctacatttt tgaagacgac cctgtggttg ataggttcaa taggtttggc acggag atg
179
                                                                    Met
                                                                    1

tct gcc atg gtc tcg gcc ttg aca cag gtg gtt tct gct cgc tct cag
227
Ser Ala Met Val Ser Ala Leu Thr Gln Val Val Ser Ala Arg Ser Gln
        5   10   15

act gag gct gaa ggt gct cac tct cag act gag gct gaa ggt gct cac
275
Thr Glu Ala Glu Gly Ala His Ser Gln Thr Glu Ala Glu Gly Ala His
        20   25   30

tct tct tcc tct tcg gct gga cat aaa aga gga tgg ctt gga atc gat
323
Ser Ser Ser Ser Ser Ala Gly His Lys Arg Gly Trp Leu Gly Ile Asp
        35   40   45

tct gct cct att ccc tca tca ttt gct cgt gta gac tct tca cat aat
371
Ser Ala Pro Ile Pro Ser Ser Phe Ala Arg Val Asp Ser Ser His Asn
50   55   60   65

847

ccg atc gaa gaa tcc atg agc aag gca ttt cca gag gaa gca agg gag
419
Pro Ile Glu Glu Ser Met Ser Lys Ala Phe Pro Glu Glu Ala Arg Glu
                  70   75   80

aaa aaa agg agg tac aga gga gta agg cag aga cca tgg ggc aaa tgg
467
Lys Lys Arg Arg Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp
              85   90   95

gca gct gag ata cgt gat cca cat aga gcc gct agg gtt tgg ctc ggg
515
Ala Ala Glu Ile Arg Asp Pro His Arg Ala Ala Arg Val Trp Leu Gly
            100   105   110

acg ttt gat aca gcg gag gcc gcg gct aga gcc tac gac gag gct gca
563
Thr Phe Asp Thr Ala Glu Ala Ala Ala Arg Ala Tyr Asp Glu Ala Ala
        115   120   125

ctc cgg ttc cgt gga aat aaa gca aag cta aat ttc cca gag gat gta
611
Leu Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn Phe Pro Glu Asp Val
130   135   140   145

agg att ctt cct cct ccc cct cct ctt ctt cgt tca cca gct gac acg
659
Arg Ile Leu Pro Pro Pro Pro Leu Leu Arg Ser Pro Ala Asp Thr
            150   155   160

gtg gcg aat aaa gca gaa gag gat ctg ata aat tat tgg agt tat aca
707
Val Ala Asn Lys Ala Glu Glu Asp Leu Ile Asn Tyr Trp Ser Tyr Thr
            165   170   175

aag ttg ttg caa agt tca ggc caa cgg tca ttt ctc gag cga gga caa
755
Lys Leu Leu Gln Ser Ser Gly Gln Arg Ser Phe Leu Glu Arg Gly Gln
        180   185   190

gaa gag agt agt aac ata ttt gaa cat tca cca atg gaa caa cct ctg
803
Glu Glu Ser Ser Asn Ile Phe Glu His Ser Pro Met Glu Gln Pro Leu
        195   200   205

cct cct tca agt tct ggt cca agt tcc tct aat ttt cct gca cct tct
851
Pro Pro Ser Ser Ser Gly Pro Ser Ser Ser Asn Phe Pro Ala Pro Ser
210   215   220   225

cta cct aat aca tag tttcactttt attaaagctc tacaaataca attaaataca
906
Leu Pro Asn Thr

tagctaaatg aaaatgattt tcttgtctgt ataccttctt aagtgctaaa caatatattg
966

tactctttgt tttccttaac taaaaaaaaa aaaaaaaaaa aaa
1009

848

<210> 456 <211> 229 <212> PRT <213> Arabidopsis thaliana <400>
456

Met Ser Ala Met Val Ser Ala Leu Thr Gln Val Val Ser Ala Arg Ser
1   5   10   15

Gln Thr Glu Ala Glu Gly Ala His Ser Gln Thr Glu Ala Glu Gly Ala
            20   25   .   30

His Ser Ser Ser Ser Ser Ala Gly His Lys Arg Gly Trp Leu Gly Ile
        35   40   .   45

Asp Ser Ala Pro Ile Pro Ser Ser Phe Ala Arg Val Asp Ser Ser His
    50   55   60

Asn Pro Ile Glu Glu Ser Met Ser Lys Ala Phe Pro Glu Glu Ala Arg
65   70   75   80

Glu Lys Lys Arg Arg Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys
                85   90   95

Trp Ala Ala Glu Ile Arg Asp Pro His Arg Ala Ala Arg Val Trp Leu
            100   105   110

Gly Thr Phe Asp Thr Ala Glu Ala Ala Ala Arg Ala Tyr Asp Glu Ala
        115   120   125

Ala Leu Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn Phe Pro Glu Asp
    130   135   140

Val Arg Ile Leu Pro Pro Pro Pro Leu Leu Arg Ser Pro Ala Asp
145   .   150   155   160

Thr Val Ala Asn Lys Ala Glu Glu Asp Leu Ile Asn Tyr Trp Ser Tyr
            165   .   170   175

Thr Lys Leu Leu Gln Ser Ser Gly Gln Arg Ser Phe Leu Glu Arg Gly
            180   185   190

Gln Glu Glu Ser Ser Asn Ile Phe Glu His Ser Pro Met Glu Gln Pro
            195   200   205

Leu Pro Pro Ser Ser Ser Gly Pro Ser Ser Ser Asn Phe Pro Ala Pro
    210   215   220

Ser Leu Pro Asn Thr

225

<210> 457 <211> 861 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(861) <223> G2007

<400> 457
atg gga agg cag cca tgt tgt gac aag ctc atg gtg aag aag ggg ccg
48
Met Gly Arg Gln Pro Cys Cys Asp Lys Leu Met Val Lys Lys Gly Pro
1   5   10   15

tgg acg gcg gag gaa gac aag aaa ctg ata aac ttt atc ttg acc aac
96
Trp Thr Ala Glu Glu Asp Lys Lys Leu Ile Asn Phe Ile Leu Thr Asn
            20   25   30

ggc cac tgt tgc tgg agg gct ttg ccg aag ctg gcc ggt ctc cgt cgc
144
Gly His Cys Cys Trp Arg Ala Leu Pro Lys Leu Ala Gly Leu Arg Arg
        35   40   45

tgt ggg aag agc tgc cgt cta cgg tgg acc aat tat ctc cga cct gac
192
Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
    50   55   60

ttg aag aga ggt ctt ctc tcc gac gcc gag gaa cag ctt gtc atc gac
240
Leu Lys Arg Gly Leu Leu Ser Asp Ala Glu Glu Gln Leu Val Ile Asp
65   70   75   80

ctt cat gct ctt ctc ggc aac aga tgg tcc aag atc gct gca aga tta
288
Leu His Ala Leu Leu Gly Asn Arg Trp Ser Lys Ile Ala Ala Arg Leu
                85   90   95

cca gga aga aca gac aac gaa ata aaa aat cat tgg aat act cat atc
336
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Thr His Ile
            100   105   110

aag aag aag ctc ctt aag atg gaa atc gat cct tcg acc cat caa cct
384
Lys Lys Lys Leu Leu Lys Met Glu Ile Asp Pro Ser Thr His Gln Pro
        115   120   125

tta aac aaa gta ttt acc gat aca aac tta gtc gat aaa tct gaa act
432
Leu Asn Lys Val Phe Thr Asp Thr Asn Leu Val Asp Lys Ser Glu Thr
    130   135   140

tca tcg aaa gcc gac aat gta aat gat aat aaa atc gta gag atc gat
480
Ser Ser Lys Ala Asp Asn Val Asn Asp Asn Lys Ile Val Glu Ile Asp
145   150   155   160

ggg aca acg aca aat aca ata gat gat agc att atc act cat caa aat
528
Gly Thr Thr Thr Asn Thr Ile Asp Asp Ser Ile Ile Thr His Gln Asn
                165   170   175

850

agt tca aat gat gat tat gaa tta ctt ggt gat ata att cat aat tat
576
Ser Ser Asn Asp Asp Tyr Glu Leu Leu Gly Asp Ile Ile His Asn Tyr
            180   185   190

gga gat tta ttt aat att cta tgg acc aac gat gaa cct cct cta gtc
624
Gly Asp Leu Phe Asn Ile Leu Trp Thr Asn Asp Glu Pro Pro Leu Val
            195   200   205

gat gat gca tca tgg agc aat cat aac gtt ggt att gga gga aca gct
672
Asp Asp Ala Ser Trp Ser Asn His Asn Val Gly Ile Gly Gly Thr Ala
            210   215   220

gca gtt gca gcc tca gac aag aac aac act gct gcc gag gaa gat ttc
720
Ala Val Ala Ala Ser Asp Lys Asn Asn Thr Ala Ala Glu Glu Asp Phe
225   230   235   240

ccg gaa aga tca ttt gaa aaa cag aac ggc gaa agt tgg atg ttc ttg
768
Pro Glu Arg Ser Phe Glu Lys Gln Asn Gly Glu Ser Trp Met Phe Leu
                245   250   255

gat tat tgc caa gaa ttt ggt gtt gaa gat ttt ggg ttc gag tgt tac
816
Asp Tyr Cys Gln Glu Phe Gly Val Glu Asp Phe Gly Phe Glu Cys Tyr
                260   265   270

cat ggt ttt ggt caa agc tcc atg aag acg ggt cac aag gac tag
861
His Gly Phe Gly Gln Ser Ser Met Lys Thr Gly His Lys Asp
                275   280   285

<210> 458 <211> 286 <212> PRT <213> Arabidopsis thaliana <400>
458

Met Gly Arg Gln Pro Cys Cys Asp Lys Leu Met Val Lys Lys Gly Pro
1   5   10   15

Trp Thr Ala Glu Glu Asp Lys Lys Leu Ile Asn Phe Ile Leu Thr Asn
            20   25   30

Gly His Cys Cys Trp Arg Ala Leu Pro Lys Leu Ala Gly Leu Arg Arg
            35   40   45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
        50   55   60

Leu Lys Arg Gly Leu Leu Ser Asp Ala Glu Glu Gln Leu Val Ile Asp
65   70   75   80

Leu His Ala Leu Leu Gly Asn Arg Trp Ser Lys Ile Ala Ala Arg Leu

851

```
                    85                      90                      95


Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Thr His Ile
          100                 105                 110


Lys Lys Lys Leu Leu Lys Met Glu Ile Asp Pro Ser Thr His Gln Pro
          115                 120                 125


Leu Asn Lys Val Phe Thr Asp Thr Asn Leu Val Asp Lys Ser Glu Thr
     130                 135                 140


Ser Ser Lys Ala Asp Asn Val Asn Asp Asn Lys Ile Val Glu Ile Asp
145                 150                 155                 160


Gly Thr Thr Thr Asn Thr Ile Asp Asp Ser Ile Ile Thr His Gln Asn
               165                 170                 175


Ser Ser Asn Asp Asp Tyr Glu Leu Leu Gly Asp Ile Ile His Asn Tyr
          180                 185                 190


Gly Asp Leu Phe Asn Ile Leu Trp Thr Asn Asp Glu Pro Pro Leu Val
          195                 200                 205


Asp Asp Ala Ser Trp Ser Asn His Asn Val Gly Ile Gly Gly Thr Ala
     210                 215                 220


Ala Val Ala Ala Ser Asp Lys Asn Asn Thr Ala Ala Glu Glu Asp Phe
225                 230                 235                 240


Pro Glu Arg Ser Phe Glu Lys Gln Asn Gly Glu Ser Trp Met Phe Leu
               245                 250                 255


Asp Tyr Cys Gln Glu Phe Gly Val Glu Asp Phe Gly Phe Glu Cys Tyr
          260                 265                 270


His Gly Phe Gly Gln Ser Ser Met Lys Thr Gly His Lys Asp
          275                 280                 285
```

<210> 459 <211> 1388 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (280)..(1095) <223> G926

<400> 459
ccaaaatcta gggttttctt ctcgcccaat ttcactttc ttctacgaaa ttctccattc
60

ctgccggctg tcgggttttc tgaatcgatt ctccttcacc aacttcttct ctggttctgt
120

tcgattctga ttttttttca aggtcaattt tttcttctct ttaaactctg caaaatcgtg
180

atcgattaaa ttcacctcag ggttttttga tttctgaaag aagttaatct tcttcgaagg
240

cgattgcaaa agagtgctct gctgtgaatt ccactgag atg caa tca aaa ccg
294
                                            Met Gln Ser Lys Pro
                                            1   5

gga aga gaa aac gaa gag gaa gtc aat aat cac cat gct gtt cag cag
342
Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His His Ala Val Gln Gln
            10   15   20

ccg atg atg tat gca gag ccc tgg tgg aaa aac aac tcc ttt ggt gtt
390
Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn Asn Ser Phe Gly Val
            25   30   35

gta cct caa gcg aga cct tct gga att cca tca aat tcc tct tct ttg
438
Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser Asn Ser Ser Ser Leu
            40   45   50

gat tgc ccc aat ggt tcc gag tca aac gat gtt cat tca gca tct gaa
486
Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val His Ser Ala Ser Glu
            55   60   65

gac ggt gcg ttg aat ggt gaa aac gat ggc act tgg aag gat tca caa
534
Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr Trp Lys Asp Ser Gln
70   75   80   85

gct gca act tcc tct cgt tca gat aat cac gga atg gaa gga aat gac
582
Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly Met Glu Gly Asn Asp
                90   95   100

cca gcg ctc tct atc cgt aac atg cat gat cag cca ctt gta caa cca
630
Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln Pro Leu Val Gln Pro
                105   110   115

cca gag ctt gtt gga cac tat atc gct tgt gtc cca aac cca tat cag
678
Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val Pro Asn Pro Tyr Gln
            120   125   130

gat cca tat tat ggg gga ttg atg gga gca tat ggt cat cag caa ttg
726
Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr Gly His Gln Gln Leu
            135   140   145

ggt ttt cgt cca tat ctt gga atg cct cgt gaa aga aca gct ctg cca
774
Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu Arg Thr Ala Leu Pro
150   155   160   165

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ctt gac atg gca caa gag ccc gtt tat gtg aat gca aag cag tac gag
822
Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn Ala Lys Gln Tyr Glu
                170             175             180


gga att cta agg cga aga aaa gca cgt gcc aag gca gag cta gag agg
870
Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys Ala Glu Leu Glu Arg
                185             190             195


aaa gtc atc cgg gac aga aag cca tat ctt cac gag tca aga cac aag
918
Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His Glu Ser Arg His Lys
            200             205             210


cat gca atg aga agg gca cga gcg agt gga ggc cgg ttt gcg aag aaa
966
His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly Arg Phe Ala Lys Lys
        215             220             225


agt gag gta gaa gcg gga gag gat gca gga ggg aga gac aga gaa agg
1014
Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly Arg Asp Arg Glu Arg
230             235             240             245


ggt tca gca acc aac tca tca ggc tct gaa caa gtt gag aca gac tct
1062
Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln Val Glu Thr Asp Ser
                250             255             260


aat gag acc ctg aat tct tct ggt gca cca taa taaaaaaagc caaagctctg
1115
Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro
                265             270


agaggagaga gagacacaca ctttggctaa tataatccat tgcctcaaac cggcaaatca
1175

ttcttggctt tttcgttttt gtgtttgcta gttgttcttg tcagagtctc atattgtgtg
1235

ggtttaacag ttatgatgaa tgtacaaaga gcgagttatg ttaggtgtta gattttggag
1295

acaagagaca aaggaatagc aagtaggtct tgtttttatt ctttgacctt ttttttctct
1355

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1388



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460


Met Gln Ser Lys Pro Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His
1               5               10              15


His Ala Val Gln Gln Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn
                20              25              30
```

854

Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser
        35   40   45

Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val
        50   55   60

His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr
65   70   75   80

Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly
                85   90   95

Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln
            100   105   110

Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val
        115   120   125

Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr
        130   135   140

Gly His Gln Gln Leu Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu
145   150   155   160

Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn
                165   170   175

Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys
            180   185   190

Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His
        195   200   205

Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly
    210   215   220

Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly
225   230   235   240

Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln
            245   250   255

Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro
            260   265   270

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60

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116
                                                    Met Ala Phe
                                                    1

gat ctc cac cat ggc tca gct tca gat acg cat tca tca gaa ctt ccg
164
Asp Leu His His Gly Ser Ala Ser Asp Thr His Ser Ser Glu Leu Pro
    5   10   15

tcg ttt tct ctc cca cct tat cct cag atg ata atg gaa gcg att gag
212
Ser Phe Ser Leu Pro Pro Tyr Pro Gln Met Ile Met Glu Ala Ile Glu
20   25   30   35

tcc ttg aac gat aag aac ggc tgc aac aaa acg acg att gct aag cac
260
Ser Leu Asn Asp Lys Asn Gly Cys Asn Lys Thr Thr Ile Ala Lys His
                40   45   50

atc gag tcg act caa caa act cta ccg ccg tca cac atg acg ctg ctc
308
Ile Glu Ser Thr Gln Gln Thr Leu Pro Pro Ser His Met Thr Leu Leu
            55   60   65

agc tac cat ctc aac cag atg aag aaa acc ggt cag cta atc atg gtg
356
Ser Tyr His Leu Asn Gln Met Lys Lys Thr Gly Gln Leu Ile Met Val
        70   75   80

aag aac aat tat atg aaa cca gat cca gat gct cct cct aag cgt ggt
404
Lys Asn Asn Tyr Met Lys Pro Asp Pro Asp Ala Pro Pro Lys Arg Gly
    85   90   95

cgt ggc cgt cct ccg aag cag aag act cag gcc gaa tct gac gcc gct
452
Arg Gly Arg Pro Pro Lys Gln Lys Thr Gln Ala Glu Ser Asp Ala Ala
100   105   110   115

gct gct gct gtt gtt gct gcc acc gtc gtc tct aca gat ccg cct aga
500
Ala Ala Ala Val Val Ala Ala Thr Val Val Ser Thr Asp Pro Pro Arg
                120   125   130

tct cgt ggc cgt cca ccg aag ccg aaa gat cca tcg gag cct ccc cag
548
Ser Arg Gly Arg Pro Pro Lys Pro Lys Asp Pro Ser Glu Pro Pro Gln
            135   140   145

gag aag gtc att acc gga tct gga agg cca cga gga cga cca ccg aag
596
Glu Lys Val Ile Thr Gly Ser Gly Arg Pro Arg Gly Arg Pro Pro Lys
            150   155   160

856

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aga ccg aga aca gat tcg gag acg gtt gct gcg ccg gaa ccg gca gct
644
Arg Pro Arg Thr Asp Ser Glu Thr Val Ala Ala Pro Glu Pro Ala Ala
    165                 170                 175

cag gcg aca ggt gag cgt agg gga cgt ggg aga cct ccg aag gtg aag
692
Gln Ala Thr Gly Glu Arg Arg Gly Arg Gly Arg Pro Pro Lys Val Lys
180                 185                 190                 195

ccg acg gtg gtt gct ccg gtt ggg tgc tga attaatcggt acttatgcaa
742
Pro Thr Val Val Ala Pro Val Gly Cys
                200

tttcggaatc tttagttact gaaaaatgga atctcttaga gagtaagaga gtgctttaat
802

ttagcttaat tagatttatt tggatttctt tcagtatttg gattgtaaac tttagaattt
862

gtgtgtgtgt tgttgcttag tcctgagata agatataaca ttagcgactg tgtattatta
922

ttattactgc attgtgttat gtgaaacttt gttctcttgt tgaaaaaaaa aaaaaaaaaa
982

a
983
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<210> 462 <211> 204 <212> PRT <213> Arabidopsis thaliana <400>
462

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1               5                   10                  15

Glu Leu Pro Ser Phe Ser Leu Pro Pro Tyr Pro Gln Met Ile Met Glu
            20                  25                  30

Ala Ile Glu Ser Leu Asn Asp Lys Asn Gly Cys Asn Lys Thr Thr Ile
        35                  40                  45

Ala Lys His Ile Glu Ser Thr Gln Gln Thr Leu Pro Pro Ser His Met
    50                  55                  60

Thr Leu Leu Ser Tyr His Leu Asn Gln Met Lys Lys Thr Gly Gln Leu
65                  70                  75                  80

Ile Met Val Lys Asn Asn Tyr Met Lys Pro Asp Pro Asp Ala Pro Pro
                85                  90                  95

Lys Arg Gly Arg Gly Arg Pro Pro Lys Gln Lys Thr Gln Ala Glu Ser
            100                 105                 110
```

857

Asp Ala Ala Ala Ala Ala Val Val Ala Ala Thr Val Val Ser Thr Asp
        115   120   125

Pro Pro Arg Ser Arg Gly Arg Pro Pro Lys Pro Lys Asp Pro Ser Glu
    130   135   140

Pro Pro Gln Glu Lys Val Ile Thr Gly Ser Gly Arg Pro Arg Gly Arg
145   150   155   160

Pro Pro Lys Arg Pro Arg Thr Asp Ser Glu Thr Val Ala Ala Pro Glu
                165   170   175

Pro Ala Ala Gln Ala Thr Gly Glu Arg Arg Gly Arg Gly Arg Pro Pro
            180   185   190

Lys Val Lys Pro Thr Val Val Ala Pro Val Gly Cys
        195   200

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<221> CDS <222> (1)..(1359) <223> G374

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48
Met Asp Asn Lys Asn Asp Gln Asp Ile Asp Val Arg Ser Val Val Glu
1   5   10   15

gct gtt tcc gcc gat ctt tcc ttt ggt gct ccc ctc tat gtg gtt gag
96
Ala Val Ser Ala Asp Leu Ser Phe Gly Ala Pro Leu Tyr Val Val Glu
            20   25   30

agc atg tgc atg cgc tgc caa gaa aat gga aca acc aga ttt cta ttg
144
Ser Met Cys Met Arg Cys Gln Glu Asn Gly Thr Thr Arg Phe Leu Leu
        35   40   45

acc tta att cct cac ttc aga aag gtc tta ata tct gca ttt gaa tgt
192
Thr Leu Ile Pro His Phe Arg Lys Val Leu Ile Ser Ala Phe Glu Cys
    50   55   60

ccg cat tgc ggg gaa agg aat aat gaa gtt cag ttc gca ggc gag att
240
Pro His Cys Gly Glu Arg Asn Asn Glu Val Gln Phe Ala Gly Glu Ile
65   70   75   80

caa ccc cgt gga tgc tgt tac aat cta gag gtt cta gct ggt gat gtg
288
Gln Pro Arg Gly Cys Cys Tyr Asn Leu Glu Val Leu Ala Gly Asp Val
                85   90   95

858

aag ata ttt gac cgg caa gtt gtg aaa tct gaa tca gcc act att aag
336
Lys Ile Phe Asp Arg Gln Val Val Lys Ser Glu Ser Ala Thr Ile Lys
            100   105   110

att cct gaa ctg gat ttt gag att cca cca gag gcc caa cgt gga agt
384
Ile Pro Glu Leu Asp Phe Glu Ile Pro Pro Glu Ala Gln Arg Gly Ser
        115   120   125

ttg tct act gtg gaa ggg ata tta gca cgg gct gct gat gaa ctg agt
432
Leu Ser Thr Val Glu Gly Ile Leu Ala Arg Ala Ala Asp Glu Leu Ser
    130   135   140

gcc ctt caa gaa gaa cgc aag aaa gtt gat cct aaa act gct gaa gca
480
Ala Leu Gln Glu Glu Arg Lys Lys Val Asp Pro Lys Thr Ala Glu Ala
145   150   155   160

ata gac caa ttc ttg tcc aaa ctg aga gct tgt gct aaa gca gag aca
528
Ile Asp Gln Phe Leu Ser Lys Leu Arg Ala Cys Ala Lys Ala Glu Thr
                165   170   175

tcc ttc acc ttc att ttg gat gat cct gct gga aac agt ttc att gag
576
Ser Phe Thr Phe Ile Leu Asp Asp Pro Ala Gly Asn Ser Phe Ile Glu
            180   185   190

aac cca cat gct cca tca cca gat ccc tct cta acc atc aaa ttc tat
624
Asn Pro His Ala Pro Ser Pro Asp Pro Ser Leu Thr Ile Lys Phe Tyr
        195   200   205

gag cga aca cca gag caa caa gca aca ctt gga tat gtt gct aac cca
672
Glu Arg Thr Pro Glu Gln Gln Ala Thr Leu Gly Tyr Val Ala Asn Pro
    210   215   220

tct cag gct gga caa tca gaa gga agc ctt ggc gca cct gtg atg act
720
Ser Gln Ala Gly Gln Ser Glu Gly Ser Leu Gly Ala Pro Val Met Thr
225   230   235   240

ttc cct tca act tgc gga gca tgt acg gag ccg tgt gag aca cgg atg
768
Phe Pro Ser Thr Cys Gly Ala Cys Thr Glu Pro Cys Glu Thr Arg Met
                245   250   255

ttc aaa ata gaa atc ccg tac ttt cag gaa gtt att gtc atg gca tct
816
Phe Lys Ile Glu Ile Pro Tyr Phe Gln Glu Val Ile Val Met Ala Ser
            260   265   270

aca tgt gac agt tgt ggc tat cgt aat tct gag ttg aag cct ggt ggt
864
Thr Cys Asp Ser Cys Gly Tyr Arg Asn Ser Glu Leu Lys Pro Gly Gly
        275   280   285

859

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gca att cct gaa aag gga aag aag att act ctc tct gtg agg aac att
912
Ala Ile Pro Glu Lys Gly Lys Lys Ile Thr Leu Ser Val Arg Asn Ile
    290             295             300

aca gac ctt agc cga gat gtt atc aag tcg gac act gca gga gtg ata
960
Thr Asp Leu Ser Arg Asp Val Ile Lys Ser Asp Thr Ala Gly Val Ile
305             310             315             320

atc cca gaa ctt gat ctg gag cta gct ggt ggt aca ctt ggt gga atg
1008
Ile Pro Glu Leu Asp Leu Glu Leu Ala Gly Gly Thr Leu Gly Gly Met
            325             330             335

gta aca aca gtt gaa ggg ttg gtt aca cag atc aga gaa agc cta gcg
1056
Val Thr Thr Val Glu Gly Leu Val Thr Gln Ile Arg Glu Ser Leu Ala
        340             345             350

aga gtt cac gga ttc act ttt ggt gat agt atg gaa gag agt aag ttg
1104
Arg Val His Gly Phe Thr Phe Gly Asp Ser Met Glu Glu Ser Lys Leu
        355             360             365

aac aaa tgg aga gaa ttt gga gcc agg ctc act aag ctc cta agc ttt
1152
Asn Lys Trp Arg Glu Phe Gly Ala Arg Leu Thr Lys Leu Leu Ser Phe
    370             375             380

gaa cag ccg tgg aca ttg att ctt gat gat gaa tta gca aat tcc ttt
1200
Glu Gln Pro Trp Thr Leu Ile Leu Asp Asp Glu Leu Ala Asn Ser Phe
385             390             395             400

att gca cca gta aca gat gat atc aaa gat gac cat cag ctc aca ttt
1248
Ile Ala Pro Val Thr Asp Asp Ile Lys Asp Asp His Gln Leu Thr Phe
            405             410             415

gaa gag tac gag agg tca tgg gat caa aac gag gag ttg ggt ctc aac
1296
Glu Glu Tyr Glu Arg Ser Trp Asp Gln Asn Glu Glu Leu Gly Leu Asn
            420             425             430

gac ata gat act tct tca gct gat gct gct tat gaa tcc aca gag acg
1344
Asp Ile Asp Thr Ser Ser Ala Asp Ala Ala Tyr Glu Ser Thr Glu Thr
            435             440             445

act aaa tta cct taa
1359
Thr Lys Leu Pro
    450


<210> 464 <211> 452 <212> PRT <213> Arabidopsis thaliana <400>
464

Met Asp Asn Lys Asn Asp Gln Asp Ile Asp Val Arg Ser Val Val Glu
1           5               10              15
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Ala Val Ser Ala Asp Leu Ser Phe Gly Ala Pro Leu Tyr Val Val Glu
            20   25   30

Ser Met Cys Met Arg Cys Gln Glu Asn Gly Thr Thr Arg Phe Leu Leu
            35   40   45

Thr Leu Ile Pro His Phe Arg Lys Val Leu Ile Ser Ala Phe Glu Cys
        50   55   60

Pro His Cys Gly Glu Arg Asn Asn Glu Val Gln Phe Ala Gly Glu Ile
65   70   75   80

Gln Pro Arg Gly Cys Cys Tyr Asn Leu Glu Val Leu Ala Gly Asp Val
            85   90   95

Lys Ile Phe Asp Arg Gln Val Val Lys Ser Glu Ser Ala Thr Ile Lys
            100   105   110

Ile Pro Glu Leu Asp Phe Glu Ile Pro Pro Glu Ala Gln Arg Gly Ser
            115   120   125

Leu Ser Thr Val Glu Gly Ile Leu Ala Arg Ala Ala Asp Glu Leu Ser
    130   135   140

Ala Leu Gln Glu Glu Arg Lys Lys Val Asp Pro Lys Thr Ala Glu Ala
145   150   155   160

Ile Asp Gln Phe Leu Ser Lys Leu Arg Ala Cys Ala Lys Ala Glu Thr
            165   170   175

Ser Phe Thr Phe Ile Leu Asp Asp Pro Ala Gly Asn Ser Phe Ile Glu
            180   185   190

Asn Pro His Ala Pro Ser Pro Asp Pro Ser Leu Thr Ile Lys Phe Tyr
    195   200   205

Glu Arg Thr Pro Glu Gln Gln Ala Thr Leu Gly Tyr Val Ala Asn Pro
    210   215   220

Ser Gln Ala Gly Gln Ser Glu Gly Ser Leu Gly Ala Pro Val Met Thr
225   230   235   240

Phe Pro Ser Thr Cys Gly Ala Cys Thr Glu Pro Cys Glu Thr Arg Met
            245   250   255

861

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Phe Lys Ile Glu Ile Pro Tyr Phe Gln Glu Val Ile Val Met Ala Ser
        260                 265                 270

Thr Cys Asp Ser Cys Gly Tyr Arg Asn Ser Glu Leu Lys Pro Gly Gly
        275                 280                 285

Ala Ile Pro Glu Lys Gly Lys Lys Ile Thr Leu Ser Val Arg Asn Ile
    290                 295                 300

Thr Asp Leu Ser Arg Asp Val Ile Lys Ser Asp Thr Ala Gly Val Ile
305                 310                 315                 320

Ile Pro Glu Leu Asp Leu Glu Leu Ala Gly Gly Thr Leu Gly Gly Met
                325                 330                 335

Val Thr Thr Val Glu Gly Leu Val Thr Gln Ile Arg Glu Ser Leu Ala
            340                 345                 350

Arg Val His Gly Phe Thr Phe Gly Asp Ser Met Glu Glu Ser Lys Leu
        355                 360                 365

Asn Lys Trp Arg Glu Phe Gly Ala Arg Leu Thr Lys Leu Leu Ser Phe
    370                 375                 380

Glu Gln Pro Trp Thr Leu Ile Leu Asp Asp Glu Leu Ala Asn Ser Phe
385                 390                 395                 400

Ile Ala Pro Val Thr Asp Asp Ile Lys Asp Asp His Gln Leu Thr Phe
                405                 410                 415

Glu Glu Tyr Glu Arg Ser Trp Asp Gln Asn Glu Glu Leu Gly Leu Asn
            420                 425                 430

Asp Ile Asp Thr Ser Ser Ala Asp Ala Ala Tyr Glu Ser Thr Glu Thr
        435                 440                 445

Thr Lys Leu Pro
    450
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/26189

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7)   :   A01H 5/00; C12P 21/00; C12N 15/82
US CL   :   435/69.1; 800/279, 281, 289, 290, 300, 301

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
    U.S. : 435/69.1; 800/279, 281, 289, 290, 300, 301

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EAST, and SEQUENCE search of SEQ ID NOs: 1, 2, 3 and 4

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KRANZ, H.D. et al. Towards functional characterisation of the members of the R2R3-MYB gene family from Arabidopsis thaliana. The Plant Journal. 1998, Vol 16, No. 2, pages 263-276, see entire document.	1-5,7-22
X --- Y	ALLEN, M.D. et al. A novel mode of DNA recognition by a beta-sheet revealed by the solution structure of the GCC-box binding domain in complex with DNA. The EMBO Journal. 1998, Vol. 17, No. 18, pages 5484-5496, in particular page 5493, left column, section under Materials and Methods.	4,5 ---------- 1-3,7-22
X --- Y	SMALLE, J. et al. The trihelix DNA-binding motif in higher plants is not restricted to the transcription factors GT-1 and GT-2. Proc. Natl. Acad. Sci. USA. 1998, Vol. 95, pages 3318-3322, see entire document, in particular Fig. 1A on page 3319.	4,5 ---------- 1-3,7-22
X,P --- Y,P	Database NCBI on WEST, AN BE522812. WHITE, J.A. et al. 'A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oi'l. Plant Physiol. 124,(4), 1582-1594. NCBI-Genbank (National Library of Medicine, Bethesda, MD), submitted 19 March 2001.	4 ---------- 1-3,5,7-22

☒ Further documents are listed in the continuation of Box C.   ☐   See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance		
"E"	earlier application or patent published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
27 November 2001 (27.11.2001)	16 JAN 2002

Name and mailing address of the ISA/US
    Commissioner of Patents and Trademarks
    Box PCT
    Washington, D.C. 20231
Facsimile No. (703)305-3230
	Authorized officer
	David H Kruse
	
	Telephone No. 703-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	OHME-TAKAGI, M. et al. Ethylene-inducible DNA binding proteins that interact with an ethylene-responsive element. The Plant Cell. February 1995, Vol. 7, pages 173-182, see entire document.	4,5 ----------- . 1-3,7-22
A	ELOMAA, P. et al. Transformation of antisense constructs of the chalcone synthase gene superfamily into Gerbera hybrida: differential effect on the expression of family members. Molecular Breeding 1996, Vol. 2, pages 41-50, see entire document.	1-5,7-22
A	QUATTROCCHIO, F. et al. Analysis of bHLH and MYB domain proteins: species-specific regulatory differences are caused by divergent evolution of target anthocyanin genes. The Plant Journal. 1998, Vol. 13, No. 4, pages 475-488, see entire document.	1-5,7-22

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/26189

Box I   Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐   Claim Nos.:
   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒   Claim Nos.: 52-70
   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
   Please See Continuation Sheet

3. ☐   Claim Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II   Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐   As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐   As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☒   As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: Please See Continuation Sheet

4. ☐   No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest   ☒   The additional search fees were accompanied by the applicant's protest.
☐   No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

Continuation of Box I Reason 2:
Claims 52-60 constitute unsearchable subject matter under PCT Rule 39.1(iii) as a process of thought or a business method and claims 61-70 constitute unsearchable subject matter under PCT Rule 39.1(v) a mere presentation of information.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING
Groups 1-232, claim(s) 1-5, 7-22 and 44-47 (Group 1 is claims 1-5, 7-22 and 44-47 and SEQ ID NOS: 1 & 2, Group 2 is claims 1-5, 7-22 and 44-47 and SEQ ID NOS: 3 & 4, etc), drawn to an isolated or recombinant polynucleotide, transgenic plants comprising said polynucleotide and a method of making said transgenic plant.

Groups 233-465, claim(s) 6 and 34-43 (Group 233 is claims 6 and 34-43 and SEQ ID NOS: 1 & 2, Group 234 is claims 6 and 34-43 and SEQ ID NOS: 3 & 4, etc), drawn to an isolated or recombinant polypeptide.

Groups 466-698, claim(s) 23-33 (Group 466 is claims 23-33 and SEQ ID NOS: 1 & 2, Group 467 is claims 23-33 and SEQ ID NOS: 3 & 4, etc), drawn to a method comprising expressing an antisense nucleic acid in a transformed plant and the plant produced by said method.

Groups 699-931, claim(s) 48-51 (Group 699 is claims 48-51 and SEQ ID NOS: 1 & 2, Group 700 is claims 48-51 and SEQ ID NOS: 3 & 4, etc), drawn to a computer readable medium.

The inventions listed as Groups 1-931 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The isolated polynucleotide is anticipated by the prior art because Applicant's SEQ ID NO: 66 is 99% identical to the MYB12 disclosed by Kranz *et al* (1998, The Plant Journal, 16(2):263-278). Because Applicant has claimed an isolated polynucleotide encoding a polypeptide having at least anywhere from 31-95% sequence identity outside of a conserved domain of the polypeptide of SEQ ID NO: 66 and an isolated polypeptide having at least 31-95% sequence identity over the entire length of the polypeptide of SEQ ID NO: 66, the claimed invention has been anticipated by the prior art and thus Unity of Invention is lacking as required under PCT Rule 13.1 and it lacks a special technical feature as required under PCT Rule 13.2.

2. Claims 52-60 constitute unsearchable subject matter under PCT Rule 39.1(iii) as a process of thought or a business method and Claims 61-70 constitute unsearchable subject matter under PCT Rule 39.1(v) as mere presentation of information.

Continuation of Box II Item 3:
1-5,7-22,44-45 and SEQ ID NOs. 1,2,3,4
Claims 46 and 47 were not searched because no additional fees were paid for the inventions to which the claims are directed.